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November 22, 2004

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APPLICATION NUMBER: 60/458,026
FILING DATE: *March 28, 2003*
RELATED PCT APPLICATION NUMBER: *PCT/US04/09510*

Certified by



Jon W Dudas

Acting Under Secretary of Commerce
for Intellectual Property
and Acting Director of the U.S.
Patent and Trademark Office

60458026 032803

Provisional Application For Patent Cover Sheet

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 C.F.R. § 1.53(c).

Express Mail Label No.

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JCE57 U.S. PTO
60/458026

03/28/03

☐ Additional inventors are being named on the _____ separately numbered sheets attached hereto.

TITLE OF THE INVENTION (500 Characters Maximum)

CORRESPONDENCE ADDRESS

Direct all correspondence to:

Place Customer Number



26111

PATENT TRADEMARK OFFICE

☒ Customer number 26111
Type Customer Number here



Bar Code Label here

OR

☐ Firm or Individual Name

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ENCLOSED APPLICATION PARTS (check all that apply)

☒ Specification Number of pages _____

☐ CD(s), Number _____

☒ Drawing(s) Number of sheets: _____

☒ Other (specify) Authorization To Treat A Reply As Incorporating An Extension Of Time Under 37 C.F.R. § 1.136(a)(3)

☒ Application Data Sheet. See 37 CFR 1.76

METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT (check one)

☐ Applicant claims small entity status. See 37 CFR 1.27.

☐ A check or money order is enclosed to cover the filing fees

Filing Fee
Amount (\$)

☒ The Commissioner is hereby authorized to charge filing fees or credit any overpayments to Deposit Account Number: 19-0036.

\$160.00

☒ Payment by credit card. Form PTO-2038 is attached.

The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☐ No

☒ Yes, the name of the U.S. Government agency and the Government contract number are:

Respectfully submitted,

Signature: Helene C. Carlson

Date: 3/28/03

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Telephone: 202-371-2600

Docket Number: 2060.0260000/EKS/HCC

USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT



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71129 U.S. PTO
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March 28, 2003

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71129 U.S. PTO
60/458026
03/28/03

Commissioner for Patents
Washington, D.C. 20231

Box Provisional Application

Re: U.S. Provisional Patent Application
Appl. No. To be assigned; Filed: March 28, 2003
For: **Methods Of Identifying Optimal Variants Of Peptide Epitopes**
Inventors: BAKER *et al.*
Our Ref: 2060.0260000/EKS/HCC

Sir:

The following documents are being submitted under 37 C.F.R. § 1.53(c) herewith for appropriate action by the U.S. Patent and Trademark Office:

1. PTO Fee Transmittal (Form PTO/SB/17);
2. U.S. Provisional Patent Application entitled:

Methods Of Identifying Optimal Variants Of Peptide Epitopes

and naming as inventors:

Denise Marie BAKER
Brian D. LIVINGSTON
Robert W. CHESNUT
Alessandro SETTE
Mark J. NEWMAN

the application consisting of:

- a. A Provisional Application for Patent Cover Sheet;

Page 2

- b. an Application Data Sheet (37 C.F.R. § 1.76);
 - c. A specification containing **457** total pages:
 - (i) **452** pages of description prior to any claims;
 - (ii) **4** pages of claims (**30** claims); and
 - (iii) a one page abstract;
 - d. **5** sheets of drawings: (Figures **1A-4**); and
3. Authorization to Treat a Reply As Incorporating An Extension of Time Under 37 C.F.R. § 1.136(a)(3);
4. Form PTO-2038 Credit Card Payment Form in the amount of \$160.00 to cover the filing fee; and
5. Two (2) return postcards.

The U.S. Patent and Trademark Office is hereby authorized to charge any fee deficiency, or credit any overpayment, to our Deposit Account No. 19-0036.

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

Helene C. Carlson
Agent for Applicants
Registration No. 47,473

SKGF DC1:117771.1

60455026-032803

PTO/SB/17 (10-02)
Approved for use through 10/31/2002. OMB 0651-0032
Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE
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FEE TRANSMITTAL **for FY 2003**

Patent fees are subject to annual revision.

☐ Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT (\$160.00)

Complete if Known

Application Number	To be assigned
Filing Date	March 28, 2003
First Named Inventor	Denise Marie BAKER
Examiner Name	To be assigned
Group Art Unit	To be assigned
Attorney Docket No.	2060.0260000/EKS/HCC

METHOD OF PAYMENT (check all that apply)

☐ Check ☒ Credit card ☐ Money Order ☒ Other** ☐ None
** Charge any deficiencies or credit any overpayments in the fees or fee calculations of Parts 1, 2 and 3 below to Deposit Account No. 19-0036.

☐ Deposit Account
Deposit Account Number 19-0036
Deposit Account Name: Sterne, Kessler, Goldstein & Fox P.L.L.C.

The Commissioner is authorized to: (check all that apply)

☐ Charge fee(s) indicated below ☐ Credit any over payments
☐ Charge any additional fee(s) during the pendency of this application
☐ Charge fee(s) indicated below, except for the filing fee to the above-identified deposit account.

FEE CALCULATION

1. BASIC FILING FEE

Large Entity Small Entity

Fee Code	Fee (\$)	Fee Code	Fee (\$)	Fee Description	Fee Paid
1001	750	2001	375	Utility filing fee	
1002	330	2002	165	Design filing fee	
1003	520	2003	260	Plant filing fee	
1004	750	2004	375	Reissue filing fee	
1105	160	2005	80	Provisional filing fee	\$160.00

SUBTOTAL (1) (\$160.00)

2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE

	Extra	Fee from below	Fee Paid
Total Claims	- 20** =	X	=
Indep. Claims	- 3** =	X	=
Multiple Dependent			=

Large Entity Small Entity

Fee Code	Fee (\$)	Fee Code	Fee (\$)	Fee Description
1202	18	2202	9	Claims in excess of 20
1201	84	2201	42	Independent claims in excess of 3
1203	280	2203	140	Multiple dependent claim, if not paid
1204	84	2204	42	**Reissue independent claims over original patent
1205	18	2205	9	**Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) (\$0)

**or number previously paid, if greater; For Reissue, see above

FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Small Entity


Fee Code	Fee (\$)	Fee Code	Fee (\$)	Fee Description	Fee Paid
1051	130	2051	65	Surcharge - late filing fee or oath	
1502	50	2052	25	Surcharge-late provisional filing fee or cover sheet	
1053	130	1053	130	Non-English specification	
1812	2,520	1812	2,520	For filing a request for <i>ex parte</i> reexamination	
1804	920*	1804	920*	Requesting publication of SIR prior to Examiner action	
1805	1,840*	1805	1,840*	Requesting publication of SIR after Examiner action	
1251	110	2251	55	Extension for reply within first month	
1252	410	2252	205	Extension for reply within second month	
1253	930	2253	465	Extension for reply within third month	
1254	1,450	2254	725	Extension for reply within fourth month	
1255	1,970	2255	985	Extension for reply within fifth month	
1401	320	2401	160	Notice of Appeal	
1402	320	2402	160	Filing a brief in support of an appeal	
1403	280	2403	140	Request for oral hearing	
1451	1,510	1451	1,510	Petition to institute a public use proceeding	
1452	110	2452	55	Petition to revive - unavoidable	
1453	1,300	2453	650	Petition to revive - unintentional	
1501	1,300	2501	650	Utility issue fee (or reissue)	
1502	470	2502	235	Design issue fee	
1503	630	2503	315	Plant issue fee	
1460	130	1460	130	Petitions to the Commissioner	
1807	50	1807	50	Processing fee under 37 CFR 1.17(q)	
1806	180	1806	180	Submission of Information Disclosure Stmt	
8021	40	8021	40	Recording each patent assignment per property (times number of properties)	
1809	750	2809	375	Filing a submission after final rejection (37 CFR 1.128(a))	
1810	750	2810	375	For each additional invention to be examined (37 CFR 1.129(b))	
1801	750	2801	375	Request for Continued Examination (RCE)	
1802	900	1802	900	Request for expedited examination of a design application	

Other fee (specify) _____

* Reduced by Basic Filing Fee Paid

SUBTOTAL (3) (\$0)

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Name (Print/Type)	Helene C. Carlson	Registration No. (Attorney/Agent)	47,473	Telephone	202-371-2600
Signature				Date	March 28, 2003

Complete (if applicable)

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

This collection of information is required by 37 CFR 1.17 and 1.27. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 12 minutes to complete, including gathering, preparing, and submitting the completed form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Commissioner for Patents, Washington, DC 20231.

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60458026 .032803

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APPLICATION INFORMATION

60156026-432943

Title Line One:: Methods Of Indentifying Optimal Variants
Title Line Two:: Of Peptide Epitopes
Formal Drawings?:: No
Application Type:: Provisional
Docket Number:: 2060.0260000
Secrecy Order in Parent Appl.?:: No

REPRESENTATIVE INFORMATION

Representative Customer Number:: 26111

Source:: PrintEFS Version 1.0.1



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

BAKER *et al.*

Appl. No. To be assigned

Filed: March 28, 2003

For: **Methods Of Identifying Optimal
Variants Of Peptide Epitopes**

Art Unit: To be assigned

Examiner: To be assigned

Atty. Docket: 2060.0260000/EKS/HCC

**Authorization To Treat A Reply As Incorporating An Extension Of
Time Under 37 C.F.R. § 1.136(a)(3)**

Commissioner for Patents
Washington, D.C. 20231

Sir:

The U.S. Patent and Trademark Office is hereby authorized to treat any concurrent or future reply that requires a petition for an extension of time under this paragraph for its timely submission, as incorporating a petition for extension of time for the appropriate length of time. The U.S. Patent and Trademark Office is hereby authorized to charge all required extension of time fees to our Deposit Account No. 19-0036, if such fees are not otherwise provided for in such reply.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

A handwritten signature in cursive script, appearing to read "Helene C. Carlson".

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Attorney Docket No: 2060.026000
EPI 0141.20 US

METHODS OF IDENTIFYING OPTIMAL VARIANTS OF PEPTIDE EPITOPES

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Assignee: Epimmune Inc.

CROSS-REFERENCE TO RELATED APPLICATIONS

Not applicable.

STATEMENT REGARDING FEDERALLY-SPONSORED RESEARCH AND DEVELOPMENT

[0001] This invention was funded, in part, by the United States government under grants with the National Institutes of Health. The U.S. government has certain rights in this invention.

REFERENCE TO MICROFICHE APPENDIX/SEQUENCE LISTING/TABLE/COMPUTER
PROGRAM LISTING APPENDIX (submitted on a compact disc and an incorporation-by-
reference of the material on the compact disc)

[0002] Not applicable.

BACKGROUND OF THE INVENTION

Field of the Invention

[0003] This invention relates to the field of biology. In a particular embodiment, it relates to peptides, polynucleotides, and compositions useful to monitor or elicit an immune response to selected antigens, and methods of identifying such peptides and polynucleotides.

Related Art

[0004] HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens, epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.

[0005] **Human Immunodeficiency Virus.** Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

[0006] The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global

epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV infection.

[0007] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections in vivo (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0008] While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, *Nature* 370:463, 1994; Walker *et al.*, *Proc. Natl. Acad. Sci.* 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g.*, Tsubota *et al.*, *J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*, *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g.*, Borrow *et al.*, *Nature Med.* 3:205-211, 1997; Price *et al.*, *Proc. Nat. Acad. Sci.* 94:12890-12895, 1997; Koenig *et al.*, *Nature Med.* 1:330-336, 1995; and Haas *et al.*, *J. Immunol.* 157:4212-4221, 1996).

[0009] Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g.*, Rosenberg *et al.*, *Science* 278:1447, 1997).

[0010] A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like some other infectious agents including retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape

anti-viral therapy and immune recognition (Borrow et al., *Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g., Lukashov et al., AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of sufficient breadth and vigor to prevent and/or clear HIV infection.

- [0011] **Hepatitis B Virus.** Chronic infection by hepatitis B virus (HBV) affects at least 5% of the world's population and is a major cause of cirrhosis and hepatocellular carcinoma (Hoofnagle, J., *N. Engl. J. Med.* 323:337, 1990; Fields, B. and Knipe, D., In: *Fields Virology* 2:2137, 1990). The World Health Organization lists hepatitis B as a leading cause of death worldwide, close behind chronic pulmonary disease, and more prevalent than AIDS. Chronic HBV infection can range from an asymptomatic carrier state to continuous hepatocellular necrosis and inflammation, and can lead to hepatocellular carcinoma.
- [0012] The immune response to HBV is believed to play an important role in controlling hepatitis B infection. A variety of humoral and cellular responses to different regions of the HBV nucleocapsid core and surface antigens have been identified. T cell mediated immunity, particularly involving class I human leukocyte antigen-restricted cytotoxic T lymphocytes (CTL), is believed to be crucial in combatting established HBV infection.
- [0013] Several studies have emphasized the association between self-limiting acute hepatitis and multispecific CTL responses (Penna, A. et al., *J. Exp. Med.* 174:1565, 1991; Nayarsina, R. et al., *J. Immunol.* 150:4659, 1993). Spontaneous and interferon-related clearance of chronic HBV infection is also associated with the resurgence of a vigorous CTL response (Guidotti, L. G. et al., *Proc. Natl. Acad. Sci. USA* 91:3764, 1994). In all such cases the CTL responses are polyclonal, and specific for multiple viral proteins including the HBV envelope, core and polymerase antigens. By contrast, in patients with chronic hepatitis, the CTL activity is usually absent or weak, and antigenically restricted.
- [0014] The crucial role of CTL in resolution of HBV infection has been further underscored by studies using HBV transgenic mice. Adoptive transfer of HBV-specific CTL into mice transgenic for the HBV genome resulted in suppression of virus

replication. This effect was primarily mediated by a non-lytic, lymphokine-based mechanism (Guidotti, L. G. et al., *Proc. Natl. Acad. Sci. USA* 91:3764, 1994; Guidotti, L. G., Guilhot, S., and Chisari, F. V. *J. Virol.* 68:1265, 1994; Guidotti, L. G. et al., *J. Virol.* 69:6158, 1995; Gilles, P. N., Fey, G., and Chisari, F. V., *J. Virol.* 66:3955, 1992).

[0015] As is the case for HLA class I restricted responses, HLA class II restricted T cell responses are usually detected in patients with acute hepatitis, and are absent or weak in patients with chronic infection (Chisari, F. V. and Ferrari, C., *Annu. Rev. Immunol.* 13:29, 1995). HLA Class II responses are tied to activation of helper T cells (HTLs) Helper T lymphocytes, which recognize Class II HLA molecules, may directly contribute to the clearance of HBV infection through the secretion of cytokines which suppress viral replication (Franco, A. et al., *J. Immunol.* 159:2001, 1997). However, their primary role in disease resolution is believed to be mediated by inducing activation and expansion of virus-specific CTL and B cells.

[0016] In view of the heterogeneous immune response observed with HBV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple epitopes appears to be important for the development of an efficacious vaccine against HBV. There is a need to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear HBV infection. Epitope-based vaccines appear useful.

[0017] **Hepatitis C Virus.** Hepatitis C virus (HCV) infection is a global human health problem with approximately 150,000 new reported cases each year in the U.S. alone. HCV is a single stranded RNA virus, and is the etiological agent identified in most cases of non-A, non-B post-transfusion and post-transplant hepatitis, and is a common cause of acute sporadic hepatitis (Choo et al., *Science* 244:359, 1989; Kuo et al., *Science* 244:362, 1989; and Alter et al., in: *Current Perspective in Hepatology*, p. 83, 1989). It is estimated that more than 50% of patients infected with HCV become chronically infected and, of those, 20% develop cirrhosis of the liver within 20 years (Davis et al., *New Engl. J. Med.* 321:1501, 1989; Alter et al., in: *Current Perspective in Hepatology*, p. 83, 1989; Alter et al., *New Engl. J. Med.* 327:1899, 1992; and Dienstag, J. L. *Gastroenterology* 85:430, 1983). Moreover, the only therapy available for treatment of HCV infection is interferon- α . Most patients are unresponsive, however, and among the responders, there is a high recurrence rate within 6-12 months of cessation of treatment (Liang et al., *J. Med. Virol.*

40:69, 1993). Ribavirin, a guanosine analog with a broad spectrum activity against many RNA and DNA viruses, has been shown in clinical trials to be effective against chronic HCV infection when used in combination with interferon- α (see, e.g., Poynard *et al.*, *Lancet* 352:1426-1432, 1998; Reichard *et al.*, *Lancet* 351:83-87, 1998). However, the response rate is still well below 50%.

[0018] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).

[0019] In view of the heterogeneous immune response observed with HCV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HCV epitopes appears to be important for the development of an efficacious vaccine against HCV. There is a need, however, to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear HCV infection.

[0020] **Human Papillomavirus.** Human papillomavirus (HPV) is a member of the papillomaviridae, a group of small DNA viruses that infect a variety of higher vertebrates. More than 80 types of HPVs have been identified. Of these, more than 30 can infect the genital tract. Some types, generally types 6 and 11, may cause genital warts, which are typically benign and rarely develop into cancer. Other strains of HPV, "cancer-associated", or "high-risk" types, can more frequently lead to the development of cancer. The primary mode of transmission of these strains of HPV is through sexual contact.

[0021] The main manifestations of the genital warts are cauliflower-like condylomata acuminata that usually involve moist surfaces; keratotic and smooth papular warts, usually on dry surfaces; and subclinical "flat" warts, which are found on any mucosal or cutaneous surface (Handsfield, H., *Am. J. Med.* 102(5A):16-20, 1997). These warts are typically benign but are a source of inter-individual spread of the virus (Ponten, J. & Guo, Z., *Cancer Surv.* 32:201-29, 1998). At least three HPV strains associated with genital warts

have been identified: type 6a (see, *e.g.*, Hofmann, K.J., *et al.*, *Virology* 209(2):506-518, 1995), type 6b (see, *e.g.*, Hofmann *et al.*, *supra*) and type 11 (see, *e.g.*, Dartmann, K. *et al.*, *Virology* 151(1):124-130, 1986).

[0022] Cancer-associated HPVs have been linked with cancer in both men and women; they include, but are not limited to, HPV-16, HPV-18, HPV-31, HPV-45, HPV-33 and HPV-56. Other HPV strains, including types 6 and 11 as well as others, *e.g.*, HPV-5 and HPV-8, are less frequently associated with cancer. The high risk types are typically associated with the development of cervical carcinoma and premalignant lesions of the cervix in women, but are also associated with similar malignant and premalignant lesions at other anatomic sites within the lower genital or anogenital tract. These lesions include neoplasia of the vagina, vulva, perineum, the penis, and the anus. HPV infection has also been associated with respiratory tract papillomas, and rarely, cancer, as well as abnormal growth or neoplasia in other epithelial tissues. See, *e.g.* VIROLOGY, 2ND ED, Fields *et al.*, Eds. Raven Press, New York, 1990, Chapters 58 and 59, for a review of HPV association with cancer.

[0023] The HPV genome consists of three functional regions, the early region, the late region, and the "long control region". The early region gene products control viral replication, transcription and cellular transformation. They include the HPV E1 and E2 proteins, which play a role in HPV DNA replication, and the E6 and E7 oncoproteins, which are involved in the control of cellular proliferation. The late region include the genes that encode the structural proteins L1 and L2, which are the major and minor capsid proteins, respectively. The "long control region" contains such sequences as enhancer and promoter regulatory regions.

[0024] HPV expresses different proteins at different stages of the infection, for example early, as well as late, proteins. Even in latent infections, however, early proteins are often expressed and are therefore useful targets for vaccine-based therapies. For example, high-grade dysplasia and cervical squamous cell carcinoma continue to express E6 and E7, which therefore can be targeted to treat disease at both early and late stages of infection.

[0025] Treatment for HPV infection is often unsatisfactory because of persistence of virus after treatment and recurrence of clinically apparent disease is common. The treatment may require frequent visits to clinics and is not directed at elimination of the virus but at clearing warts. Because of persistence of virus after treatment, recurrence of clinically apparent disease is common.

- [0026] Thus, a need exists for an efficacious vaccine to both prevent and treat HPV infection and to treat cancer that is associated with HPV infection. Effective HPV vaccines would be a significant advance in the control of sexually transmissible infections and could also protect against clinical disease, particularly cancers such as cervical cancer. (see, e.g., Rowen, P. & Lacey, C., *Dermatologic Clinics* 16(4):835-838, 1998).
- [0027] Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982).
- [0028] Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al.*, *New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL plays a role in viremia (see, e.g., Rosenberg *et al.*, *Science* 278:1447, 1997).
- [0029] The development of vaccines with prophylactic and therapeutic efficacy against HPV is ongoing. Early vaccine development was hampered by the inability to culture HPV. With the introduction of cloning techniques and protein expression, however, some attempts have been made to stimulate humoral and CTL response to HPV (See, e.g., Rowen, P. & Lacey, C., *Dermatologic Clinics* 16(4):835-838 (1998)). Studies to date, however, have been inconclusive.
- [0030] Activation of T helper cells and cytotoxic lymphocytes (CTLs) in the development of vaccines has also been analyzed. Lehtinen, M., *et al.* for instance, has shown that some peptides from the E2 protein of HPV type 16 activate T helper cells and CTLs (*Biochem. Biophys. Res. Commun.* 209(2):541-6 (1995)). Similarly, Tarpey *et al.*, has shown that some peptides from HPV type 11 E7 protein can stimulate human HPV-specific CTLs *in*

vitro (*Immunology* 81:222-227 (1994)) and Borysiewicz *et al.* have reported a recombinant vaccinia virus expressing HPV 16 and HPV 17 E6 and E7 that stimulated CTL responses in at least one patient (*Lancet* 347:1347-1357, 1996).

- [0031] ***Plasmodium falciparum* and Malaria.** Malaria, which is caused by infection with the parasite *Plasmodium falciparum* (PF), represents a major world health problem. Approximately 500 million people in the world are at risk from the disease, with approximately 200 million people actually harboring the parasites. An estimated 1 to 2 million deaths occur each year due to malaria. (Miller *et al.*, *Science* 234:1349, 1986).
- [0032] Fatal outcomes are not confined to first infections, and constant exposure is apparently a prerequisite for maintaining immunity. Naturally acquired sterile immunity is rare, if it exists at all. Accordingly, major efforts to develop an efficacious malaria vaccine have been undertaken.
- [0033] Human volunteers injected with irradiated PF sporozoites are resistant to subsequent sporozoite challenges, which demonstrates that development of a malaria vaccine is indeed immunologically feasible. Furthermore, these immune individuals developed a vigorous response, including antibodies, and cytotoxic T lymphocyte (CTL) and helper T lymphocyte (HTL) components, directed against multiple antigens. Reproducing the breadth and multiplicity of this response in a vaccine, however, is a task of large proportions. The epitope approach, as described herein, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine composition.
- [0034] Anti-sporozoite antibodies are by themselves, in general, not completely efficacious in clearing the infection (Egan *et al.*, *Science* 236:453, 1987). However, high concentrations of antibodies directed against the repeated region of the major B cell antigen of the sporozoite/circumsporozoite protein (CSP) have been shown to prevent liver cell infection in certain experimental models (Egan *et al.*, *Science* 236:453, 1987; Potocnjak, P. *et al.*, *Science* 207:71, 1980). The present inventors have shown that constructs encompassing CSP-repeat B cell epitopes and the optimized helper epitope PADRE™ (San Diego, CA) are highly immunogenic, and can protect *in vitro* against sporozoite invasion in both mouse and human liver cells, and protect mice *in vivo* against live sporozoite challenge (Franke *et al.*, *Vaccine* 17:1201-1205, 1999).

- [0035] PF-specific CD4⁺ T cells also have a role in malarial immunity beyond providing help for B cell and CTL responses. Experiments by Renia *et al.* (Renia, *et al.*, *Proc. Natl. Acad. Sci. USA* 88:7963, 1991) demonstrated that HTLs directed against the *Plasmodium yoelli* CS protein could in fact adoptively transfer protection against malaria.
- [0036] Considerable data implicate CTLs in protection against pre-erythrocytic-stage malaria. CD8⁺ CTLs can eliminate *Plasmodium berghei*- or *Plasmodium yoelii*-infected mouse hepatocytes from in vitro culture in a major histocompatibility complex (MHC)-restricted and antigen-restricted manner (Hoffman *et al.*, *Science* 244:1078-1081, 1989; Weiss *et al.*, *J. Exp. Med.* 171:763-773, 1990). Further, it has also been shown that the immunity that developed in mice vaccinated with irradiated sporozoites is also dependent upon the presence of CD8⁺ T cells. These T cells accumulate in inflammatory liver infiltrates subsequent to challenge. Passive transfer of circumsporozoite (CSP)-specific CTL clones as long as three hours after inoculation of sporozoites (*i.e.*, after the parasites have left the bloodstream and infected liver cells) were capable of protecting animals against infection (Romero *et al.*, *Nature* 341:323, 1989).
- [0037] It is notable that CTL-restricted responses directed against a single antigen are insufficient to protect mice with different MHC alleles, and a combination of multiple antigens was required even to protect mice from the most common laboratory strains of *Plasmodium*. These data indicate that a combination of epitopes from several antigens is necessary to elicit a protective CTL response.
- [0038] Indirect evidence that CTLs are important in protective immunity against Pf in humans has also accumulated. It has been reported that cytotoxic CD8⁺ T cells can be identified in humans immunized with PF sporozoites (Moreno, *et al.*, *Int. Immunol.* 3:997, 1991). Further, humans immunized with irradiated sporozoites or naturally exposed to malaria can generate a CTL response to the pre-erythrocytic-stage antigens, CSP, sporozoite surface protein 2 (SSP2), liver-stage antigen-1 (LSA-1), and exported protein-1 (Exp-1) (*see, e.g.* Malik *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 3300-3304, 1991; Doolan *et al.*, *Int. Immunol.* 3:511-516, 1991; Hill *et al.*, *Nature* 360:434-439, 1992). Additionally, there is evidence that the polymorphism within the CSP may be the result of selection by CTLs of parasites that express variant forms (McCutchan and Water, *Immunol. Lett.* 25:23-26, 1990). This is based on the observation that the variation is nonsynonymous at the nucleotide level, thereby indicating selective pressure at the protein level. The polymorphism primarily maps to identified CTL and T helper epitopes (Doolan *et al.*, *Int.*

Immunol. 5:27-46, 1993); and CTL responses to some of the parasite variants do not cross-react (Hill *et al.*, *supra*). Finally, the MHC class I human leukocyte antigen (HLA)-Bw53 has been associated with resistance to severe malaria in The Gambia, and CTLs to a conserved epitope restricted by the HLA-Bw53 allele have been identified on *P. falciparum* LSA-1 (Hill *et al.*, *Nature* 352:595-600, 1991; Hill *et al.*, *Nature* 340:434-439, 1992). Since HLA-Bw53 is found in 15%-40% of the population of sub-Saharan Africa but in less than 1% of Caucasians and Asians, these data suggest evolutionary selection on the basis of protection against severe malaria.

[0039] Thus, antibody, and both HLA class I and class II restricted responses directed against multiple sporozoite antigens appear to be involved in generating protective immunity to malaria. Furthermore, several important antigenic epitopes against which humoral and cellular immunity is focused have already been exactly delineated.

[0040] In view of the heterogeneous immune response observed with PF infection, induction of a multi-specific cellular immune response directed simultaneously against multiple PF epitopes appears to be important for the development of an efficacious vaccine against PF. There is a need, however, to establish vaccine embodiments that elicit immune responses that correspond to responses seen in patients that clear PF infection.

[0041] **Epitope-Based Vaccines.** The use of epitope-based vaccines has several advantages over current vaccines. The epitopes for inclusion in such a vaccine are to be selected from conserved regions of viral or tumor-associated antigens, in order to reduce the likelihood of escape mutants. The advantage of an epitope-based approach over the use of whole antigens is that there is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

[0042] Additionally, with an epitope-based vaccine approach, there is an ability to combine selected epitopes (CTL and HTL) and additionally to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

- [0043] Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.
- [0044] An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion of epitopes from multiple antigens from that pathogen in a vaccine composition. A "pathogen" may be an infectious agent or a tumor associated molecule.
- [0045] One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics has been the extreme polymorphism of HLA molecules. In the past, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used specific for HLA molecules corresponding to each individual HLA allele. Therefore, impractically large numbers of epitopes would be required in order to cover ethnically diverse populations. Recently, methods have been developed that allow the identification of epitopes that bind multiple HLA molecules. Therefore, epitope-based vaccines can be designed that contain epitopes which, either individually or in combination, bind a greater number of HLA molecules. The resulting epitope-based vaccines have a greater breadth of population coverage across one or more continents and even worldwide.
- [0046] **Variation in Epitopes of Infectious Agents.** A challenge in the development of effective vaccines against infectious agents such as hepatitis B virus (HBV) (47, 60) hepatitis C virus (HCV) (61-63), human papilloma virus (HPV) (64, 65) *Plasmodium falciparum* (66), and human immunodeficiency virus (HIV-1) is the protein sequence variation associated with different isolates. This variation is the result of gene sequence mutations. When such mutations occur in regions encoding epitopes recognized by cytotoxic T-lymphocytes (CTL), they provide a mechanism for escape of the agent from immune system control.
- [0047] HIV-1 represents an infectious agent with an especially high frequency of sequence variation. The sequence variation associated with HIV-1 proteins from related isolates, members of the same clades or types, as well as unrelated isolates, is well documented (1). Viral escape from CTL induced as the result of natural infection or vaccines was documented in nonhuman primate models where the mechanism behind this

escape was mutation of the primary anchor residues in dominant CTL epitopes (5-9). Viral escape from HIV-specific CTL has also been strongly implied by data obtained from HIV-1 infected individuals whose disease status change, including the transition from acute to chronic infection (10, 11), loss of stable control of viral replication and subsequent progression to AIDS (4, 12) or mother-to-child transmission (13). Thus, HIV-1 genetic and protein sequence variation represent a significant challenge to immune system-based control of viral replication, both within infected individuals and within populations.

[0048] While the public health need for a vaccine against HIV-1 is well recognized and accepted, the genetic variation of HIV-1 isolates represents a highly significant obstacle (1, 14-16). Several strategies have been proposed, some of which include:

- (1) Designing vaccines on HIV-1 types prevalent within small, well defined populations or geographical regions, such as individual countries or regions, and producing multiple different vaccines for exclusive use within these countries or regions (16).
- (2) Use of HIV-1 ancestral or consensus sequences based on HIV types present in larger target populations, such as groups of neighboring countries or continents (15, 17-19).
- (3) Incorporation of viral gene products obtained from multiple different virus isolates, representing diversely different types or clades, into a single 'multi-valent' vaccine.

[0049] Related vaccine design concepts that incorporate many of the advantages associated with the approaches described above are the use of highly conserved regions or epitopes derived from these regions as the basis of the vaccine. The logic behind this approach is that conserved regions of the viral genome are those that have been maintained through the evolution of HIV-1 because changes impact gene product function and general viral fitness. This theory is consistent with analyses of HIV-1 protein sequence data which demonstrated that CTL epitopes are concentrated in conserved regions and that regions devoid of CTL epitopes are the most variable (20). Additional support comes from published reports describing CTL responses, induced as the result of

natural infection or vaccination, that recognize viral proteins or epitopes common to viral isolates from diverse types or clades (21-26). Broad function CTL responses are also known to be correlated with slower progression to AIDS, at least for certain carefully studied populations (27, 28). Despite these reports and the clustering of CTL epitopes in conserved regions of HIV-1 gene products, amino acid sequence variation of analogous regions and epitopes from different viral isolates, both within the same type or clade and from different types, remains significant. There are currently no rules guiding the selection of conserved regions of CTL epitopes for use in vaccines other than the use of amino acid sequence identity (29).

[0050] A clear understanding of how CTL recognize pathogen infected cells has emerged over the past decade. It is now well established that small fragments of pathogen-derived proteins are generated, defined as peptide epitopes generally 8-11 amino acids in length, which bind to HLA-A, -B, or -C (human Class I Major Histocompatibility Molecules) molecules expressed on the cell surface. Sequencing of naturally processed peptides bound to HLA molecules provided a means to identify the amino acid residues required for allele-specific epitope-peptide binding (30-32). Data obtained from X-ray crystallographic analysis of HLA-epitope peptide complexes, allowed for the identification and structural characterization of 'binding pockets' within the peptide binding cleft of HLA molecules. More refined epitope anchor motif definitions were then developed using data obtained from *in vitro* peptide-MHC binding assays. It is now well known that the main anchor residues typically occur at position 2 and the carboxyl terminus of peptides 8-11 amino acids in length, thus positions 8, 9, 10 or 11 (33-40). The definition of epitope peptide binding anchor motifs is the key to most, if not all, epitope prediction methods.

[0051] Initial CTL epitope identification methods were developed using common HLA alleles, such as HLA-A2.1. Motifs defined using different HLA molecules were found to be similar and this lead to the definition of HLA supertype families (41). The biological effect of this supertype relationship was first demonstrated for HIV-1 epitopes in a study where the HLA-A3 and -A11 epitope peptide binding patterns repertoires were demonstrated to be overlapping, not only with each other but also with HLA-A31, -A33 and -A*6801 (42). This binding specificity was defined as the HLA-A3 supertype. A significant overlap in peptide binding patterns was also demonstrated amongst several serologically distant HLA-B alleles (43, 44), and multiple HLA-A2 alleles (45, 46),

resulting in the definition of the HLA-B7 and HLA-A2 supertype families. Recognition of epitopes by CTL in a supertype manner has since been demonstrated to occur naturally in infectious diseases and cancer (47-53).

[0052] While only two positions within CTL epitopes are typically characterized as the primary binding anchor positions, the amino acids that can serve as the anchor residues are more variable. The preferred and tolerated amino acids that can serve as anchor residues for the HLA-A2, -A3 and -B7 supertype families of epitopes are listed in Table 1. It is possible for analogous HIV-1 epitope peptides derived from different isolates, which differ with respect to the amino acids used as anchor residues, to bind to HLA molecules similarly. This type of variation can be as conserved since it is likely that CTL produced against one epitope would recognize the related epitope. Thus, variation limited to changes in anchor residues that result in sufficient epitope peptide binding to HLA molecules does not result in immune escape from CTL. Epitopes that contain this type of variation can be identified using the appropriately designed motif search algorithms.

[0053] The TCR of CTL has been reported to be somewhat flexible or promiscuous with respect to recognition of epitope peptides bound to HLA molecules. For HIV-1, this flexibility was demonstrated as CTL recognition of related, but slightly variable, epitopes by single clones of CTL produced following natural infection (54, 55). Similar flexibility of CTL epitope recognition was demonstrated using rhesus macaques and natural infection with SIV or immunization (56, 57). This observation is not unique to HIV-1 and SIV but rather the TCR appears to have evolved to allow promiscuous recognition of peptide epitope bound to MHC molecules (58).

[0054] Selective replacement of certain amino acids in CTL epitope peptides, amino acids thought to represent TCR contact points, is not only tolerated but can increase the recognition of the epitopes by CTL clones (59). The types of amino acid substitutions that can be incorporated, typically amino acids that are similar in chemical properties are best tolerated, and their positions, independent of primary anchor positions, within a selected number of CTL epitopes from tumor associated antigens were also defined.

[0055] For HIV-1 and other infectious agents, reproducible methods for predicting the CTL recognition of related variant epitopes that occur amongst isolates have not been developed. Nor have methods for identifying CTL epitopes that are most likely to induce broadly functional responses when used in vaccine. Thus, there exists a need to develop

such methods to overcome the challenge associated with protein sequence variation in HIV and other infectious agents.

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SUMMARY OF THE INVENTION

[0056] The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s).

[0057] In some embodiments, antigen sequences from a population of an infectious agent, said antigens comprising variants of a peptide epitope, are optionally aligned (manually or by computer) along their length, preferably their full length. Variant(s) of a peptide epitope (preferably naturally occurring variants), each 8-11 amino acids in length and comprising the same MHC class I supermotif or motif, are identified manually or with the aid of a computer. In some embodiments, a variant is optionally chosen which comprises preferred anchor residues of said motif and/or which occurs with high frequency within the population of variants. In other embodiments, a variant is randomly chosen. The randomly or otherwise chosen variant is compared to from one to all the remaining variant(s) to determine whether it comprises only conserved residues in the non-anchor positions relative to from one to all the remaining variant(s).

[0058] The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

- [0059] FIGS. 1A-1E. Recognition of variant peptides by CTL generated against a single epitope. Variant peptides were identified from 167 HIV strains for 5 HIV epitopes, 3 HLA-A2 restricted (Env 134, A, Gag 386, B, and Vpr 62, C) and 2 HLA-A11 restricted (Pol 98, D, and Env 47, E). These are listed according to their relationship to a previously determined parent (P) into single anchor substitutions (A), single non-anchor substitutions (NA) or multiple substitutions (M). Binding of each variant peptide is also shown. The number of viral sequences containing each variant peptide is shown in the column labeled # Isolates, and is reported for the total sequences, Clade B sequences (B), and Clade C sequences (C). Finally, the ability of CTL primed against the parent peptide to recognize the variant peptides is shown in the bar graphs.
- [0060] FIGS. 2A-2C. Characterization of the peptide-specific T cell lines. A. FACS analysis of the TCRs expressed by peptide-stimulated cells after 0, 1, and 5 peptide stimulations, using a panel of commercially available mAb for mouse TCR 2-14. B-C. Peptide affinity. Parent and variant peptides were titrated against CTL that had been stimulated 5 times with the parent peptide.
- [0061] FIGS. 2A-2B. Recognition of a panel of variant peptides by PBL from an HIV-infected individual.
- [0062] FIG 4. Prediction of immunological conservation. Gag 271 variants and their binding are shown, along with the number of isolates that express each variant. Immunological recognition was predicted for each variant based on two different choices in the immunizing peptide. On the right, the immunogenicity for each variant is shown.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

- [0063] The invention can be better understood with reference to the following definitions:
- [0064] An "antigen" refers to a polypeptide encoded by the genome of an infectious agent, or other another source, but preferably an infectious agent in the present invention.

Examples of HIV antigens include Env, Gag, Nef, Pol, Tat, Rev, Vif, Vpr, Vpu, p17, p24, p2, p7, p1, p6, Protease, RT, Integrase, and gp160 (preferably Env, Gag, Nef, Pol, Tat, Rev, Vif, Vpr, Vpu). Examples of HBV antigens include Core, Env, and Pol. Examples of HCV antigens include Core, E1, E2, Ns1, Ns2, Ns3, Ns4, and Ns5. Examples of HPV antigens include E1, E2, E3, E4, E5, E6, E7, L1, and L2. Examples of *Plasmodium falciparum* antigens include CSP, SSP2, Exp1, and LSA1.

[0065] Throughout this disclosure, "binding data" results are often expressed in terms of "IC₅₀'s." IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205, and other publications such as Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); and Sette, *et al.*, *Mol. Immunol.* 31:813 (1994). It should be noted that IC₅₀ values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

[0066] Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC₅₀'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good (*i.e.* high), intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀ of a standard peptide. The Tables included in this application present binding data in a preferred biologically relevant form of IC₅₀ nM.

[0067] Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, *Nature* 339:392 (1989); Christnick *et al.*, *Nature* 352:67 (1991); Busch *et al.*, *Int. Immunol.* 2:443 (1990); Hill *et al.*, *J. Immunol.* 147:189 (1991); del Guercio *et al.*, *J. Immunol.* 154:685 (1995)), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069 (1991)), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890 (1994); Marshall *et al.*, *J. Immunol.* 152:4946 (1994)), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829 (1992)), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425 (1993)), high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353 (1994)), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476 (1990);

Schumacher *et al.*, *Cell* 62:563 (1990); Townsend *et al.*, *Cell* 62:285 (1990); Parker *et al.*, *J. Immunol.* 149:1896 (1992)).

- [0068] As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} or K_D value, of 50 nM or less, "intermediate affinity" is binding with an IC_{50} or K_D value of between 50 and about 500 nM, weak affinity is binding with an IC_{50} or K_D value of between about 500 and about 5000 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.
- [0069] A "computer" or "computer system" generally includes: a processor and related computer programs; at least one information storage/retrieval apparatus such as a hard drive, a disk drive or a tape drive; at least one input apparatus such as a keyboard, a mouse, a touch screen, or a microphone; and display structure, such as a screen or a printer. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.
- [0070] "Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.
- [0071] A "cryptic epitope" elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein, which comprises the epitope, is used as an antigen.
- [0072] The term "derived" when used to discuss an epitope is a synonym for "prepared." A derived epitope can be isolated from a natural source, or it can be synthesized in accordance with standard protocols in the art. Synthetic epitopes can comprise artificial amino acids "amino acid mimetics," such as D isomers of natural occurring L amino acids or non-natural amino acids such as cyclohexylalanine. A derived/prepared epitope can be an analog of a native epitope.
- [0073] A "diluent" includes sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred diluent for pharmaceutical compositions. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as diluents, particularly for injectable solutions.
- [0074] A "dominant epitope" is an epitope that induces an immune response upon immunization with a whole native antigen (see, *e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.
- [0075] An "epitope" is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Alternatively, an epitope can be defined as a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T

cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. Epitopes are present in nature, and can be isolated, purified or otherwise prepared/derived by humans. For example, epitopes can be prepared by isolation from a natural source, or they can be synthesized in accordance with standard protocols in the art. Synthetic epitopes can comprise artificial amino acids, "amino acid mimetics," such as D isomers of naturally-occurring L amino acids or non-naturally-occurring amino acids such as cyclohexylalanine. Throughout this disclosure, epitopes may be referred to in some cases as peptides. The variants of the invention are set forth in Tables 6-9 and Figures 1A-4.

[0076] It is to be appreciated that proteins or peptides that comprise a variant of the invention as well as additional amino acid(s) are still within the bounds of the invention. In certain embodiments, the peptide comprises a fragment of an antigen. A "fragment of an antigen" or "antigenic fragment" or simply "fragment" is a portion of an antigen which has 100% identity with a wild type antigen or naturally-occurring variant thereof. The fragment may or may not comprise an epitope of the invention. The fragment may be less than or equal to 600 amino acids, less than or equal to 500 amino acids, less than or equal to 400 amino acids, less than or equal to 250 amino acids, less than or equal to 100 amino acids, less than or equal to 85 amino acids, less than or equal to 75 amino acids, less than or equal to 65 amino acids, or less than or equal to 50 amino acids in length. In certain embodiments, a fragment is e.g., less than 101 or less than 51 amino acids in length, in any increment down to 5 amino acids in length. For example, the fragment may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length.

[0077] In certain embodiments, there is a limitation on the length of a peptide of the invention. The embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid the definition of epitope from reading, e.g., on whole natural molecules, there is a limitation on the length of any region that has 100% identity with a native peptide sequence. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence, the region with 100% identity to a native sequence generally has a length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an "epitope" of the invention

is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment down to 5 amino acids.

[0078] Accordingly, peptide or protein sequences longer than 600 amino acids are within the scope of the invention, so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence. For any peptide that has five contiguous residues or less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a peptide of the invention (e.g., a peptide comprising an epitope of the invention) be less than 600 residues long in any increment down to eight amino acid residues.

[0079] A peptide epitope occurring with "high frequency" is one that occurs in at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the infectious agents in a population. A "high frequency" peptide epitope is one of the more common in a population, preferably the first most common, second most common, third most common, or fourth most common in a population of variant peptide epitopes.

[0080] "Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g., Stites, et al., IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA (1994).*

[0081] An "HLA supertype or HLA family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into such HLA superotypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where "xx" denotes a particular HLA type), are synonyms. See Tables 1-4.

[0082] As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} , or K_D value, of 50 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 50 and about 500 nM; "weak affinity" is binding with an IC_{50} or K_D value between about 500 and about 5000 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM. See "binding data."

[0083] An " IC_{50} " is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. See "binding data."

[0084] The terms "identical" or percent "identity," in the context of two or more peptide sequences or antigen fragments, refer to two or more sequences or subsequences that are the same

or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

[0085] An "immunogenic" peptide or an "immunogenic" epitope or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T lymphocyte (CTL) response, or a helper T lymphocyte (HTL) response, to the peptide.

[0086] An "infectious agent" refers to a disease-causing microorganism, including viruses, bacteria, fungi, and protozoa against which a cellular immune response, preferably a CTL response, plays a role in acquired immunity. Examples of infectious agents include viruses such as human immunodeficiency virus (HIV), hepatitis B virus (HBV), hepatitis C virus (HCV), human papilloma virus (HPV), Influenza virus, Dengue virus, Epstein-Barr virus, bacteria such as *Mycobacterium tuberculosis* and *Chlamydia*, fungi such as *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.* and *Aspergillus fumigatis*, protozoa such as *Plasmodium spp.*, including *P. falciparum*, *Trypanosoma spp.*, *Schistosoma spp.*, *Leishmania spp.* and the like. Preferred infectious agents include HIV, HBV, HCV, HPV, Epstein-Barr virus, *Plasmodium falciparum*, Influenza virus and Dengue virus.

[0087] The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. An "isolated" epitope refers to an epitope that does not include the whole sequence of the antigen or polypeptide from which the epitope was derived. Typically the "isolated" epitope does not have attached thereto additional amino acids that result in a sequence that has 100% identity with a native sequence. The native sequence can be a sequence such as a tumor-associated antigen from which the epitope is derived. Thus, the term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or peptide present in a living animal is not isolated, but the same polynucleotide or peptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such a polynucleotide could be part of a vector, and/or such a polynucleotide or peptide could be part of a composition, and still be "isolated" in that such vector or composition is not part of its natural environment. Isolated RNA molecules include *in vivo* or *in vitro* RNA

transcripts of the DNA molecules of the present invention, and further include such molecules produced synthetically.

- [0088] "Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the human leukocyte antigen (HLA) complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York (1993).
- [0089] The term "motif" refers to a pattern of residues in an amino acid sequence of defined length, preferably a peptide of less than about 15 amino acids in length, or less than about 13 amino acids in length, usually from about 8 to about 13 amino acids (*e.g.*, 8, 9, 10, 11, 12, or 13) for a class I HLA motif and from about 6 to about 25 amino acids (*e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) for a class II HLA motif, which is recognized by a particular HLA molecule. Motifs are typically different for each HLA protein encoded by a given human HLA allele. These motifs often differ in their pattern of the primary and secondary anchor residues. See Tables 1-3.
- [0090] A "native" or a "wild type" sequence refers to a sequence found in nature.
- [0091] A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.
- [0092] The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids.
- [0093] A "PanDR binding" peptide or "PADRE[®]" peptide (Epimmune, San Diego, CA) is a member of a family of molecules that binds more than one HLA class II DR molecule. The pattern that defines the PADRE[®] family of molecules can be referred to as an HLA Class II supermotif. A PADRE[®] molecule binds to HLA-DR molecules and stimulates *in vitro* and *in vivo* human helper T lymphocyte (HTL) responses. For a further definition of the PADRE[®] family, see copending application US serial Nos. 09/709,774, filed November 11, 2000; and 09/707,738, filed November 6, 2000; PCT publication Nos WO 95/07707, and WO 97/26784; U.S. Patent Nos. 5,736,142 issued April 7, 1998; 5,679,640, issued October 21, 1997; and 6,413,935, issued July 2, 2002.
- [0094] "Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition or component of a composition.

- [0095] A "pharmaceutical excipient" or "excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like. A "pharmaceutical excipient" is an excipient which is pharmaceutically acceptable.
- [0096] A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One, two or three, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment of an HLA class I motif, the primary anchor residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif of HLA Class I are set forth in Tables 1-2. For example, analog peptides can be created by altering the presence or absence of particular residues in these anchor positions. Such analogs are used to modulate the binding affinity of an epitope comprising a particular motif or supermotif. A "preferred primary anchor residue" is an anchor residue of a motif or supermotif that is associated with optimal binding. Preferred primary anchor residues are indicated in bold-face in Tables 1-2. A "tolerated primary anchor residue" is an anchor residue of a motif or supermotif that is associated with binding to a lesser extent than a preferred residue. Tolerated primary anchor residues are indicated in italicized text in Tables 1-2.
- [0097] "Promiscuous recognition" by a TCR is where a distinct peptide is recognized by the various T cell clones in the context of various HLA molecules. Promiscuous binding by an HLA molecule is synonymous with cross-reactive binding.
- [0098] A "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an antigen of an infectious agent, which in some way prevents or at least partially arrests disease symptoms, side effects or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.
- [0099] By "ranking" the variants in a population of peptide epitopes is meant ordering each variant by its frequency of occurrence relative to the other variants.
- [00100] The term "residue" refers to an amino acid or amino acid mimetic incorporated into a peptide or protein by an amide bond or amide bond mimetic.
- [00101] A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst HLA-bound peptides than would be expected by random

distribution of amino acids at a given position. A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. The secondary anchor residues are said to occur at "secondary anchor positions." For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of an epitope comprising a particular motif or supermotif. The terminology "fixed peptide" is generally used to refer to an analog peptide that has changes in primary anchor position; not secondary.

[00102] A "subdominant epitope" is an epitope which evokes little or no response upon immunization with a whole antigen or a fragment of the whole antigen comprising a subdominant epitope and a dominant epitope, which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole antigen or a fragment of the whole antigen comprising a subdominant epitope and a dominant epitope is used to recall the response *in vitro* or *in vivo*.

[00103] A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

[00104] "Synthetic peptide" refers to a peptide that is obtained from a non-natural source, *e.g.*, is man-made. Such peptides may be produced using such methods as chemical synthesis or recombinant DNA technology. "Synthetic peptides" include "fusion proteins."

[00105] As used herein, a "vaccine" is a composition used for vaccination, *e.g.*, for prophylaxis or therapy, that comprises one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more peptides of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150, *e.g.*, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I-binding peptides of the invention can be linked to HLA class II-binding peptides, *e.g.*, a PADRE® universal HTL-binding peptide, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can comprise peptide pulsed antigen presenting cells, *e.g.*, dendritic cells.

[00106] A "variant of a peptide epitope" refers to a peptide that is identified from a different viral strain at the same position in an aligned sequence, and that varies by one or

more amino acids from the parent peptide epitope. Examples of peptide epitope variants include those shown in Tables 6-9 and Figures 1A-4. A "variant of an antigen" refers to an antigen that comprises at least one variant of a peptide epitope. Examples of antigen variants include those listed by sequence and/or accession number in Tables 10-22. A "variant of an infectious agent" refers to an infectious agent whose genome encodes at least one variant of an antigen. Variants of infectious agents are related viral, bacterial, fungal, or protozoan strains or isolates that vary in sequence but cause the same disease symptoms. Examples of infectious agent variants include HIV Clade A, B, and C subtypes, HBV subtypes adr, ayr, adw, and ayw, HCV types 1, 2, 3, 4, 5, and 6, HPV strains 1-92 (preferably strains 16, 18, 31, 33, 45, 52, 56, and 58) (see Table 10, listing accession numbers for the complete genome sequences of 167 HIV variants; Table 22, showing an alignment of the complete polyprotein sequences of 50 HCV variants) (see also, *Human Retroviruses and AIDS 2000: A Compilation and Analysis of Nucleic Acid and Amino Acid Sequences*, Kuiken CL, et al., Eds. Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, NM).

[00107] The nomenclature used to describe peptides/proteins follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. However, when three letter symbols or full names are used without capitals, they may refer to L amino acids. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or "G". The amino acid sequences of peptides set forth herein are generally designated using the standard single letter symbol. (A, Alanine; C, Cysteine; D, Aspartic Acid; E, Glutamic Acid; F, Phenylalanine; G, Glycine; H, Histidine; I, Isoleucine; K, Lysine; L, Leucine; M, Methionine; N, Asparagine; P, Proline; Q, Glutamine; R, Arginine; S, Serine; T, Threonine; V, Valine; W, Tryptophan; and Y, Tyrosine.) In addition to these symbols, "B" in the single letter abbreviations used herein

designates α -amino butyric acid. In some embodiments, α -amino butyric acid may be replaced with cysteine.

Acronyms used herein are as follows:

APC:	Antigen presenting cell
CD3:	Pan T cell marker
CD4:	Helper T lymphocyte marker
CD8:	Cytotoxic T lymphocyte marker
CEA:	Carcinoembryonic antigen (see, e.g., SEQ ID NO: 363)
CTL:	Cytotoxic T lymphocyte
DC:	Dendritic cells. DC functioned as potent antigen presenting cells by stimulating cytokine release from CTL lines that were specific for a model peptide derived from hepatitis B virus. <i>In vivo</i> experiments using DC pulsed <i>ex vivo</i> with an HBV peptide epitope have stimulated CTL immune responses <i>in vivo</i> following delivery to naïve mice.
DLT:	Dose-limiting toxicity, an adverse event related to therapy.
DMSO:	Dimethylsulfoxide
ELISA:	Enzyme-linked immunosorbant assay
E:T:	Effector:Target ratio
G-CSF:	Granulocyte colony-stimulating factor
GM-CSF:	Granulocyte-macrophage (monocyte)-colony stimulating factor
HBV:	Hepatitis B virus
HER2/neu:	A tumor associated antigen; c-erbB-2 is a synonym (see, e.g., SEQ ID NO: 364)
HLA:	Human leukocyte antigen
IILA-DR:	Human leukocyte antigen class II
HPLC:	High Performance Liquid Chromatography
HTC:	Helper T Cell
HTL:	Helper T Lymphocyte. A synonym for HTC.
ID:	Identity
IFN γ :	Interferon gamma
IL-4:	Interleukin-4
IV:	Intravenous
LU _{30%} :	Cytotoxic activity for 10 ⁶ effector cells required to achieve 30% lysis of a target cell population, at a 100:1 (E:T) ratio.
MAb:	Monoclonal antibody
MAGE:	Melanoma antigen (see, e.g., SEQ ID NO: 365 and 366 for MAGE2 and MAGE3)
MLR:	Mixed lymphocyte reaction
MNC:	Mononuclear cells
PB:	Peripheral blood
PBMC:	Peripheral blood mononuclear cell
ProGP TM :	Progenipoietin TM product (Searle, St. Louis, MO), a chimeric flt3/G-CSF receptor agonist.
SC:	Subcutaneous
S.E.M.:	Standard error of the mean
QD:	Once a day dosing
TAA:	Tumor Associated Antigen
TNF:	Tumor necrosis factor
WBC:	White blood cells

[00108] The following describes the peptides, nucleic acid molecules, compositions, and methods of the invention in more detail.

Methods of Identifying Candidate Peptide Epitopes

[00109] The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s).

[00110] In some embodiments, antigen sequences from a population of an infectious agent, said antigens comprising variants of a peptide epitope, are optionally aligned (manually or by computer) along their length, preferably their full length. Variant(s) of a peptide epitope (preferably naturally occurring variants), each 8-11 amino acids in length and comprising the same MHC class I supermotif or motif, are identified manually or with the aid of a computer. In some embodiments, a variant is optionally chosen which comprises preferred anchor residues of said motif and/or which occurs with high frequency within the population of variants. In other embodiments, a variant is randomly chosen. The randomly or otherwise chosen variant is compared to from one to all the remaining variant(s) to determine whether it comprises only conserved residues in the non-anchor positions relative to from one to all the remaining variant(s).

[00111] The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

[00112] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and

- b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

[00113] In some embodiments, (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00114] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;
- b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
- c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

[00115] In some embodiments, (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00116] In some embodiments, the invention is directed to a method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
- b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and

- ii) a variant which occurs with high frequency within the population of variants; and
- c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

[00117] In some embodiments, (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00118] In some embodiments, the invention is directed to method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

- a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
- b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and
 - ii) a variant which occurs with high frequency within the population of variants; and
- c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
- d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

[00119] In some embodiments, (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

[00120] In some embodiments, (a) comprises aligning the sequences of said antigens.

- [00121] In some embodiments, (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif.
- [00122] In some embodiments, (b) comprises choosing a variant which occurs with high frequency within said population.
- [00123] In some embodiments, (b) comprises ranking said variants by frequency of occurrence within said population.
- [00124] In some embodiments, (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif and which occurs with high frequency within said population.
- [00125] In some embodiments, (b) comprises ranking said variants by frequency of occurrence within said population.
- [00126] In some embodiments, the identified variant comprises the fewest conserved anchor residues in comparison to each of the remaining variants.
- [00127] In some embodiments, the remaining variants comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, or 300 variants.
- [00128] In some embodiments, the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis*, *Chlamydia*, *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, *Aspergillus fumigatis*, *Plasmodium spp.*, *Trypanosoma spp.*, *Schistosoma spp.*, and *Leishmania spp.*
- [00129] In some embodiments, the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus.
- [00130] In some embodiments, the infectious agent is HIV and the antigen is selected from the group consisting of: Gag, Env, Pol, Nef, Rev, Tat, Vif, Vpr, and Vpu.
- [00131] In some embodiments, the infectious agent is HBV and the antigen is selected from the group consisting of: Pol, Env, Core, and NS1/Env2.
- [00132] In some embodiments, the infectious agent is HCV and the antigen is selected from the group consisting of: Core, E1, E2, NS1, NS2, NS3, NS4, and NS5.
- [00133] In some embodiments, the infectious agent is HPV and the antigen is selected from the group consisting of: E1, E2, E3, E4, E5, E6, E7, L1, and L2.

- [00134] In some embodiments, the infectious agent is *Plasmodium falciparum* and the antigen is selected from the group consisting of: CSP, SSP2, EXP1, LSA1.
- [00135] In some embodiments, the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.
- [00136] In some embodiments, the motif or supermotif is selected from the group consisting of those in Tables 1-2.
- [00137] In some embodiments, the conserved non-anchor residues are at any of positions 3-7 of said variant.
- [00138] In some embodiments, the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.
- [00139] In some embodiments, the variant comprises only 1-2 conserved non-anchor residues compared to at least one remaining variant.
- [00140] In some embodiments, the variant comprises only 1 conserved non-anchor residue compared to at least one remaining variant.
- [00141] In some embodiments, the infectious agent is HPV, and further wherein, the HPV infectious agent is selected from the group consisting of HPV strains 16, 18, 31, 33, 45, 52, 56, and 58.
- [00142] In some embodiments, the variants are a population of naturally occurring variants.
- [00143] **Optional Alignment.** Optionally, antigen sequences, either full-length or partial, may be aligned manually or by computer. Convenient computer programs for aligning multiple sequences include Omega, Oxford software, version 1.1.3, using ClustalW alignment, using an open gap penalty of 10.0, extend gap penalty of 0.05, and delay divergent sequences of 40.0 (See, e.g., Table 21); and BLASTP 2.2.5 (Nov-16-2002) (Altschul, S.F., et al., Nucleic Acids Res. 25:3389-3402 (1997)) using a cutoff = $3e-88$ (to select human sequences) (see, e.g., Table 20). Alternatively, alignments may be obtained through publicly available sources such as published journal articles and published patent documents or as disclosed herein (see, e.g., Tables 10-22).
- [00144] **HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes.** A large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each respective supertype characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus,

peptides of the present invention are preferably identified by the primary residues of any one of several HLA-specific amino acid motifs, or if the presence of the motif corresponds to the ability to bind several allele-specific HLA antigens, a supermotif (*see, e.g.*, Tables 1-2). The preferred primary residues are indicated in bold, while the tolerated primary residues are indicated by italics.

[00145] The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs are summarized in Tables 1-2. Preferred primary anchors are shown in bold, while tolerated primary anchors are shown in italics. Primary and secondary anchor positions for HLA Class I are summarized in Table 3. Allele-specific HLA molecules that fall within the various HLA class I supertypes are listed in Table 4. In some cases, patterns of amino acid residues are present in both a motif and a supermotif. The relationship of a particular motif and any related supermotif is indicated in the description of the individual motifs.

[00146] Thus, the peptide motifs and supermotifs described below, and summarized in Tables 1-2, provide guidance for the identification and use of peptide epitopes comprising primary anchor residues of motifs or supermotifs in accordance with the invention.

[00147] Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table 4.

[00148] **HLA-A1 supermotif.** The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table 4. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00149] **HLA-A2 supermotif.** Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and cross-reactive binding among HLA-A2 and -A28 molecules have been

described. (See, e.g., Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

[00150] The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table 4. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00151] The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

[00152] **HLA-A3 supermotif.** The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (see, *e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA molecules predicted to be members of the A3 supertype are shown in Table 4. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

[00153] **HLA-A24 supermotif.** The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (see, *e.g.*, Sette and Sidney, *Immunogenetics*, in press,

1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.*, the A24 supertype) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00154] **HLA-B7 supermotif.** The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.*, the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g.*, Sidney, *et al.*, *J. Immunol.* 154:247, 1995; Barber, *et al.*, *Curr. Biol.* 5:179, 1995; Hill, *et al.*, *Nature* 360:434, 1992; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table 4. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

[00155] **HLA-B27 supermotif.** The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.*, the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00156] HLA-B44 supermotif. The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.,* the B44 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

[00157] HLA-B58 supermotif. The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.,* the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00158] HLA-B62 supermotif. The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.,* the B62 supertype) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table 4. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

[00159] HLA-A1 motif. The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a

primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, *J. Immunol.*, 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data). Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

[00160] Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also HLA-A1 supermotif-bearing peptide epitopes, as these residues are a subset of the A1 supermotif primary anchors.

[00161] **HLA-A*0201 motif.** An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g.*, Hunt *et al.*, *Science* 255:1261-1263, March 6, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g.*, Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Ruppert *et al.*, *Cell* 74:929-937, 1993; Sidney *et al.*, *Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g.*, Ruppert *et al.*, *Cell* 74:929-937, 1993). These are shown in Table 3. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

- [00162] **HLA-A3 motif.** The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., DiBrino et al., Proc. Natl. Acad. Sci USA 90:1508, 1993; and Kubo et al., J. Immunol. 152:3913-3924, 1994*). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.
- [00163] The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.
- [00164] **HLA-A11 motif.** The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Zhang et al., Proc. Natl. Acad. Sci USA 90:2217-2221, 1993; and Kubo et al., J. Immunol. 152:3913-3924, 1994*). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.
- [00165] There is extensive overlap between the A3 and A11 motif primary anchor specificities.
- [00166] **HLA-A24 motif.** The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kondo et al., J. Immunol. 155:4307-4312, 1995; and Kubo et al., J. Immunol. 152:3913-3924, 1994*). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the motif.
- [00167] The primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.
- [00168] **Computer or Manual Screening.** Peptides bearing HLA Class I or Class II supermotifs or motifs may be identified by computer searches or manually, e.g., as follows. In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devèreux, *et al. Nucl. Acids Res. 12:387-395*,

1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

[00169] Translated antigen protein sequences may be analyzed using a text string search software program, *e.g.*, MotifSearch 1.4 (D. Brown, San Diego) to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally.

[00170] Identified supermotif or motif sequences may be scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$"\Delta G" = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (*i.e.*, independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

[00171] The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average

relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

[00172] Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (see, e.g., Milik *et al.*, *Nature Biotechnology* 16:753, 1998; Altuvia *et al.*, *Hum. Immunol.* 58:1, 1997; Altuvia *et al.*, *J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al.*, *Bioinformatics* 14:121-130, 1998; Parker *et al.*, *J. Immunol.* 152:163, 1993; Meister *et al.*, *Vaccine* 13:581, 1995; Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994; Sturniolo *et al.*, *Nature Biotechnol.* 17:555 1999).

[00173] **Conserved, Semi-conserved, and Non-conserved Non-anchor Residues.** The determination of non-anchor residues as being conserved (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative) in comparison to the non-anchor positions of from one to all of the remaining variant(s) is defined by as follows, the results of which are summarized in Table 5.

[00174] Table 5 shows the similarity assignments between any given amino acid pair so that a given amino acid substitution could be characterized as being a (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative) residue.

[00175] The degree of similarity between amino acid pairs was quantified by averaging, for each amino acid pair, the rank coefficient scores for PAM250, hydrophobicity, and side chain volume as described below. Based on the average values of these composite rankings, Table 5 shows each pair to be conserved, semi-conserved or non-conserved.

[00176] The Dayhoff PAM250 score (Dayhoff, M.O., *et al.*, *Atlas of Protein Sequence and Structure*, Vol. 5, suppl.3. (1978) M.O. Dayhoff, ed. National Biomedical Research Foundation, Washington DC, p. 345; Creighton, T.E., *Proteins: structures and molecular properties* (1993) (2nd edition) W.H. Freeman and Company, NY; <http://prowl.rockefeller.edu/aainfo/pam250.html>) is a commonly utilized protein

alignment scoring matrix which measures the percentage of acceptable point mutations (PAM) within a defined time frame. The frequencies of these mutations are different from what would be expected from the probability of random mutations, and presumably reflect a bias due to the degree of physical and chemical similarity of the amino acid pair involved in the substitution. To obtain a score of amino acid similarity that could be standardized with other measures of similarity, the PAM250 scores were converted to a rank value, where 1 indicates the highest probability of being an accepted mutation.

[00177] The most commonly utilized scales to represent the relative hydrophobicity of the 20 naturally occurring amino acids (Cornette, J., *et al.*, *J. Mol. Biol.* (1987) 195:659) are those developed on the basis of experimental data by Kyte and Doolittle (Kyte, J. and R.F. Doolittle, *J. Mol. Biol.* (1982) 157:105), and by Fauchere and Pliska (Fauchere, J. and V. Pliska, *Eur. J. Med. Chem.* (1983) 18:369). The Kyte/Doolittle scale measures the H₂O/organic solvent partition of individual amino acids. Because it considers the position of amino acids in folded proteins, it may most accurately reflect native hydrophobicity in the context of proteins. The Fauchere/Pliska scale measures the octanol/H₂O partitioning of N-acetyl amino acid amides, and most accurately reflects hydrophobicity in the context of denatured proteins and/or small synthetic peptides. To obtain scores for hydrophobicity, each amino acid residue was ranked on both the Kyte/Doolittle and Fauchere/Pliska hydrophobicity scales. An average rank between the two scales was calculated and the average difference in hydrophobicity for each pair was calculated.

[00178] Finally, for calculating amino acid side-chain volume, the partial volume in solution obtained by noting the increase in volume of water after adding either one molecule or one gram of amino acid residue was considered (Zamyatnin, A.A., *Ann. Rev. Biophys. Bioeng.* (1984) 13:145; Zamyatnin, A.A., *Prog. Biophys. Mol. Biol.* (1972) 24:107). The absolute difference in the partial volume of each possible pairing of the 20 naturally occurring amino acids was calculated and ranked, where 1 indicated residues with the most similar volumes, and 20 the most dissimilar.

[00179] Thus, by consulting Table 5, one can determine whether a residue in a variant is considered to be conserved, semi-conserved, or non-conserved in comparison to a residue in another variant(s). The residue of the parent variant (randomly or otherwise chosen variant) is shown across the top of Table 5, and the residue of the variant(s) it is compared with is shown below the parent residue.

[00180] As shown in Table 5, each of the amino acids shown across the top of the table bears a numerically defined relationship to the remaining 19 genetically encoded amino acids. The lower the index, the higher the conservation; the same amino acid will have a similarity assignment of 1.0; maximally different amino acids will have similarity assignments approaching 20. Using the method set forth above, amino acids which are not gene-encoded can also be assigned similarity indices and can be classified with respect to any natively occurring amino acid as conserved (conservative) or semi-conserved (semi-conservative) or non-conserved (non-conservative).

Variant Peptide Epitopes

[00181] In some embodiments, the invention is directed to an isolated peptide comprising or consisting of a variant. In some embodiments, the invention is directed to an isolated polynucleotide encoding such a peptide.

[00182] The isolated variants of the invention are all class I binding peptides, i.e., CTL peptides. In particular, the variants of the invention comprise a motif or supermotif, as described above. Variants of the invention are those set forth in Tables 6-9 and Figures 1A-4 (SEQ ID Nos:__). Variants of the invention may be referred to herein as "variants" and "variant peptide epitopes" or referred to by Table or referred to by SEQ ID NO. Other peptide epitopes are referred to herein as CTL epitopes or CTL peptides and HTL epitopes or HTL peptides.

[00183] **Peptides and Polynucleotides.** In some embodiments, the invention is directed to an isolated peptide comprising or consisting of a variant, wherein the variant consists of a sequence selected from those in Tables 6-9 and Figures 1A-4 (SEQ ID Nos:__).

[00184] Peptides of the invention may be fusion proteins of variant(s) to CTL epitope(s), and/or HTL epitope(s), and/or linker(s), and/or spacer(s), and/or carrier(s), and/or additional amino acid(s), and/or may comprise or consist of homopolymers of a variant or heteropolymers of more than one variant, as is described in detail below.

[00185] Peptides which comprise a variant of the invention may comprise or consist of a fragment of an antigen ("fragment" or "antigenic fragment"), wherein the fragment comprises a variant. The fragment may be a portion of any antigen of an infectious agent, e.g., the sequences in Tables 11-22 (SEQ ID Nos:__, respectively). The variant of the invention may be within the fragment or may be linked, directly or indirectly, to the fragment.

[00186] The fragment may comprise or consist of a region of a native antigen that contains a high concentration of class I and/or class II epitopes, preferably it contains the greatest number of epitopes per amino acid length. Such epitopes can be present in a frame-shifted manner, e.g. a 10

amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope.

[00187] The fragment may be less than or equal to 600 amino acids, less than or equal to 500 amino acids, less than or equal to 400 amino acids, less than or equal to 250 amino acids, less than or equal to 100 amino acids, less than or equal to 85 amino acids, less than or equal to 75 amino acids, less than or equal to 65 amino acids, or less than or equal to 50 amino acids in length. In certain embodiments, a fragment is less than 101 amino acids in length, in any increment down to 5 amino acids in length. For example, the fragment may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100 amino acids in length. Fragments of full length antigens may be fragments from about residue 1-20, 21-40, 41-60, 61-80, 81-100, 101-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-680, 681-700, 701-720, 721-740, 741-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981 to the C-terminus of the antigen.

[00188] Peptides which comprise a variant of the invention may be a fusion protein comprising one or more amino acid residues in addition to the variant or fragment. Fusion proteins include homopolymers and heteropolymers, as described below.

[00189] In some embodiments, the peptide comprises or consists of multiple variants, *e.g.*, 2, 3, 4, 5, 6, 7, 8, or 9 variants of the invention. In some embodiments, the peptide comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 variants of the invention.

[00190] The peptide may also be a homopolymer of one variant or the peptide may be a heteropolymer which contains at least two different variants. Polymers have the advantage of increased probability for immunological reaction and, where different variants are used to make up the polymer, the ability to induce antibodies and/or T cells that react with different antigenic determinants of the antigen(s) targeted for an immune response.

[00191] A homopolymer may comprise 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 copies of the same variant.

[00192] A heteropolymer may comprise one or more copies of an individual variant and one or more copies of one or more different variants of the invention. The variants that form a heteropolymer may all be from the same antigen, *e.g.*, may be from any of those in Tables 11-22

(SEQ ID NOS:_) or other antigens herein or known in the art, or may be from different antigens, preferably from infectious agents. Combinations of variants that may form a heteropolymer include, for example, Gag 545 variants EPLTSLKSLF (SEQ ID NO:_) and YPLASLKSLF (SEQ ID NO:_), or combinations of peptides from different tables in Tables 6-9 and/or Figures 1A-4 or those combinations in Tables 23-28. Heteropolymers may contain multiple copies of one or more variants.

[00193] Thus, peptides of the invention such as heteropolymers may comprise a first variant and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 other (different) variants.

[00194] In some embodiments, the peptide comprising a variant may also comprise a number of CTL and/or HTL epitopes, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 CTL and/or HTL epitopes.

[00195] The CTL and/or HTL epitope and the variant of the invention may be from the same antigen of an infectious agent or from different antigens. Thus, for example, if the variant is from HIV pol, the CTL peptide and/or HTL peptide may also be from HIV pol. Alternatively, if the variant is from HIV pol, the CTL peptide and/or HTL peptide may be from another antigen such as HIV env or HIV vpr. As another example, if the variant is from HBV E6, the CTL peptide and/or HTL peptide may be from HBV E7. The CTL and/or HTL epitope and the variant of the invention may be from the same infectious agent or different infectious agents. Thus, for example, the variant may be from HIV, and the CTL and/or HTL epitope may be from HIV or may be from another infectious agent such as HBV, HCV, HPV, or *Plasmodium falciparum*.

[00196] The CTL peptide and/or HTL peptide may be from other antigens including hepatitis B core and surface antigens (HBVc, HBVs), hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency virus (HIV) antigens and human papilloma virus (HPV) antigens (in particular antigens from HPV-16, HPV-18, HPV-31, HPV-33, HPV-45, HPV-52, HPV-56 and HPV-58, *Mycobacterium tuberculosis* and *Chlamydia*. Examples of suitable fungal antigens include those derived from *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, and *Aspergillus fumigatis*. Examples of suitable protozoan parasitic antigens include those derived from *Plasmodium spp.*, including *P. falciparum*, *Trypanosoma spp.*, *Schistosoma spp.*, *Leishmania spp* and the like.

[00197] Alternatively, the CTL peptide and/or HTL peptide may be from tumor-associated antigens such as but not limited to, melanoma antigens MAGE-1, MAGE-2, MAGE-3, MAGE-11, MAGE-A10, as well as BAGE, GAGE, RAGE, MAGE-C1, LAGE-1, CAG-3, DAM, MUC1, MUC2, MUC18, NY-ESO-1, MUM-1, CDK4, BRCA2, NY-LU-1, NY-LU-7, NY-LU-12,

CASP8, RAS, KIAA-2-5, SCCs, p53, p73, CEA, HER2/neu, Melan-A, gp100, tyrosinase, TRP2, gp75/TRP1, kallikrein, prostate-specific membrane antigen (PSM), prostatic acid phosphatase (PAP), prostate-specific antigen (PSA), PT1-1, β -catenin, PRAME, Telomerase, FAK, cyclin D1 protein, NOEY2, EGF-R, SART-1, CAPB, HPVE7, p15, Folate receptor CDC27, PAGE-1, and PAGE-4.

[00198] Examples of CTL peptides and HTL peptides are disclosed in WO 01/42270, published 14 June 2001; WO 01/41788, published 14 June 2001; WO 01/42270, published 14 June 2001; WO 01/45728, published 28 June 2001; and WO 01/41787, published 14 June 2001.

[00199] The HTL peptide may comprise a "loosely HLA-restricted" or "promiscuous" sequence. Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: 627), *Plasmodium falciparum* CS protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: 628), and Streptococcus 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; SEQ ID NO: 629). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

[00200] The HTL peptide may comprise a synthetic peptide such as a Pan-DR-binding epitope (e.g., a PADRE[®] peptide, Epimmune Inc., San Diego, CA, described, for example, in U.S. Patent Number 5,736,142), for example, having the formula aKXVAAZTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine; "Z" is either tryptophan, tyrosine, histidine or asparagine; and "a" is either D-alanine or L-alanine (SEQ ID NO: 746). Certain pan-DR binding epitopes comprise all "L" natural amino acids; these molecules can be provided as peptides or in the form of nucleic acids that encode the peptide. See also, U.S. Patent Nos. 5,679,640 and 6,413,935.

[00201] The peptide comprising a variant may comprise additional amino acid(s). Such additional amino acids may be Ala, Arg, Asn, Asp, Cys, Gln, Gly, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, Trp, Val, amino acid mimetics, and other unnatural amino acids such as those described below. Additional amino acids may provide for ease of linking peptides one to another, for linking variants to one another, for linking variants to CTL and/or HTL epitopes, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as Ala, Arg, Asn, Asp, Cys, Gln, Gly, Glu, His, Ile, Leu, Lys, Met, Phe,

Pro, Ser, Thr, Tyr, Trp, or Val, or the like, can be introduced at the C- and/or N-terminus of the peptide and/or can be introduced internally.

[00202] The peptide comprising a variant may comprise an amino acid spacer(s), which may be joined to the variants, CTL epitopes, HTL epitopes, carriers, etc. within a peptide or may be joined to the peptide at the N-and/or C-terminus. Thus, spacers may be at the N-terminus or C-terminus of peptide, or may be internal such that they link or join variants, CTL epitopes, HTL epitopes, carriers, additional amino acids, and/or antigenic fragments one to the other.

[00203] The spacer is typically comprised of one or more relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer may be composed of the same residues or may be composed of one or more different residues and thus may be a homo- or hetero-oligomer of spacer residues. Thus, the spacer may contain more than one Ala residue (poly-alanine) or more than one Gly residue (poly-glycine), or may contain both Ala and Gly residues, *e.g.*, Gly, Gly-Gly-, Ser, Ser-Ser-, Gly-Ser-, Ser-Gly-, etc. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues, *e.g.*, 3, 4, 5, 6, 7, 8, 9, or 10, or even more residues. (Livingston, B.D. *et al. Vaccine* 19:4652-4660 (2000)).

[00204] Peptides comprising a variant may comprise carrier(s) such as those well known in the art, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like. (See Table 29).

[00205] In addition, the peptide comprising or consisting of a variant may be modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

[00206] The peptides in accordance with the invention can contain modifications such as but not limited to glycosylation, side chain oxidation, biotinylation, phosphorylation, addition of a surface active material, *e.g.* a lipid, or can be chemically modified, *e.g.*,

acetylation, *etc.* Moreover, bonds in the peptide can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds, *etc.*

[00207] Peptides of the present invention may contain substitutions to modify a physical property (*e.g.*, stability or solubility) of the resulting peptide. For example, peptides may be modified by the substitution of a cysteine (C) with α -amino butyric acid ("B"). Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding and crossbinding capability in certain instances. Substitution of cysteine with α -amino butyric acid may occur at any residue of a peptide, *e.g.*, at either anchor or non-anchor positions of a variant within a peptide, or at other positions of a peptide.

[00208] The peptides comprising a variant can comprise amino acid mimetics or unnatural amino acids, *e.g.* D- or L-naphylalanine; D- or L-phenylglycine; D- or L-2-thieneylalanine; D- or L-1, -2, 3, or 4-pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-*p*-fluorophenylalanine; D- or L-*p*-biphenylphenylalanine; D- or L-*p*-methoxybiphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylalanines, where the alkyl group can be a substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, *e.g.*, thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings. Modified peptides that have various amino acid mimetics or unnatural amino acids are particularly useful, as they tend to manifest increased stability *in vivo*. Such peptides may also possess improved shelf-life or manufacturing properties.

[00209] Peptide stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. *See, e.g.*, Verhoef, *et al.*, *Eur. J. Drug Metab. Pharmacokinetics* 11:291 (1986). Half-life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows: Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI-1640 or another suitable tissue culture medium. At predetermined time intervals, a small amount of reaction solution is removed and added to

either 6% aqueous trichloroacetic acid (TCA) or ethanol. The cloudy reaction sample is cooled (4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

[00210] As indicated above, the peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention can contain modifications such as glycosylation, side chain oxidation, or phosphorylation, generally subject to the condition that modifications do not destroy the biological activity of the peptides.

[00211] The peptides of the invention may be lyophilized, or may be in crystal form.

[00212] It is generally preferable that the variant peptide epitope be as small as possible while still maintaining substantially all of the immunologic activity of the native protein. When possible, it may be desirable to optimize HLA class I binding epitopes of the invention to a length of about 8 to about 13 amino acid residues, for example, 8, 9, 10, 11, 12 or 13, preferably 8 to 11 or 9 to 10. It is to be appreciated that one or more epitopes in this size range can be comprised by a longer peptide (see the Definition Section for the term "epitope" for further discussion of peptide length). HLA class II binding epitopes are preferably optimized to a length of about 6 to about 30 amino acids in length, *e.g.*, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30, preferably to between about 13 and about 20 residues, *e.g.*, 13, 14, 15, 16, 17, 18, 19 or 20. Preferably, the epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules. The identification and preparation of peptides of various lengths can be carried out using the techniques described herein.

[00213] Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or can be isolated from natural sources such as native tumors or pathogenic organisms. Epitopes may be synthesized individually or joined directly or indirectly in a peptide. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to be joined to native fragments or particles.

[00214] The peptides of the invention can be prepared in a wide variety of ways. For relatively short sizes, the peptides can be synthesized in solution or on a solid support in

accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (See, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptides can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

[00215] Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes a peptide inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant peptides, which comprise or consist of one or more epitopes of the invention, can be used to present the appropriate T cell epitope.

[00216] Polynucleotides encoding each of the peptides above are also part of the invention. As appreciated by one of ordinary skill in the art, various nucleic acids will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acids falls within the scope of the present invention. This embodiment of the invention comprises DNA and RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any polynucleotide that encodes a peptide in accordance with the invention falls within the scope of this invention.

[00217] The polynucleotides encoding peptides contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Polynucleotides encoding peptides comprising or consisting of a variant can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode a related (e.g., analogous) epitope.

[00218] The polynucleotide, e.g. minigene (see below), may be produced by assembling oligonucleotides that encode the plus and minus strands of the polynucleotide, e.g. minigene. Overlapping oligonucleotides (15-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. A polynucleotide, e.g. minigene, encoding the peptide of the invention, can be cloned into a desired vector such as an expression vector. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly

available in the art, and the vectors used to transform suitable hosts to produce the desired peptide such as a fusion protein.

[00219] A large number of such vectors and suitable host systems are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, phagescript, psiX174, pBluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); pCR (Invitrogen). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia); p75.6 (valentis); pCEP (Invitrogen); pCEI (Epimmune). However, any other plasmid or vector can be used as long as it is replicable and viable in the host.

[00220] As representative examples of appropriate hosts, there can be mentioned: bacterial cells, such as *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*; fungal cells, such as yeast; insect cells such as *Drosophila* and Sf9; animal cells such as COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines or Bowes melanoma; plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

[00221] Thus, the present invention is also directed to vectors, preferably expression vectors useful for the production of the peptides of the present invention, and to host cells comprising such vectors.

[00222] Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which can be, for example, a cloning vector or an expression vector. The vector can be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the polynucleotides. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[00223] For expression of the peptides, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For

example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts.

[00224] Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), α -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

[00225] Yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. Such promoters may also be derived from viral sources, such as, *e.g.*, human cytomegalovirus (CMV-IE promoter) or herpes simplex virus type-1 (HSV TK promoter). Nucleic acid sequences derived from the SV40 splice, and polyadenylation sites can be used to provide the required nontranscribed genetic elements.

[00226] Polynucleotides encoding peptides of the invention may also comprise a ubiquitination signal sequence, and/or a targeting sequence such as an endoplasmic reticulum (ER) signal sequence to facilitate movement of the resulting peptide into the endoplasmic reticulum.

[00227] Polynucleotides of the invention, *e.g.*, minigenes, may be expressed in human cells. A human codon usage table can be used to guide the codon choice for each amino

acid. Such polynucleotides preferably comprise spacer amino acid residues between variants, such as those described above, or may comprise naturally-occurring flanking sequences adjacent to the variants (and/or CTL and HTL epitopes).

[00228] The peptides of the invention can also be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. As an example of this approach, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the polypeptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein. A preferred vector is Modified Vaccinia Ankara (MVA) (*e.g.*, Bavarian Noridic (MVA-BN)).

[00229] Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the human target cells. Several vector elements are desirable: a promoter with a downstream cloning site for polynucleotide, *e.g.*, minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences. A preferred promoter is the CMV-IE promoter.

[00230] Polynucleotides, *e.g.* minigenes, may comprise one or more synthetic or naturally-occurring introns in the transcribed region. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing polynucleotide, *e.g.* minigene, expression.

[00231] In addition, the polynucleotide, *e.g.* minigene, may comprise immunostimulatory sequences (ISSs or CpGs). These sequences may be included in the vector, outside the polynucleotide (*e.g.* minigene) coding sequence to enhance immunogenicity.

[00232] In some embodiments, a bi-cistronic expression vector which allows production of both the polynucleotide- (*e.g.* minigene-) encoded peptides of the invention and a second protein (*e.g.*, one that modulates immunogenicity) can be used. Examples of proteins or

polypeptides that, if co-expressed with peptides of the invention, can enhance an immune response include cytokines (e.g., IL-2, IL-12, GM-CSF), cytokine-inducing molecules (e.g., LeIF), costimulatory molecules, or pan-DR binding proteins (PADRE[®] molecules, Epimmune, San Diego, CA). Helper T cell (HTL) epitopes such as PADRE[®] molecules can be joined to intracellular targeting signals and expressed separately from expressed peptides of the invention. Specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

[00233] Once an expression vector is selected, the polynucleotide, e.g. minigene, is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the polynucleotide, e.g. minigene, as well as all other elements included in the vector, are confirmed using restriction mapping, DNA sequence analysis, and/or PCR analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.

[00234] Therapeutic/prophylactic quantities of DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and are grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA is purified using standard bioseparation technologies such as solid phase anion-exchange resins available, e.g., from QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

[00235] Purified polynucleotides, e.g. minigenes, can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized polynucleotide, e.g. DNA, in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of polynucleotide vaccines, alternative methods of formulating purified plasmid DNA may be used. A variety of such methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, e.g., WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Patent No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) can also be complexed to purified plasmid DNA to

influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00236] Known methods in the art can be used to enhance delivery and uptake of a polynucleotide *in vivo*. For example, the polynucleotide can be complexed to polyvinylpyrrolidone (PVP), to prolong the localized bioavailability of the polynucleotide, thereby enhancing uptake of the polynucleotide by the organism (*see e.g.*, U.S. Patent No. 6,040,295; EP 0 465 529; WO 98/17814). PVP is a polyamide that is known to form complexes with a wide variety of substances, and is chemically and physiologically inert.

[00237] Target cell sensitization can be used as a functional assay of the expression and HLA class I presentation of polynucleotide- (e.g. minigene-) encoded peptides. For example, the polynucleotide, e.g. plasmid DNA, is introduced into a mammalian cell line that is a suitable target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. For example, electroporation can be used for "naked" DNA, whereas cationic lipids or PVP-formulated DNA allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). The transfected cells are then chromium-51 (^{51}Cr) labeled and used as targets for epitope-specific CTLs. Cytolysis of the target cells, detected by ^{51}Cr release, indicates both production and HLA presentation of, polynucleotide-, e.g. minigene-, encoded variants of the invention, or peptides comprising them. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTI activity.

[00238] *In vivo* immunogenicity is a second approach for functional testing of polynucleotides, e.g. minigenes. Transgenic mice expressing appropriate human HLA proteins are immunized with the polynucleotide, e.g. DNA, product. The dose and route of administration are formulation dependent (*e.g.*, IM for polynucleotide (*e.g.*, naked DNA or PVP-formulated DNA) in PBS, intraperitoneal (IP) for lipid-complexed polynucleotide (*e.g.*, DNA)). Eleven to twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of polynucleotides encoding each peptide being tested. Thereafter, for peptides comprising or consisting of variants, standard assays are conducted to determine if there is cytolysis of peptide-loaded, ^{51}Cr -labeled target cells. Once again, lysis of target cells that were exposed to variants corresponding to those encoded by the polynucleotide (e.g. minigene) demonstrates polynucleotide (e.g., DNA)

vaccine function and induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

[00239] Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of a polynucleotide such as DNA are administered. In a further alternative embodiment for ballistic delivery, polynucleotides such as DNA can be adhered to particles, such as gold particles.

[00240] The use of polynucleotides such as multi-epitope minigenes is described herein and in, e.g. co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a polynucleotide such as a multi-epitope DNA plasmid can be engineered which encodes an epitope derived from multiple regions of a infectious agent (e.g., p53, HER2/nev, MAGE-2/3, or CEA), a pan-DR binding peptide such as the PADRE® universal helper T cell epitope, and an endoplasmic reticulum-translocating signal sequence. As described in the sections above, a peptide/polynucleotide may also comprise/encode epitopes that are derived from other infectious agents.

[00241] Thus, the invention includes peptides as described herein, polynucleotides encoding each of said peptides, as well as compositions comprising the peptides and polynucleotides, and includes methods for producing and methods of using the peptides, polynucleotides, and compositions, as further described below.

[00242] **Compositions.** In other embodiments, the invention is directed to a composition comprising one or more peptides and/or polynucleotides of the invention and optionally another component(s).

[00243] In some embodiments, the composition comprises or consists of multiple peptides, e.g., 2, 3, 4, 5, 6, 7, 8, or 9 peptides of the invention. In some embodiments, the composition comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 peptides of the invention. Combinations of peptides include, for example, a peptide comprising or alternatively consisting of the Gag 545 variant EPLTSLKSLF (SEQ ID NO:_) and a peptide comprising or alternatively consisting of the Gag 545 variant YPLASLKSLF (SEQ ID NO:_), or combinations of peptides from different tables in Tables 6-9 and/or Figures 1A-4.

[00244] Compositions of the invention may comprise polynucleotides encoding the above peptides and/or combinations of peptides.

[00245] The composition can comprise at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 peptides and/or polynucleotides selected from those described above or below. At least one of the one or more peptides can be a heteropolymer or a homopolymer. Additionally, the composition can comprise a CTL and/or HTL epitope, which can be derived from a tumor-associated antigen. The additional epitope can also be a PanDR binding molecule, (*e.g.*, a PADRE® universal helper T cell epitope).

[00246] Optional components include excipients, diluents, proteins such as peptides comprising a CTL epitope, and/or an HTL epitope such as a pan-DR binding peptide (*e.g.*, a PADRE® universal helper T cell epitope), and/or a carrier, polynucleotides encoding such proteins, lipids, or liposomes, as well as other components described herein. There are numerous embodiments of compositions in accordance with the invention, such as a cocktail of one or more peptides and/or polynucleotides (*e.g.*, minigenes); a cocktail of one or more peptides and/or polynucleotides (*e.g.*, minigenes) and one or more CTL and/or HTL epitopes.

[00247] Compositions may comprise one or more peptides (and/or polynucleotides such as minigenes) of the invention, along with one or more other components as described above and herein. "One or more" refers to any whole unit integer from 1-150, *e.g.*, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 peptides, polynucleotides, or other components.

[00248] Compositions of the invention may be, for example, polynucleotides or polypeptides of the invention combined with or complexed to cationic lipid formulations; lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), encapsulated *e.g.*, in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995); peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998); multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996); viral, bacterial, or, fungal delivery vectors (Perkus, M. E. *et*

al., In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990); particles of viral or synthetic origin (e.g., Kofler, N. *et al.*, *J. Immunol. Methods* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995); adjuvants (e.g., incomplete Freund's adjuvant) (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993); liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996); or, particle-absorbed cDNA or other polynucleotides of the invention (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993), etc. Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) or attached to a stress protein, e.g., HSP 96 (Stressgen Biotechnologies Corp., Victoria, BC, Canada) can also be used.

[00249] Compositions of the invention comprise polynucleotide-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and, WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers (e.g., PVP, PNC, etc.), peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687). Accordingly, peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as Modified Vaccinia Ankara (MVA) (e.g., Bavarian Noridic), vaccinia or fowlpox. For example, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin).

BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, alpha virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, are apparent to those skilled in the art from the description herein.

[00250] In certain embodiments, components that induce T cell responses are combined with components that induce antibody responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. Alternatively, a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE[®] molecule (Epimmune, San Diego, CA).

[00251] Compositions of the invention can comprise antigen presenting cells, such as dendritic cells. Antigen presenting cells, *e.g.*, dendritic cells, may be transfected, *e.g.*, with a polynucleotide such as a minigene construct in accordance with the invention, in order to elicit immune responses. The peptide can be bound to an HLA molecule on the antigen-presenting cell, whereby when an HLA-restricted cytotoxic T lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the peptide.

[00252] The compositions of the invention may also comprise antiviral drugs such as interferon- α , or immune adjuvants such as IL-12, GM-CSF, etc.

[00253] Compositions may comprise an HLA heavy chain, β_2 -microglobulin, streptavidin, and/or biotin. The streptavidin may be fluorescently labeled. Compositions may comprise tetramers (*see e.g.*, U.S. Pat. No. 5,635,363; *Science* 274:94-96 (1996)). A tetramer composition comprising an HLA heavy chain, β_2 -microglobulin, streptavidin, and biotin. The streptavidin may be fluorescently labeled. Compositions may also comprise dimers. A dimer composition comprises as MHC molecule and an Ig molecule (*see e.g.*, *PNAS* 95:7568-73 (1998)).

[00254] In some embodiments it may be desirable to include in the compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or

emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. A preferred composition comprises palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the peptide.

[00255] As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P_3 CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3 CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3 CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

[00256] Another preferred embodiment is a composition comprising one or more peptides of the invention emulsified in IFA.

[00257] Compositions of the invention may also comprise CTL and/or HTL peptides. Such CTL and HTL peptides can be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or naturally or unnaturally occurring amino acid residues, can be introduced at the carboxyl- or amino-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule. CTL and HTL epitopes may comprise additional amino acids, such as those described above including spacers.

[00258] A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more peptides in accordance with the invention. The antigen presenting cell can be a "professional" antigen presenting cell, such as a dendritic cell. The antigen presenting cell can comprise the peptide of the invention by any means known or to be determined in the art. Such means include pulsing

of dendritic cells with one or more individual peptides, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

[00259] Compositions may comprise carriers. Carriers that can be used with compositions of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like.

[00260] The compositions (*e.g.* pharmaceutical compositions) can contain a physiologically tolerable diluent such as water, or a saline solution, preferably phosphate buffered saline. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glyceryl-cysteinyl-seryl-serine (P₃CSS).

[00261] Compositions of the invention may be pharmaceutically acceptable compositions. Pharmaceutical compositions preferably contain an immunologically effective amount of one or more peptides and/or polynucleotides of the invention, and optionally one or more other components which are pharmaceutically acceptable. A preferred composition comprises one or more peptides of the invention and IFA. A more preferred composition of the invention comprises one or more peptides of the invention, one or more peptides, and IFA.

[00262] Upon immunization with a peptide and/or polynucleotide and/or composition in accordance with the invention, via injection (*e.g.*, SC, ID, IM), aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by an immune response comprising the production of antibodies, CTLs and/or HTLs specific for the desired antigen(s). Consequently, the host becomes at least partially immune to subsequent exposure to the infectious agent(s), or at least partially resistant to further development of infectious agent-bearing cells and thereby derives a prophylactic or therapeutic benefit.

[00263] Furthermore, the peptides, primers, and epitopes of the invention can be used in any desired immunization or administration regimen; *e.g.*, as part of periodic vaccinations such as annual vaccinations as in the veterinary arts or as in periodic vaccinations as in the human medical arts, or as in a prime-boost regime wherein an inventive vector or recombinant is administered either before or after the administration of the same or of a different epitope of interest or recombinant or vector expressing such as a same or different epitope of interest (including an inventive recombinant or vector expressing such

as a same or different epitope of interest), see, e.g., U.S. Pat. Nos. 5,997,878; 6,130,066; 6,180,398; 6,267,965; and 6,348,450. An useful viral vector of the present invention is Modified Vaccinia Ankara (MVA) (e.g., Bavarian Noridic (MVA-BN)).

[00264] Recent studies have indicated that a prime-boost protocol, whereby immunization with a poxvirus recombinant expressing a foreign gene product is followed by a boost using a purified subunit preparation form of that gene product, elicits an enhanced immune response relative to the response elicited with either product alone. Human volunteers immunized with a vaccinia recombinant expressing the HIV-1 envelope glycoprotein and boosted with purified HIV-1 envelope glycoprotein subunit preparation exhibit higher HIV-1 neutralizing antibody titers than individuals immunized with just the vaccinia recombinant or purified envelope glycoprotein alone (Graham *et al.*, *J. Infect. Dis.*, 167:533-537 (1993); Cooney *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:1882-1886 (1993)). Humans immunized with two injections of an ALVAC-HIV-1 env recombinant (vCP125) failed to develop HIV specific antibodies. Boosting with purified rgp160 from a vaccinia virus recombinant resulted in detectable HIV-1 neutralizing antibodies. Furthermore, specific lymphocyte T cell proliferation to rgp160 was clearly increased by the boost with rgp160. Envelope specific cytotoxic lymphocyte activity was also detected with this vaccination regimen (Pialoux *et al.*, *AIDS Res. and Hum. Retroviruses*, 11:272-381 (1995)). Macaques immunized with a vaccinia recombinant expressing the simian immunodeficiency virus (SIV) envelope glycoprotein and boosted with SIV envelope glycoprotein from a baculovirus recombinant are protected against SIV challenge (Hu *et al.*, *AID Res. and Hum. Retroviruses*, 3:615-620 (1991); Hu *et al.*, *Science* 255:456-459 (1992)). In the same fashion, purified HCMVgB protein can be used in prime-boost protocols with NYVAC or ALVAC-gB recombinants.

[00265] In certain embodiments, the polynucleotides are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:74137416 (1987), which is herein incorporated by reference); mRNA (Malone *et al.*, *Proc. Natl. Acad. Sci. USA* 86:60776081 (1989), which is herein incorporated by reference); and purified transcription factors (Debs *et al.*, *J. Biol.*

Chem. 265:1018910192 (1990), which is herein incorporated by reference), in functional form.

- [00266] Cationic liposomes are readily available. For example, N-[12,3-dioleoyloxy]-propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner *et al.*, *Proc. Natl Acad. Sci. USA* 84:74137416 (1987)). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).
- [00267] Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner *et al.*, *Proc. Natl. Acad. Sci. USA* 84:74137417. Similar methods can be used to prepare liposomes from other cationic lipid materials.
- [00268] Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.
- [00269] For example, commercially available dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

[00270] The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The various liposome nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger *et al.*, *Methods of Immunology* 101:512527 (1983). For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include Ca^{2+} -EDTA chelation (Papahadjopoulos *et al.*, *Biochim. Biophys. Acta* 394:483 (1975); Wilson *et al.*, *Cell* 17:77 (1979)); ether injection (Deamer, D. and Bangham, A., *Biochim. Biophys. Acta* 443:629 (1976); Ostro *et al.*, *Biochem. Biophys. Res. Commun.* 76:836 (1977); Fraley *et al.*, *Proc. Natl. Acad. Sci. USA* 76:3348 (1979)); detergent dialysis (Enoch, H. and Strittmatter, P., *Proc. Natl. Acad. Sci. USA* 76:145 (1979)); and reversephase evaporation (REV) (Fraley *et al.*, *J. Biol. Chem.* 255:10431 (1980); Szoka, F. and Papahadjopoulos, D., *Proc. Natl. Acad. Sci. USA* 75:145 (1978); SchaeferRidder *et al.*, *Science* 215:166 (1982)).

[00271] Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

[00272] U.S. Patent No. 5,676,954 reports on the injection of genetic material, complexed with cationic liposome carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 provide methods for delivering DNA-cationic lipid complexes to mammals.

Binding Affinity of Variants for HLA Molecules

- [00273] As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to developing therapeutics and diagnostics. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules. However, in some embodiments, it is preferred that all epitopes in a given composition bind to the alleles of a single HLA supertype or a single HLA molecule.
- [00274] Variants of the invention preferably include those that have an IC_{50} or binding affinity value for a class I HLA molecule(s) of 500 nM or better (*i.e.*, the value is ≤ 500 nM). In certain embodiments of the invention, peptides of interest have an IC_{50} or binding affinity value for a class I HLA molecule(s) of 200 nM or better. In certain embodiments of the invention, peptides of interest, such as A1 and A24 peptides, have an IC_{50} or binding affinity value for a class I HLA molecule(s) of 100 nM or better. If HTL epitopes are included, they preferably are HTL epitopes that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is $\leq 1,000$ nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are generally tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.
- [00275] The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens was determined for the first time by inventors at Epimmune. As disclosed in greater detail herein, higher HLA binding affinity is correlated with greater immunogenicity.
- [00276] Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance

with these principles, close to 90% of high binding peptides have been found to elicit a response and thus be "immunogenic," as contrasted with about 50% of the peptides that bind with intermediate affinity. (See, e.g., Schaeffer *et al.* PNAS (1988)) High affinity-binding class I peptides generally have an affinity of less than or equal to 100 nM. Moreover, not only did peptides with higher binding affinity have an enhanced probability of generating an immune response, the generated response tended to be more vigorous than the response seen with weaker binding peptides. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used rather than a lower affinity one. Thus, in some preferred embodiments of the invention, high affinity binding epitopes are used.

[00277] The correlation between binding affinity and immunogenicity was analyzed by the present inventors by two different experimental approaches (*see, e.g., Sette, et al., J. Immunol.* 153:5586-5592 (1994)). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g., Schaeffer et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653 (1989)).

[00278] An affinity threshold associated with immunogenicity in the context of HLA class II (*i.e.*, HLA DR) molecules has also been delineated (*see, e.g., Southwood et al. J. Immunology* 160:3363-3373 (1998), and U.S. Patent No. 6,413,527, issued July 2, 2002). In order to define a biologically significant threshold of HLA class II binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the epitope) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC₅₀

of 1000 nM or greater. Thus, 1000 nM is defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

[00279] The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

Enhancing Population Coverage of the Vaccine

[00280] The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs are summarized in Tables 1-2. Allele-specific HLA molecules that are comprised by the various HLA class I supertypes are listed in Table 4. In some cases, patterns of amino acid residues are present in both a motif and a supermotif. The relationship of a particular motif and any related supermotif is indicated in the description of the individual motifs.

[00281] By inclusion of one or more epitopes from several motifs or supermotifs in a vaccine composition, enhanced population coverage for major global ethnicities can be obtained.

Assays to Detect T-Cell Responses

[00282] Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to relevant HLA proteins. These assays may involve evaluation of peptide binding to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* cell surface HLA molecules that lack any bound peptide) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to an HLA class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL

responses that can give rise to CTL populations capable of reacting with selected target cells associated with pathology.

[00283] Analogous assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

[00284] Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant, non-human mammalian cell lines that have been transfected with a human class I MHC gene, and that are deficient in their ability to load class I molecules with internally processed peptides, are used to evaluate the capacity of the peptide to induce *in vitro* primary CTL responses. Peripheral blood mononuclear cells (PBMCs) can be used as the source of CTL precursors. Antigen presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that lyse radio-labeled target cells, either specific peptide-pulsed targets or target cells that express endogenously processed antigen from which the specific peptide was derived. Alternatively, the presence of epitope-specific CTLs can be determined by IFN γ *in situ* ELISA.

[00285] In an embodiment of the invention, directed to diagnostics, a method has been devised which allows direct quantification of antigen-specific T cells by staining with fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other options include staining for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998). Additionally, DimerX technology can be used as a means of quantitation (*see, e.g.*, *Science* 274:94-99 (1996) and *Proc. Natl. Acad. Sci.* 95:7568-73 (1998)).

- [00286] HTL activation may also be assessed using techniques known to those in the art, such as T cell proliferation or lymphokine secretion (*see, e.g. Alexander et al., Immunity* 1:751-761, 1994).
- [00287] Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse strains, *e.g.*, mice with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized. Other transgenic mice strains (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. Moreover, HLA-DR1 and HLA-DR3 mouse models have been developed. In accordance with principles in the art, additional transgenic mouse models with other HLA alleles are generated as necessary.
- [00288] Such mice can be immunized with peptides emulsified in Incomplete Freund's Adjuvant; thereafter any resulting T cells can be tested for their capacity to recognize target cells that have been peptide-pulsed or transfected with genes encoding the peptide of interest. CTL responses can be analyzed using cytotoxicity assays described above. Similarly, HTL responses can be analyzed using, *e.g.*, T cell proliferation or lymphokine secretion assays.

Minigenes

- [00289] A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding multiple epitopes are a useful embodiment of the invention; discrete peptide epitopes or polyepitopic peptides can be encoded. The epitopes to be included in a minigene are preferably selected according to the guidelines set forth in the previous section. Examples of amino acid sequences that can be included in a minigene include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or a targeting sequence such as an endoplasmic reticulum (ER) signal sequence to facilitate movement of the resulting peptide into the endoplasmic reticulum. Examples of minigene constructs are shown in Tables 23-28.
- [00290] The use of multi-epitope minigenes is also described in, *e.g.*, co-pending applications U.S.S.N. 09/311,784, 09/894,018, 60/419,973, 60/415,463; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid

encoding nine dominant HLA-A*0201- and A11-restricted CTL epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), a PADRE® universal helper T cell (HTL) epitope, and an endoplasmic reticulum-translocating signal sequence has been engineered. Immunization of HLA transgenic mice with this plasmid construct resulted in strong CTL induction responses against the nine CTL epitopes tested. This CTL response was similar to that observed with a lipopeptide of known immunogenicity in humans, and significantly greater than immunization using peptides in oil-based adjuvants. Moreover, the immunogenicity of DNA-encoded epitopes *in vitro* was also correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. These data show that the minigene served: 1.) to generate a CTL response and 2.) to generate CTLs that recognized cells expressing the encoded epitopes. A similar approach can be used to develop minigenes encoding epitopes of an infectious agent.

[00291] For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous peptide sequence is created. However, to optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design such as spacer amino acid residues between epitopes. HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention. In one embodiment, spacer amino acid residues between one or more CTL and/or HTL epitopes are designed so as to minimize junctional epitopes that may result from the juxtaposition of 2 CTL and/or HTL epitopes.

[00292] The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope peptide, can then be cloned into a desired expression vector.

- [00293] Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a downstream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) CMV-IE promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.
- [00294] Optimized peptide expression and immunogenicity can be achieved by certain modifications to a minigene construct. For example, in some cases introns facilitate efficient gene expression, thus one or more synthetic or naturally-occurring introns can be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.
- [00295] Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping, PCR and/or DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.
- [00296] In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence to enhance immunogenicity.
- [00297] In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (*e.g.*, one that modulates immunogenicity) can be used. Examples of proteins or polypeptides that, if co-expressed with epitopes, can enhance an immune response include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or pan-DR binding proteins (PADRE[®], Epimmune, San Diego, CA). Helper T cell (HTL) epitopes such as PADRE[®] molecules can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes. This can be done in order to direct HTL epitopes to a cell compartment different than that of the CTL epitopes, one that provides for more efficient entry of HTL epitopes into the HLA class II pathway, thereby

improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

[00298] Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and are grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA is purified using standard bioseparation technologies such as solid phase anion-cxchange resins available, e.g., from QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

[00299] Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene vaccines, alternative methods of formulating purified plasmid DNA may be used. A variety of such methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, e.g., WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Patent No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) can also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00300] Known methods in the art can be used to enhance delivery and uptake of a polynucleotide *in vivo*. For example, the polynucleotide can be complexed to polyvinylpyrrolidone (PVP), to prolong the localized bioavailability of the polynucleotide, thereby enhancing uptake of the polynucleotide by the organism (see e.g., U.S. Patent No. 6,040,295; EP 0 465 529; WO 98/17814). PVP is a polyamide that is known to form complexes with a wide variety of substances, and is chemically and physiologically inert.

[00301] Target cell sensitization can be used as a functional assay of the expression and HLA class I presentation of minigene-encoded epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is a suitable target for standard CTL chromium release assays. The transfection method used will be dependent on the final

formulation, electroporation can be used for "naked" DNA, whereas cationic lipids or DNA:PVP compositions allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). The transfected cells are then chromium-51 (^{51}Cr) labeled and used as targets for epitope-specific CTLs. Cytolysis of the target cells, detected by ^{51}Cr release, indicates both the production and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

[00302] *In vivo* immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Eleven to twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTLs, standard assays are conducted to determine if there is cytolysis of peptide-loaded, ^{51}Cr -labeled target cells. Once again, lysis of target cells that were exposed to epitopes corresponding to those in the minigene, demonstrates DNA vaccine function and induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

[00303] Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment for ballistic delivery, DNA can be adhered to particles, such as gold particles.

Vaccine Compositions

[00304] Vaccines that contain an immunologically effective amount of one or more peptides or polynucleotides of the invention are a further embodiment of the invention. The peptides can be delivered by various means or formulations, all collectively referred to as "vaccine" compositions. Such vaccine compositions, and/or modes of administration, can include, for example, naked DNA, DNA formulated with PVP, DNA in cationic lipid formulations; lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), DNA or peptides, encapsulated *e.g.*, in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*,

Vaccine 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995); peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998); multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996); viral, bacterial, or, fungal delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990); particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995); adjuvants (*e.g.*, incomplete freund's adjuvant) (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993); liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996); or, particle-absorbed DNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993), etc. Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) or attached to a stress protein, *e.g.*, HSP 96 (Stressgen Biotechnologies Corp., Victoria, BC, Canada) can also be used.

[00305] Vaccines of the invention comprise nucleic acid mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and, WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers (*e.g.*, PVP), peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687). Accordingly, peptide vaccines of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. For example, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention

(e.g., MVA). Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g. adeno and adeno-associated virus vectors, alpha virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, are apparent to those skilled in the art from the description herein.

[00306] Furthermore, vaccines in accordance with the invention can comprise one or more peptides of the invention. Accordingly, a peptide can be present in a vaccine individually; alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased probability for immunological reaction and, where different peptide epitopes are used to make up the polymer, the ability to induce antibodies and/or T cells that react with different antigenic determinants of the antigen targeted for an immune response. The composition may be a naturally occurring region of an antigen or can be prepared, e.g., recombinantly or by chemical synthesis.

[00307] Carriers that can be used with vaccines of the invention are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza virus proteins, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable diluent such as water, or a saline solution, preferably phosphate buffered saline. Generally, the vaccines also include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glyceryl-cysteinyl-serine (P₃CSS).

[00308] Upon immunization with a peptide composition in accordance with the invention, via injection (e.g., SC, ID, IM), aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing antibodies, CTLs and/or HTLs specific for the desired antigen.

Consequently, the host becomes at least partially immune to subsequent exposure to the infectious agent, and thereby derives a prophylactic or therapeutic benefit.

[00309] In certain embodiments, components that induce T cell responses are combined with components that induce antibody responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. Alternatively, a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE[®] molecule (Epimmune, San Diego, CA).

[00310] Vaccines of the invention can comprise antigen presenting cells, such as dendritic cells, as a vehicle to present peptides of the invention. For example, dendritic cells are transfected, *e.g.*, with a minigene construct in accordance with the invention, in order to elicit immune responses. Minigenes are discussed in greater detail in a following section. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*.

[00311] The vaccine compositions of the invention may also be used in combination with antiviral drugs such as interferon- α , or immune adjuvants such as IL-12, GM-CSF, etc.

[00312] Preferably, the following principles are utilized when selecting epitope(s) and/or analogs for inclusion in a vaccine, either peptide-based or nucleic acid-based formulations. Exemplary variants that may be utilized in a vaccine to treat or prevent infectious agent-mediated disease are set out in Tables 6-9 and Figures 1A-4. Each of the following principles can be balanced in order to make the selection. When multiple epitopes are to be used in a vaccine, the epitopes may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived. Such multiple epitopes can refer to the order of epitopes within a peptide, or to the selection of epitopes that come from the same region, for use in either individual peptides or in a multi-epitopic peptide.

1.) Variants are selected which, upon administration, mimic immune responses that have been observed to be correlated with prevention or clearance of infectious disease. For HLA Class I, this generally includes 3-7 variants from at least one infectious agent or antigen thereof.

2.) Variants are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC₅₀ of 500 nM or less, or for Class II an IC₅₀ of 1000 nM or less. For HLA Class I it is presently preferred to select a peptide having an IC₅₀ of 200 nM or less, as this is believed to better correlate not only to induction of an immune response, but to *in vitro* tumor cell killing as well. For HLA A1 and A24, it is especially preferred to select a peptide having an IC₅₀ of 100 nM or less.

3.) Supermotif bearing-variants, or a sufficient array of allele-specific motif-bearing variants, are selected to give broad population coverage. In general, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth of population coverage.

4.) Of particular relevance are "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. For example, a nested epitope can be a fragment of an antigen from a region that contains multiple epitopes that are overleapping, or one epitope that is completely encompassed by another, *e.g.*, A2 peptides MAGE3.159 and MAGE3.160 are nested epitopes. A peptide comprising "transcendent nested epitopes" is a peptide that has both HLA class I and HLA class II epitopes in it. When providing nested epitopes, it is preferable to provide a sequence that has the greatest number of epitopes per provided sequence. Preferably, one avoids providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a sequence comprising nested epitopes, it is important to evaluate the sequence in order to insure that it does not have pathological or other deleterious biological properties; this is particularly relevant for vaccines directed to infectious organisms.

5.) If a protein with multiple epitopes or a polynucleotide (*e.g.*, minigene) is created, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial peptide comprising multiple epitopes, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polypeptidic protein. Spacer amino acid residues can be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

[00313] The principles are the same, except junctional epitopes applies to the sequences surrounding the epitope. One must also take care with other sequences in construct to avoid immune response.

T CELL PRIMING MATERIALS

[00314] In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T

lymphocytes. Lipids have been identified as agents capable of facilitating the priming *in vitro* CTL response against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α - amino groups of a lysine residue and then linked to an immunogenic peptide. One or more linking moieties can be used such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like. The lipidated peptide can then be administered directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. A preferred immunogenic composition comprises palmitic acid attached to ϵ - and α - amino groups of Lys via a linking moiety, *e.g.*, Ser-Ser, added to the amino terminus of an immunogenic peptide.

[00315] In another embodiment of lipid-facilitated priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glyceryl-cysteinyl-seryl-serine (P_3CSS) can be used to prime CTL when covalently attached to an appropriate peptide. (*See, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Thus, peptides of the invention can be coupled to P_3CSS , and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3CSS -conjugated epitopes, two such compositions can be combined to elicit both humoral and cell-mediated responses.

DENDRITIC CELLS PULSED WITH CTL AND/OR HTL PEPTIDES

[00316] An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoiectin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes in HLA molecules on their surfaces.

[00317] The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to one or more antigens of interest, *e.g.*, antigens from infectious agents such as HIV env, HIV pol, HIV gag, HIV vpu, HBV and/or the antigens in Tables 11-22, or otherwise described herein or known in the art. Optionally, a helper T cell (HTL) peptide such as PADRE®, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention comprising epitopes from an infectious agent is used to

treat or prevent disease mediated by these agents in patients. A vaccine can be used prior to, during, or following other therapies including, for example, antibiotic therapy, anti-viral therapy (e.g., highly active antiretroviral therapy (HAART) in the case of HIV-AIDS), antibody therapy, cancer therapy, and adjunct therapy, whereupon the vaccine provides decreased morbidity, increased disease free survival and overall survival in recipients.

DIAGNOSTIC AND PROGNOSTIC USES

[00318] In one embodiment of the invention, HLA class I and class II binding peptides can be used as reagents to evaluate an immune response. Preferably, the following principles are utilized when selecting a variant(s) for diagnostic, prognostic and similar uses. Potential principles include having the binding affinities described earlier, and/or matching the HLA-motif/supermotif of a peptide with the HLA-type of a patient.

[00319] The evaluated immune response can be induced by any immunogen. For example, the immunogen may result in the production of antigen-specific CTLs or HTLs that recognize the peptide epitope(s) employed as the reagent. Thus, a peptide of the invention may or may not be used as the immunogen. Assay systems that can be used for such analyses include tetramer-based protocols (e.g., DimerX technology (*see, e.g., Science* 274:94-99 (1996) and *Proc. Natl. Acad. Sci.* 95:7568-73 (1998)), staining for intracellular lymphokines, interferon release assays, or ELISPOT assays.

[00320] For example, following exposure to a putative immunogen, a peptide of the invention can be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of any antigen-specific CTLs. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs and thereby determine the frequency of such antigen-specific CTLs in a sample of peripheral blood mononuclear cells (*see, e.g., Ogg et al., Science* 279:2103-2106, 1998; and Altman *et al., Science* 174:94-96, 1996).

[00321] A tetramer reagent comprising a peptide of the invention is generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2 -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the HLA heavy chain, at a site that was previously engineered into the protein. Tetramer formation is then induced by adding streptavidin. When fluorescently labeled streptavidin is used, the tetrameric complex is

used to stain antigen-specific cells. The labeled cells are then readily identified, *e.g.*, by flow cytometry. Such procedures are used for diagnostic or prognostic purposes; the cells identified by the procedure can be used for therapeutic purposes.

[00322] Peptides of the invention are also used as reagents to evaluate immune recall responses. (*see, e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991.) For example, a PBMC sample from an individual expressing a disease-associated antigen (*e.g.* an antigen from an infectious agent) can be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

[00323] Thus, the peptides can be used to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed by methods such as those described herein. The patient is HLA typed, and peptide epitopes that are bound by the HLA molecule(s) present in that patient are selected for analysis. The immunogenicity of the vaccine is indicated by the presence of CTLs and/or HTLs directed to epitopes present in the vaccine.

[00324] The peptides of the invention may also be used to make antibodies, using techniques well known in the art (*see, e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual* Harlow, Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989). Such antibodies are useful as reagents to determine the presence of disease-associated antigens. Antibodies in this category include those that recognize a peptide when bound by an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

ADMINISTRATION FOR THERAPEUTIC OR PROPHYLACTIC PURPOSES

[00325] The peptides and polynucleotides of the present invention, including cells and compositions comprising them, are useful for administration to mammals, particularly humans, to treat and/or prevent infection by an infectious agent such as HIV, HBV, HCV, HPV, *Plasmodium falciparum* and other agents described herein or known in the art. Vaccine compositions containing the peptides of the invention are administered to a

patient infected with a particular infectious agent or to an individual susceptible to, or otherwise at risk for, infection with such an agent to elicit an immune response against antigens of that agent and thus enhance the patient's own immune response capabilities. Where susceptible individuals are identified prior to infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

[00326] In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective immune response to the infectious agent antigen and to thereby cure, arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

[00327] The vaccine compositions of the invention can be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 µg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 µg of peptide. Dosage values for a human typically range from about 500 µg to about 50,000 µg of peptide per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 µg to about 50,000 µg of peptide, administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

[00328] As noted above, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vitro* or *in vivo*. If the contacting occurs *in vivo*, peptide can be administered directly, or in other forms/vehicles, *e.g.*, DNA vectors encoding one or more peptides, viral vectors encoding the peptide(s), liposomes, antigen presenting cells such as dendritic cells, and the like.

[00329] Accordingly, for pharmaceutical compositions of the invention in the form of peptides or polypeptides, the peptides or polypeptides can be administered directly. Alternatively, the peptide/polypeptides can be administered indirectly presented on APCs, or as DNA encoding them. Furthermore, the peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences.

[00330] For therapeutic use, administration should generally begin at the first diagnosis of infectious agent-related disease. This is followed by boosting doses at least until symptoms are

substantially abated and for a period thereafter. In chronic disease states, loading doses followed by boosting doses may be required.

[00331] The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg of peptide. Dosage values for a human typically range from about 500 μg to about 50,000 μg of peptide per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide, administered pursuant to a boosting regimen over weeks to months, can be administered depending upon the patient's response and condition. Patient response can be determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

[00332] In certain embodiments, peptides and compositions of the present invention are used in serious disease states. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be desirable to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

[00333] For treatment of chronic disease, a representative dose is in the range disclosed above, namely where the lower value is about 1, 5, 50, 500, or 1,000 μg of peptide and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg of peptide, preferably from about 500 μg to about 50,000 μg of peptide per 70 kilogram patient. Initial doses followed by boosting doses at established intervals, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic disease, administration should continue until at least clinical symptoms or laboratory tests indicate that the disease has been eliminated or substantially abated, and for a follow-up period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

[00334] The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly.

[00335] Thus, in a preferred embodiment the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances or pharmaceutical excipients as may be required to approximate physiological conditions, such as pH-adjusting and

buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

[00336] The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

[00337] A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that also comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g., Remington's Pharmaceutical Sciences*, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

[00338] The peptides of the invention can also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells (such as monoclonal antibodies which bind to the CD45 antigen) or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

[00339] For targeting compositions of the invention to cells of the immune system, a ligand can be incorporated into the liposome, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

[00340] For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, often at a concentration of 25%-75%.

[00341] For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form, along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, often 1%-10%. The surfactant must, of course, be pharmaceutically acceptable, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant, although an atomizer may be used in which no propellant is necessary and other percentages are adjusted accordingly. A carrier can also be included, *e.g.*, lecithin for intranasal delivery.

[00342] Antigenic peptides of the invention have been used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTLs or HTLs can be used to treat chronic infections, or tumors in patients that do not respond to other conventional forms of therapy, or who do not respond to a therapeutic peptide or nucleic acid vaccine in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (an infected cell or a tumor cell).

KITS

[00343] The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired composition(s) of the invention in a container, preferably in unit dosage form and instructions for administration. For example, a kit would include an APC, such

as a dendritic cell, previously exposed to and now presenting peptides of the invention in a container, preferably in unit dosage form together with instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

[00344] The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

EXAMPLES

EXAMPLE 1. HLA CLASS I AND CLASS II BINDING ASSAYS

[00345] The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

[00346] Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). The cell lines used as sources of HLA molecules and the antibodies used for the extraction of the HLA molecules from the cell lysates are also described in these publications and are well known in the art.

[00347] Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These cells were cultured in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50µM 2-ME, 100µg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA).

[00348] Cell lysates were prepared as follows. Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka

Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.

[00349] HLA molecules were purified from lysates by affinity chromatography. Lysates were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

[00350] A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ¹²⁵I-radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301, which was performed at pH 4.5, and DRB1*1601 (DR2w21β₁) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

[00351] Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN₃. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2β₁) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1*1501 (DR2w2β₁) assays were performed using a 7.8mm x

30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

[00352] Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC_{50} nM, are known in the art. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

[00353] Since under these conditions $[label] < [HLA]$ and $IC_{50} \geq [HLA]$, the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 $\mu\text{g/ml}$ to 1.2 ng/ml , and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

[00354] Because the antibody used for HLA-DR purification (LB3.1) is α -chain specific, β_1 molecules are not separated from β_3 (and/or β_4 and β_5) molecules. The β_1 specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2), and DRB1*0803 (DR8w3), where no β_3 is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2 β_1), DRB5*0101 (DR2w2 β_2), DRB1*1601 (DR2w21 β_1), DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use

of fibroblasts. Development and validation of assays with regard to DR β molecule specificity have been described previously (*see, e.g., Southwood et al., J. Immunol.* 160:3363-3373, 1998).

[00355] Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes.

EXAMPLE 2. RECOGNITION OF VARIANT PEPTIDES BY CTL DERIVED FROM DNA IMMUNIZATION

[00356] Variants corresponding to five HLA-A2 and -A3 restricted epitopes from 167 HIV variant were identified and synthesized. These represented all the complete sequences in the Los Alamos database at the time (116 strains), as well as 51 complete clade C sequences from Botswana, and included 22 subtype B and 62 subtype C sequences. These peptides were then characterized with regard to MHC binding, variant distribution, and immunogenicity. To measure immunogenicity, HLA-A2/K^b or HLA-A11/K^b transgenic mice were immunized with the epitopes encoded in a DNA based format (). Eleven days after immunization, splenocytes were restimulated with either the epitope corresponding to the epitope encoded by the DNA (parent) or each of the variant peptides. After 6 days in culture, IFN- γ secretion was measured in response to the peptide used to stimulate each culture.

[00357] The data for these epitopes are shown in Figure 1. The HLA-A2-restricted epitope corresponding to the Env 134 epitope (KLTPLCVTL; Figure 1A) used as the immunogen was the form observed most often (134/167). All single anchor variants were recognized to approximately the same extent as the parent peptide. Many of the single non-anchor variants (9/13) were also recognized within 10-fold of the parent peptide. Conservative substitutions (R and Q for K; see Table 4) at position 1 (P1) were tolerated, while the non-conservative substitution (E for K; see Table 4) lowered binding and eliminated recognition. Three P4 variants were observed. Two of these (F or S for P) were recognized within 10-fold of the recognition of the parent peptide, while one substitution (Q for P) completely eliminated recognition. The binding for these peptides was not significantly different from the parent peptide, indicating that this residue may be involved in TCR recognition. Both the conservative (F for L) and non-conservative (R for L) substitutions

seen at P5 completely abrogated recognition, indicating that this residue is important in TCR recognition. Finally, one substitution at P8 (I for V), and four substitutions at P9 show little effect on recognition. None of the variants with multiple substitutions were recognized, although this may be due to the poor binding of these peptides.

[00358] The Gag 386 sequence utilized as the immunogen was the second most common form (VLAEAMSQV), present in 54 strains (Figure 1B). The most prevalent variant, differing by a single tolerated C terminal anchor residue (V to A; 67 strains), was recognized equally to the parent epitope by CTL raised against the parent, as were the remaining single-anchor variants. Single substitutions were also tolerated at the non-anchor positions, P1 (I for V) and P8 (R, K, or H for Q). Only the P7 variant (G for S), probably a TCR contact residue, was not recognized.

[00359] Many of the multiple variants for Gag 386 were also recognized by CTL raised against the parent peptide. All the variants with multiple changes combined a change of V to A or T at the C terminus with 1-3 additional substitutions. Two variants with N terminal changes (V to A or I) were observed. The non-conservative A substitution was not recognized, while the conservative I substitution was. A double variant with a conservative substitution at P3 (A to G) was not recognized, implicating P3 in TCR recognition. Double variants with conservative changes at position 8 (Q to R, K, or H) were not well recognized, although the variants with single changes at the same positions were recognized. The variant combining a non-conservative A residue at position 8 with A at the C terminus was recognized as well as the parent. Equally surprising was the observation that all the variants with 3 or 4 substitutions were recognized within 10-fold of the parent peptide.

[00360] The parent form of the HLA-A2-restricted epitope, Vpr 62 (RILQQLFI; Figure 1C) was the most common form observed (86/167). Seven well-tolerated single anchor substitutions, 4 P2 and 3 C terminal, were also observed, accounting for most of the remaining variants (47/167). Single substitutions were, in general, also well tolerated. The single exception was the non-conservative substitution (P for L) at P6, while an M for L substitution at the same site was well tolerated. Binding was not affected for either variant, indicating that the reduction in activity is due to a change in a contact residue. Most variants with multiple changes also showed recognition to approximately the same extent as the parent. Several variants however did show reduced recognition. The variant with changes at both anchors (I to T at P2 and I to T at P9) had reduced binding (IC₅₀ of 9700),

and recognition of the peptide was reduced, although not lost completely. Two variants with Q to H changes at P5, in combination with anchor residue changes (I to M at P2 and I to A at P9), exhibited greatly reduced recognition although binding was not affected. Other changes at P5 (Q to R or L at P5) reduced recognition only slightly.

[00361] The HLA-A3/11-restricted epitope, Pol 98 (Figure 1D), represented the most diverse epitope in terms of the number of variant epitopes identified. The peptide encoded in the DNA was represented in only 18 out of 167 strains. Approximately a third of the peptides identified at that position (49 out of 167) did not have recognizable A3/A11 motifs. The most common variant (30 strains) differed from the parent peptide at 3 residues (VSIKVGQIK), but was recognized within 10-fold of the parent peptide. Two variants with conservative changes at anchor residues were both recognized, although the T to A substitution at P2 resulted in a 10-fold reduction in recognition of the variant peptide. All peptides with single changes in non-anchor positions were also recognized, although the P5 variant (G to E) exhibited a decrease in recognition. As the binding was not affected, this probably indicates involvement in T cell recognition.

[00362] Peptides with two changes showed mixed results. In general, peptides with a V substitution at position 3, in combination with another substitution were recognized to the same extent as the corresponding single substitution, indicating the V substitution was tolerated well and is not a TCR contact residue. Combinations including the P2 anchor residue (T to A or N) were not recognized, although the binding of these peptides was also low. Variants with 3 substitutions were generally not recognized well. Two exceptions with very conservative substitutions were noted (Figure 1D). CTL were unable to recognize peptides with four or more substitutions.

[00363] The HLA-A3/11- restricted Env 47 epitope (Figure 1E; VTVYYGVPVWK) was highly conserved, with only 9 variants identified. The most common form observed was the parent peptide (99 strains), while the second most common form, a single anchor substitution observed in 40 strains, was recognized to the same extent as the parent. All the variants were recognized within 10-fold of the parent epitope.

[00364] Taken together, these data show trends towards promiscuous recognition of variant peptides by CTL generated from immunization with a single peptide. In general, changes that disrupted binding also decreased recognition. Recognition was also affected by the position of the change, with potential TCR contact residues (P3-7) exerting a greater effect on recognition than other residues. In general, conservative residue changes were more

widely tolerated than were non-conservative changes. Recognition was also dependent on the number of changes, with progressively lower recognition with a greater number of changes.

[00365] Recognition after multiple restimulations The observed recognition of variant peptides by CTL raised against the parent peptide might be due to either promiscuous recognition at the level of a single TCR or simply a mixture of TCRs against the immunizing peptide which are each able to recognize subtly different peptides. To distinguish between these two possibilities, Env 134- or Gag 386-specific T cell lines were generated by stimulating five times with the immunizing peptide, and then tested for recognition of a partial panel of variant peptides. These T cell lines were also characterized for V β TCR usage against a panel of antibodies predicted to react with the TCR of the mouse strains utilized for these experiments.

[00366] The data for these peptide-specific lines are shown in Table 5. Because the SU is a measure of the number of cells needed to secrete a defined amount of IFN- γ , a higher SU value would correspond to an enrichment of IFN- γ producing cells. A comparison of one and five peptide stimulations indeed shows an enrichment of CTL specific for the immunizing peptide for both of the peptide lines generated (Table 5A and 5B, first line). The Gag 386 line (Table 5A) also demonstrated increased recognition of all the variant peptides measured except one peptide (ILAEAMSKA) that was never recognized. The Env 134 line also demonstrated enrichment for CTL able to recognize several of the variant peptides (Table 5B).

[00367] To further characterize these lines, we examined them for V β usage, utilizing a panel of commercially available antibodies available for mouse TCR V β 2-14. To determine background levels for the various TCR V β molecules, primary splenocytes from mice that had been immunized with EP HIV-1090 were also examined. The results for the Gag 386 line are shown in Figure 2A. After a single stimulation with the parent peptide, the Gag 386 line showed a mixture of TCR positive populations, including V β 3, 5, and 14. After 5 stimulations, those populations had been reduced to background levels, and approximately 50% of the CD8+ cells expressed the V β 6 TCR. The Env 134 line showed a similar pattern of multiple TCR positive populations after a single round of stimulation with reduction to background levels after 5 stimulations (data not shown). However, no

single V β usage significantly above background could be demonstrated, probably due to lack of the relevant TCR V β antibody.

[00368] Both lines were also characterized with regard to the affinity of certain of the variant peptides by titrating the variant peptides examined above (Table 5A and 5B). The data for both the Gag 386 and Env 134 lines are shown in Figure 2B. For the Gag 386 line, the parent peptide along with two single anchor variants (VLAEAMSQI and VLAEAMSQA) showed the highest affinity. Four other peptides demonstrated lower affinity, but still produced IFN- γ in response to higher peptide concentrations. A single peptide (ILAEAMSKA) was not recognized.

[00369] As expected, the parent peptide, which was used to generate the Env 134 line, showed the highest affinity for the TCR. The other 2 variant peptides, KITPLCVTL and QLTPLCVTL, also demonstrated higher affinity, but reduced from the parent peptide by approximately 10-fold and 100-fold, respectively. It was notable that only at the highest peptide concentration examined (1 μ g/ml) was any IFN- γ secretion detected for five of the peptides (QITPLCVTL, ELTPLCVTL, KLTPFCVTL, KLTPLCVIL, and KLTPLCVPL). These five peptides showed little or no enrichment of CTL able to recognize them, and exhibited the lowest activity as measured by SU after five restimulations (see Table 5B).

[00370] In summary, these cell lines seem to consist of a narrow, possibly single, TCR population. This TCR population recognizes the parent peptide with the highest affinity, but is also able to recognize a number of other variant peptides with equal or lesser affinity.

[00371] **Recognition of variant peptides by CTL derived from an HIV infected patient.**

[00372] To determine if the same immunological conservation was observed in natural infections, we identified an HIV-infected individual expressing the HLA-A3 allele. The HIV strain and subtype with which this patient was infected is unknown. We had previously shown that T cells from this individual responded to the HLA-A3 restricted epitopes Pol 98 and Env 47. PBL from this patient were examined in an ELISPOT assay to determine if they also showed the capacity for broad cross-reactivity. The data are shown in Figure 3. Although the actual peptide represented in the HIV strain with which this individual is infected is unknown, we observed recognition of a large number of the variant peptides for both Pol 98 (Figure 3A) and Env 47 (Figure 3B). The recognition patterns were remarkably similar for the mouse and patient data (compare Figure 1 and

Figure 3), although the mouse expressed a transgene for HLA-A11 and the patient was HLA-A3.

[00373] Prediction of Immunological Conservation. We had observed that the variant peptides that were recognized by CTL raised against the parent epitope had amino acid substitutions that followed previous observations. For example, the anchor residue changes that were tolerated in the variant peptides were also described as anchors that to define the respective HLA supertypes (). In general, conservative substitutions were tolerated at non-anchor residues, while non-conservative substitutions were less well tolerated. These followed closely the prediction model used to identify heteroclitic analogs (Tangri et al).

[00374] Based on these observations, we designed a computer program to predict immunological conservation. For anchor positions, this program utilized the conserved anchor residues described for the A2, A3, and B7 supertypes. For non-anchor positions only conservative substitutions, as defined in Tangri et.al. (), were allowed. All substitutions at non-anchor positions were analyzed independently and all conservative substitutions were allowed regardless of the number of substitutions. Finally, the position of the substitution was not factored into analysis. Each variant was compared with the parent epitope, and its ability to be recognized was predicted as either positive or negative.

[00375] The first sets of epitopes to be evaluated by this program were the five HIV epitopes and variants previously described. For the Env 134 epitope, the program predicted that 13 of the variant peptides should be immunologically conserved, while 6 should not be recognized. Comparison of the observed immunological data with the prediction showed that the program predicted correctly for 14 of the peptides and incorrectly for 5. Of the incorrect predictions, in two cases the program predicted negative results for peptides that were recognized, while in 3 cases the program predicted positive results for peptides that were not recognized. A similar analysis was performed for all five peptides. Of 101 total variant peptides, 68 were correctly identified (67%). The discordant data were fairly evenly split between peptides incorrectly predicted negative (15) and those incorrectly predicted positive (18).

[00376] As noted previously, the more substitutions present in a variant peptide, the lower the likelihood of its immunogenicity. Since the prediction program treated all substitutions independently, and did not take into account the number of substitutions, we hypothesized

that prediction of single substitutions would be more accurate. Indeed, the immunogenicity of 38 of 47 single substitution variants (80%) was correctly predicted.

[00377] With the limitations of the program in mind, it is useful to predict the recognition of the variants for a package of HLA-A2, -A3, and -B7 supertype epitopes. These epitopes had been identified as being well conserved in Clade B variants. When comparing the conservation of this group of epitopes based on sequence identity versus immunological conservation, it is interesting to note that the predicted recognition gains taking into account immunological conservation are significant (Table 6).

[00378] This particular group of 21 epitopes was selected based on their identity conservation in Clade B HIV sequences, with conservation across HIV clades as a secondary consideration. Because of this criteria, the form of epitope chosen as the parent peptide was not the most common variant (e.g. Gag 386, Gag 271, Pol 98). In some cases (e.g., see Gag 386 data), the "parent" epitope and the most common variant were recognized to the same extent. However, in some cases the selection of epitope to include as the "parent" epitope was predicted to make a difference in the immunological conservation. An example of this was the Gag 271 epitope (Figure 4). The variant most commonly seen in clade B sequences was the MTNNPPIP form, while the most common form of the epitope was MTSNPPIP. Not all amino acids are considered equal to each other in their ability to substitute (Tangri). For example, asparagine (N) is considered a conservative substitution for serine (S), while the opposite substitution is only considered semi-conserved. When the program calculated immunological conservation using the MTNNPPIP peptide as the parent peptide, only two variants were predicted to be immunogenic. However, when the immunological conservation was predicted using the MTSNPPIP peptide, most of the variants were predicted to be recognized (Figure 4). This prediction was tested using HLA-A2 transgenic mice. The results show that if the MTSNPPIP form of the peptide was utilized in vaccines, approximately 152 of 167 variants would be recognized, while if the MTNNPPIP form of the epitope was utilized, only 39 of 167 variants would be recognized. This has important implications in epitope selection for vaccine development, and epitope performance can be predicted.

EXAMPLE 3. A PADRE[®] MOLECULE AS A HELPER EPITOPE FOR ENHANCEMENT OF CTL INDUCTION

- [00379] There is increasing evidence that HTL activity is critical for the induction of long lasting CTL responses (Livingston *et al. J. Immunol* 162:3088-3095 (1999); Walter *et al., New Engl. J. Med.* 333:1038-1044 (1995); Hu *et al., J. Exp. Med.* 177:1681-1690 (1993)). Therefore, one or more peptides that bind to HLA class II molecules and stimulate HTLs can be used in accordance with the invention. Accordingly, a preferred embodiment of a vaccine includes a molecule from the PADRE[®] family of universal T helper cell epitopes (HTL) that target most DR molecules in a manner designed to stimulate helper T cells. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAZTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine; "Z" is either tryptophan, tyrosine, histidine or asparagine; and "a" is either D-alanine or L-alanine (SEQ ID NO:29), has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type.
- [00380] A particularly preferred PADRE[®] molecule is a synthetic peptide, aKXVAAWTLKAAa (a = D-alanine, X = cyclohexylalanine), containing non-natural amino acids, specifically engineered to maximize both HLA-DR binding capacity and induction of T cell immune responses.
- [00381] Alternative preferred PADRE[®] molecules are the peptides, aKFVAAWTLKAAa, aKYVAAWTLKAAa, aKFVAAWTLKAAa, aKXVAAWTLKAAa, aKYVAAWTLKAAa, aKFVAAHTLKAAa, aKXVAAHTLKAAa, aKYVAAHTLKAAa, aKFVAAHTLKAAa, aKXVAAHTLKAAa, aKYVAAHTLKAAa, aKFVAAANTLKAAa, aKXVAAANTLKAAa, aKYVAAANTLKAAa, aKXVAAWTLKAAA (SEQ ID NO:30), aKFVAAWTLKAAA (SEQ ID NO:31), aKYVAAWTLKAAA (SEQ ID NO:32), aKFVAAWTLKAAA (SEQ ID NO:33), aKXVAAWTLKAAA (SEQ ID NO:34), aKYVAAWTLKAAA (SEQ ID NO:35), aKFVAAHTLKAAA (SEQ ID NO:36), aKXVAAHTLKAAA (SEQ ID NO:37), aKYVAAHTLKAAA (SEQ ID NO:38), aKFVAAANTLKAAA (SEQ ID NO:39), aKXVAAANTLKAAA (SEQ ID NO:40), aKYVAAANTLKAAA (SEQ ID NO:41) (a = D-alanine, X = cyclohexylalanine).
- [00382] In a preferred embodiment, the PADRE[®] peptide is amidated. For example, a particularly preferred amidated embodiment of a PADRE[®] molecule is conventionally written aKXVAAWTLKAAa-NH₂.

- [00383] Competitive inhibition assays with purified HLA-DR molecules demonstrated that the PADRE[®] molecule aKXVAAWTLKAAa-NH₂ binds with high or intermediate affinity ($IC_{50} \leq 1,000$ nM) to 15 out of 16 of the most prevalent HLA-DR molecules ((Kawashima *et al.*, *Human Immunology* 59:1-14 (1998); Alexander *et al.*, *Immunity* 1:751-761 (1994)). A comparison of the DR binding capacity of PADRE[®] and tetanus toxoid (TT) peptide 830-843, a "universal" epitope has been published (Panina-Bordignon *et al.*, *Eur. J. Immunology* 19:2237-2242 (1989)). The TT 830-843 peptide bound to only seven of 16 DR molecules tested, while PADRE[®] bound 15 of 16. At least 1 of the 15 DR molecules that bind PADRE[®] is predicted to be present in >95% of all humans. Therefore, this PADRE[®] molecule is anticipated to induce an HTL response in virtually all patients, despite the extensive polymorphism of HLA-DR molecules in the human population.
- [00384] PADRE[®] has been specifically engineered for optimal immunogenicity for human T cells. Representative data from *in vitro* primary immunizations of normal human T cells with TT 830-843 antigen and the PADRE[®] molecule aKXVAAWTLKAAa-NH₂ are shown in Figure 1. Peripheral blood mononuclear cells (PBMC) from three normal donors were stimulated with the peptides *in vitro*. Following the third round of stimulation, it was observed that PADRE[®] generated significant primary T cell responses for all three donors as measured in a standard T cell proliferation assay. With the PADRE[®] peptide, the 10,000 cpm proliferation level was generally reached with 10 to 100 ng/ml of antigen. In contrast, TT 830-843 antigen generated responses for only 2 out of 3 of the individuals tested. Responses approaching the 10,000 cpm range were reached with about 10,000 ng/ml of antigen. In this respect, it was noted that PADRE[®] was, on a molar basis, about 100-fold more potent than TT 830-843 antigen for activation of T cell responses.
- [00385] Early data from a phase I/II investigator-sponsored trial, conducted at the University of Leiden (C.J.M. Melief), support the principle that the PADRE[®] molecule aKXVAAWTLKAAa, possibly the amidated aKXVAAWTLKAAa -NH₂, is highly immunogenic in humans (Ressing *et al.*, *J. Immunother.* 23(2):255-66 (2000)). In this trial, a PADRE[®] molecule was co-emulsified with various human papilloma virus (HPV)-derived CTL epitopes and was injected into patients with recurrent or residual cervical carcinoma. However, because of the late stage of carcinoma with the study patients, it was expected that these patients were immunocompromised. The patients' immunocompromised status was demonstrated by their low frequency of influenza virus-

specific CTL, reduced levels of CD3 expression, and low incidence of proliferative recall responses after *in vitro* stimulation with conventional antigens. Thus, no efficacy was anticipated in the University of Leiden trial, rather the goal of that trial was essentially to evaluate safety. Safety was, in fact, demonstrated. In addition to a favorable safety profile, PADRE® T cell reactivity was detected in four of 12 patients (Figure 2) in spite of the reduced immune competence of these patients.

[00386] Thus, the PADRE® peptide component(s) of the vaccine bind with broad specificity to multiple allelic forms of HLA-DR molecules. Moreover, PADRE® peptide component(s) bind with high affinity ($IC_{50} \leq 1000$ nM), i.e., at a level of affinity correlated with being immunogenic for HLA Class II restricted T cells. The *in vivo* administration of PADRE® peptide(s) stimulates the proliferation of HTL in normal humans as well as patient populations.

[00387] One or more PADRE® peptide(s) may be included in a composition, e.g., a vaccine, comprising one or more peptides, either as an individual peptide(s), fused to one or more variant peptides, or both.

EXAMPLE 4. CTL RECOGNITION OF ENDOGENOUS PROCESSED ANTIGENS AFTER PRIMING

[00388] This example determines that CTL induced by native or analoged peptide epitopes recognize endogenously synthesized, i.e., native antigens.

[00389] Effector cells isolated from transgenic mice that are immunized with peptide epitopes are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/ K^b target cells in the absence or presence of peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, i.e. cells that are stably transfected with HIV expression vectors.

[00390] The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A*0201/ K^b transgenic mice, several other transgenic

mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (e.g., transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

EXAMPLE 5. ACTIVITY OF CTL-HTL CONJUGATED EPITOPES IN TRANSGENIC MICE

- [00391] This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope, or an analog of that epitope. The peptides may be lipidated, if desired.
- [00392] Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or IILA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.
- [00393] Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (e.g., Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991).
- [00394] *In vitro* CTL activation: One week after priming, spleen cells (30×10^6 cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated

lymphoblasts (10×10^6 cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

[00395] Assay for cytotoxic activity: Target cells (1.0 to 1.5×10^6) are incubated at 37°C in the presence of $200 \mu\text{l}$ of ^{51}Cr . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of $1 \mu\text{g/ml}$. For the assay, 10^4 ^{51}Cr -labeled target cells are added to different concentrations of effector cells (final volume of $200 \mu\text{l}$) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C , a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = $100 \times (\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/ 10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/ 10^6 , the lytic units/ 10^6 obtained in the absence of peptide is subtracted from the lytic units/ 10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio of 50:1 (i.e., 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., 5×10^4 effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000) - (1/500,000)] \times 10^6 = 18 \text{ LU}$.

[00396] The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in above. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

EXAMPLE 6. SELECTION OF CTL AND HTL EPITOPES FOR INCLUSION IN AN HIV-SPECIFIC VACCINE.

[00397] This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or can be single and/or polypeptidic peptides.

[00398] The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

[00399] Epitopes are selected which, upon administration, mimic immune responses that correlate with virus clearance. For example, if it has been observed that patients who clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen, then 3-4 epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

[00400] When selecting an array of HIV epitopes, it is preferred that at least some of the epitopes are derived from early and late proteins. The early proteins of HIV are expressed when the virus is replicating, either following acute or dormant infection. Therefore, it is particularly preferred to use epitopes from early stage proteins to alleviate disease manifestations at the earliest stage possible.

[00401] Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less.

[00402] Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

[00403] When creating a polypeptidic compositions, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes.

[00404] In cases where the sequences of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy.

For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

[00405] Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables 6-9 or Figures 1A-4. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

EXAMPLE 7. CONSTRUCTION OF MINIGENE MULTI-EPITOPE DNA PLASMIDS

[00406] This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.

[00407] A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables 6-9 and Figures 1A-4. HLA class I supermotif or motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

[00408] Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99,

wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

[00409] This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

[00410] The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

[00411] Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated T_m of each primer pair) for 30 sec, and 72°C for 1 min.

[00412] For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

EXAMPLE 8. THE PLASMID CONSTRUCT AND THE DEGREE TO WHICH IT
INDUCES IMMUNOGENICITY.

- [00413] The degree to which a plasmid construct, for example a plasmid constructed in accordance as above is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines "antigenicity" and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.,* Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.,* Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).
- [00414] Alternatively, immunogenicity can be evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.,* in copending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994.
- [00415] For example, to assess the capacity of a DNA minigene construct (*e.g.,* a pMin minigene construct generated as described in U.S.S.N. 09/311,784) containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.
- [00416] Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polypeptidic peptide), then assayed for peptide-specific cytotoxic activity in a ⁵¹Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polypeptidic vaccine. It is, therefore, found that the minigene elicits immune responses

directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

[00417] To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4⁺ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ³H-thymidine incorporation proliferation assay, (*see, e.g.*, Alexander et al. *Immunity* 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

[00418] DNA minigenes, constructed as described above or below, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

[00419] For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 µg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10⁷ pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are

stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN- γ ELISA.

[00420] It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

[00421] The use of prime boost protocols in humans is described in below.

EXAMPLE 9. PEPTIDE COMPOSITION FOR PROPHYLACTIC USES

[00422] Vaccine compositions of the present invention can be used to prevent HIV infection in persons who are at risk for such infection. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV infection.

[00423] For example, a peptide-based composition can be provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freund's Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 μ g, generally 100-5,000 μ g, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

[00424] Alternatively, a composition typically comprising transfecting agents can be used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

EXAMPLE 10. POLYEPITOPIC VACCINE COMPOSITIONS DERIVED FROM NATIVE HIV SEQUENCES

[00425] A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify "relatively short" regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping, for example, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

[00426] The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

[00427] The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

[00428] Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

EXAMPLE 11. POLYEPITOPIC VACCINE COMPOSITIONS DIRECTED TO MULTIPLE DISEASES

[00429] The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

[00430] For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

EXAMPLE 12. USE OF PEPTIDES TO EVALUATE AN IMMUNE RESPONSE

[00431] Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

[00432] In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-

microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

[00433] For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300 x g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

EXAMPLE 13. USE OF PEPTIDE EPITOPES TO EVALUATE RECALL RESPONSES

[00434] The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected with HIV, or who have been vaccinated with an HIV vaccine.

[00435] For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA

supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

[00436] PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

[00437] In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.*, *J. Clin. Invest.* 98:1432-1440, 1996).

[00438] Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al.*, *J. Virol.* 66:2670-2678, 1992).

[00439] Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 µM, and labeled with 100 µCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

[00440] Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times \frac{[(\text{experimental release} - \text{spontaneous})]}{(\text{total release} - \text{spontaneous})}$

release)/maximum release-spontaneous release)]. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

[00441] The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

[00442] The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 $\mu\text{g/ml}$ synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μCi ^3H -thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^3H -thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^3H -thymidine incorporation in the presence of antigen divided by the ^3H -thymidine incorporation in the absence of antigen.

EXAMPLE 14. INDUCTION OF SPECIFIC CTL RESPONSE IN HUMANS

[00443] A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

[00444] A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μg of peptide composition.

[00445] After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

- [00446] The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.
- [00447] Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.
- [00448] Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.
- [00449] The vaccine is found to be both safe and efficacious.

EXAMPLE 15. PHASE II TRIALS IN PATIENTS INFECTED WITH HIV

- [00450] Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to HIV-infected patients. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4⁺ cells counts. Such a study is designed, for example, as follows:
- [00451] The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.
- [00452] There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic

backgrounds. All of them are infected with HIV for over five years and are HCV, HBV and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.

[00453] The viral load and CD4⁺ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

EXAMPLE 16. INDUCTION OF CTL RESPONSES USING A PRIME BOOST PROTOCOL

[00454] A prime boost protocol can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

[00455] For example, the initial immunization is performed using an expression vector, such as that constructed above, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 µg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster is, for example, recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polypeptidic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

[00456] Analysis of the results indicates that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

EXAMPLE 17. ADMINISTRATION OF VACCINE COMPOSITIONS USING DENDRITIC CELLS

[00457] Vaccines comprising peptide epitopes of the invention can be administered using APCs, or “professional” APCs such as DC. In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction of the specific target cells that bear the proteins from which the epitopes in the vaccine are derived.

[00458] For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoiectin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

[00459] As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (see, e.g., *Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although $2\text{--}50 \times 10^6$ DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

[00460] In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment with an agent such as Progenipoiectin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10} . Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoiectin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5×10^6 DC, then the patient will be injected with a total of 2.5×10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoiectin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

Ex vivo activation of CTL/HTL responses

[00461] Alternatively, *ex vivo* CTL or HTL responses to HIV antigens can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy or facilitate destruction of their specific target cells.

[00462] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, patent applications and sequence listings cited herein are hereby incorporated by reference in their entirety for all purposes.

TABLE 1

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T , <i>I, L, V, M, S</i>		F, W, Y
A2	L, I, V, M, A, T, Q		I, V, M, A, T, L
A3	V, S, M, A, T, L, I		R, K
A24	Y, F, W, I, V, L, M, T		F, I, Y, W, L, M
B7	P		V, I, L, F, M, W, Y, A
B27	R, H, K		F, Y, L, W, M, I, V, A
B44	E, D		F, W, L, I, M, V, A
B58	A, T, S		F, W, Y, L, I, V, M, A
B62	Q, I, I, V, M, P		F, W, Y, M, I, V, L, A
MOTIFS			
A1	T, S, M		Y
A1		D, E, A, S	Y
A2.1	L, M, V, Q, I, A, T		V, L, I, M, A, T
A3	L, M, V, I, S, A, T, F, C, G, D		K, Y, R, H, F, A
A11	V, T, M, L, I, S, A, G, N, C, D, F		K, R, Y, H
A24	Y, F, W, M		F, L, I, W
A*3101	M, V, T, A, L, I, S		R, K
A*3301	M, V, A, L, F, I, S, T		R, K
A*6801	A, V, T, M, S, L, I		R, K
B*0702	P		L, M, F, W, Y, A, I, V
B*3501	P		L, M, F, W, Y, I, V, A
B51	P		L, I, V, F, W, Y, A, M
B*5301	P		I, M, F, W, Y, A, L, V
B*5401	P		A, T, I, V, L, M, F, W, Y

Bolded residues are preferred, italicized residues are tolerated: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE 2

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T, I, L, V, M, S		F, W, Y
A2	V, Q, A, T		I, V, L, M, A, T
A3	V, S, M, A, T, L, I		R, K
A24	Y, F, W, I, V, L, M, T		F, I, Y, W, L, M
B7	P		V, I, L, F, M, W, Y, A
B27	R, H, K		F, Y, L, W, M, I, V, A
B58	A, T, S		F, W, Y, L, I, V, M, A
B62	Q, L, I, V, M, P		F, W, Y, M, I, V, L, A
MOTIFS			
A1	T, S, M		Y
A1		D, E, A, S	Y
A2.1	V, Q, A, T*		V, L, I, M, A, T
A3.2	L, M, V, I, S, A, T, F, C, G, D		K, Y, R, H, F, A
A11	V, T, M, L, I, S, A, G, N, C, D, F		K, R, H, Y
A24	Y, F, W		F, L, I, W

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are tolerated: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE 3

POSITION								
	1	2	3	4	5	6	7	8
								C-terminus
<u>SUPERMOTIFS</u>								
A1		1° Anchor T,I,L,V,M,S						1° Anchor F,W,Y
A2		1° Anchor L,I,V,M,A, T,Q						1° Anchor L,I,V,M,A,T
A3	preferred	1° Anchor V,S,M,A,T, L,I	Y,F,W, (4/5)			Y,F,W, (3/5)	Y,F,W, (4/5)	1° Anchor R,K
	deleterious	D,E (3/5); P, (5/5)	D,E, (4/5)					
A24		1° Anchor Y,F,W,I,V, L,M,T						1° Anchor F,I,Y,W,L,M
B7	preferred	F,W,Y (5/5) L,I,V,M, (3/5)	1° Anchor P	F,W,Y (4/5)			F,W,Y, (3/5)	1° Anchor V,I,L,F,M,W,Y,A
	deleterious	D,E (3/5); P(5/5); G(4/5); A(3/5); Q,N, (3/5)		D,E, (3/5)	G, (4/5)	Q,N, (4/5)	D,E, (4/5)	
B27		1° Anchor R,H,K						1° Anchor F,Y,L,W,M,V,A
B44		1° Anchor E,D						1° Anchor F,W,Y,I,I,M,V,A
		1° Anchor						1° Anchor

TABLE 3 (Continued)

		POSITION									C-terminus or C-terminus us
		1	2	3	4	5	6	7	8	9	
B58			A,T,S								F,W,Y,L,I,V,M,A
B62			1°Anchor Q,L,I,V,M, P							1°Anchor F,W,Y,M,I,V,L,A	
<u>MOTIFS</u>											
A1 9-mer	preferred	G,F,Y,W,	1°Anchor S,T,M,	D,E,A,	Y,F,W,	P,	D,E,Q,N,	Y,F,W,	1°Anchor Y		
	deleterious	D,E,	R,H,K,L,I,V M,P,	A,	G,	A,					
A1 9-mer	preferred	G,R,H,K	A,S,T,C,L,I V,M,	1°Anchor D,E,A,S	G,S,T,C,	A,S,T,C,	L,I,V,M,	D,E,	1°Anchor Y		
	deleterious	A	R,H,K,D,E, P,Y,F,W,	D,E,	P,Q,N,	R,H,K,	P,G,	G,P,			
A1 10-mer	preferred	Y,F,W,	1°Anchor S,T,M	D,E,A,Q,N,	A,	Y,F,W,Q,N,	P,A,S,T,C,	G,D,E,	P,	1°Anchor Y	
	deleterious	G,P,	R,H,K,G,L,I V,M,	D,E,	R,H,K,	Q,N,A	R,H,K,Y,F, W,	R,H,K,	A		

TABLE 3 (Continued)

		POSITION									
		1	2	3	4	5	6	7	8	9	C-terminus or C-terminus
A1 10-mer	preferred	Y,F,W,	S,T,C,L,I,V M,	<u>1°Anchor</u> D,E,A,S	A,	Y,F,W,	P,G,	G,	Y,F,W,	<u>1°Anchor</u> Y	
	deleterious	R,H,K,	R,H,K,D,E, P,Y,F,W,			P,	G,	P,R,H,K,	Q,N,		
A2.1 9-mer	preferred	Y,F,W,	<u>1°Anchor</u> L,M,I,V,Q, A,T	Y,F,W,	S,T,C,	Y,F,W,	A,	P	<u>1°Anchor</u> V,L,I,M,A,T		
	deleterious	D,E,P,	D,E,R,K,H			R,K,H	D,E,R,K,H				
A2.1 10-mer	preferred	A,Y,F,W,	<u>1°Anchor</u> L,M,I,V,Q, A,T	L,V,I,M,	G,		G,	F,Y,W,L, V,I,M,	<u>1°Anchor</u> V,L,I,M,A,T		
	deleterious	D,E,P,	D,E,	R,K,H,A,	P,	R,K,H,	D,E,R,K, H,				

TABLE 3 (Continued)

POSITION								
1	2	3	4	5	6	7	8	9
								C-terminus or C-terminus

TABLE 4 (Continued)

A3	preferred	R,H,K,	<u>1°Anchor</u> L,M,V,I,S, A,T,F,C,G D	Y,F,W,	P,R,H,K,Y, A, F,W,	Y,F,W,	P,	<u>1°Anchor</u> K,Y,R,H,F,A
----	-----------	--------	---	--------	-----------------------	--------	----	--------------------------------

deleterious D,E,P,

D,E

A11 preferred

1°Anchor
V,T,L,M,I,
S,A,G,N,C,
D,F

Y,F,W,

Y,F,W,

A,

Y,F,W,

Y,F,W,

P,

1°Anchor
K,,R,Y,H

deleterious

D,E,P,

G,

A

A24
9-mer

preferred

1°Anchor
Y,F,W,M

S,T,C

Y,F,W,

Y,F,W,

Y,F,W,

1°Anchor
F,L,I,W

deleterious

D,E,G,

D,E,

G,

Q,N,P,

D,E,R,H,K,

G,

A,Q,N,

A24
10-mer

preferred

1°Anchor
Y,F,W,M

P,

Y,F,W,P,

P,

1°Anchor
F,L,I,W

deleterious

G,D,E

Q,N

R,H,K

D,E

A

Q,N,

D,E,A,

A3101 preferred

1°Anchor
M,V,T,A,L,
I,S

P,

Y,F,W,

Y,F,W,

A,P,

1°Anchor
R,K

TABLE 3 (Continued)

		POSITION							C-terminus or terminus	
		1	2	3	4	5	6	7	8	9
deleterious	D,E,P,			D,E,		A,D,E,	D,E,	D,E,	D,E,	
A3301 preferred			<u>1°Anchor</u> M,V,A,L,F, I,S,T	Y,F,W				A,Y,F,W		<u>1°Anchor</u> R,K
deleterious	G,P			D,E						
A6801 preferred	Y,F,W,S,T,C,		<u>1°Anchor</u> A,V,T,M,S, L,I			Y,F,W,L,I, V,M		Y,F,W,	P,	<u>1°Anchor</u> R,K
deleterious	G,P,			D,E,G,		R,H,K,			A,	
B0702 preferred	R,H,K,F,W,Y,		<u>1°Anchor</u> P	R,H,K,		R,H,K,	R,H,K,	R,H,K,	P,A,	<u>1°Anchor</u> L,M,F,W,Y,A, I,V
deleterious	D,E,Q,N,P,			D,E,P,	D,E,	D,E,	G,D,E,	Q,N,	D,E,	
B3501 preferred	F,W,Y,L,I,V,M,		<u>1°Anchor</u> P	F,W,Y,				F,W,Y,		<u>1°Anchor</u> L,M,F,W,Y,I, V,A
deleterious	A,G,P,					G,	G,			

TABLE 3 (Continued)

		POSITION										
		1	2	3	4	5	6	7	8	9	C-terminus	C-terminus
											us	
B51	preferred	L,I,V,M,F,W,Y, S,T,C	<u>1°Anchor</u> P	F,W,Y,	S,T,C,	F,W,Y,	G,	F,W,Y,	<u>1°Anchor</u> L,I,V,F,W, Y,A,M			
	deleterious	A,G,P,D,E,R,H,K, S,T,C				D,E,	G,	D,E,Q,N,	G,D,E,			
B5301	preferred	L,I,V,M,F,W,Y, S,T,C	<u>1°Anchor</u> P	F,W,Y,	S,T,C,	F,W,Y,	L,I,V,M,F, W,Y,	F,W,Y,	<u>1°Anchor</u> I,M,F,W,Y, A,L,Y			
	deleterious	A,G,P,Q,N,					G,	R,H,K,Q,N,	D,E,			
B5401	preferred	F,W,Y,	<u>1°Anchor</u> P	F,W,Y,L,I,V M,		L,I,V,M,	A,L,I,V,M,	F,W,Y,A,P,	<u>1°Anchor</u> A,T,I,V,L, M,F,W,Y			
	deleterious	G,P,Q,N,D,E,		G,D,E,S,T,C,		R,H,K,D,E,	D,E,	Q,N,D,G,E,	D,E,			

Italicized residues indicate "tolerated" residues.

The information in Table II is specific for 9-mers unless otherwise specified.

Secondary anchor specificities are designated for each position independently.

Table 4

HLA-supertype	Allele-specific HLA-supertype members	
	Verified ^a	Predicted ^b
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6801	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1801, B*1802, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	
B62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

- Verified alleles include alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.
- Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.

Table 5. Compiled rankings and similarity assignments.

A	C	D	E	F	G	H	I	K	L
A	1.0	D	1.0	F	1.0	H	1.0	K	1.0
S	4.5	N	3.5	L	3.8	Q	2.0	R	2.7
T	4.8	E	4.0	Y	4.3	E	5.8	Q	6.0
P	5.3	Q	6.2	I	4.8	N	6.2	H	6.8
G	5.7	S	7.7	M	6.2	R	8.2	V	5.2
C	1.0	S	7.7	V	6.7	K	8.7	Y	8.8
V	9.9	H	7.8	W	7.2	P	9.0	D	8.5
D	10.0	G	8.8	H	10.2	D	9.2	M	9.2
M	10.0	P	9.2	C	10.2	S	10.5	A	11.5
N	10.2	R	10.5	T	11.5	T	11.5	S	11.5
P	11.5	A	9.3	R	11.5	V	11.0	K	12.0
O	11.5	K	9.3	R	11.8	G	11.5	P	12.0
H	12.5	R	11.5	A	13.0	M	12.2	L	12.5
Y	13.0	C	12.2	K	13.3	V	12.2	Q	12.2
T	13.7	V	13.3	P	13.3	F	13.3	R	13.7
I	14.3	Y	13.8	S	13.8	A	13.8	S	14.3
W	14.3	A	13.8	Q	14.2	R	14.3	A	14.3
F	15.3	L	13.5	N	14.2	C	14.3	C	14.3
K	15.8	L	13.5	E	14.3	E	14.3	W	14.8
R	16.3	W	13.5	G	14.3	E	14.3	W	14.8
R	17.3	R	13.5	G	14.3	E	14.3	W	14.8
R	17.3	R	13.5	G	14.3	E	14.3	W	14.8

Conserved (1-7)

Semi-conserved (7.1-13)

Non-conserved (13.1-20)

Table 5 (continued)

[illegible]

Conserved (1-7)

Semi-conserved (7.1-13)

Non-conserved (13.1-20)

60458026 . 032803

Table 6. Recognition of variant peptides by CTL generated after one and five stimulations with the parent peptide.

A. Gag 386 (VLAEAMSQV)			
Peptide Sequence	Binding IC50 (nM)	1 Stimulation (SU)	5 Stimulations (SU)
VLAEAMSQV	49.9	31.6	222.0
VLAEAMSQA	23.8	17.0	133.5
VLAEAMSQI	70.9	21.2	246.1
VLAEAMSKV	230.5	10.8	130.9
VLAEAMSKA	69.4	NT	36.6
ILAEAMSQA	29.3	4.0	49.7
ILAEAMSKA	72.4	--	--
VLAEAMAAA	17	16.3	90.3

B. Env 134 (KLTPLCVTL)			
KLTPLCVTL	77.0	278.4	683.6
KITPLCVTL	461	231.8	700.8
QLTPLCVTL	63.6	166.2	361.5
QITPLCVTL	975	105.0	166.9
ELTPLCVTL	7190	91.7	100.0
KLTPFCVTL	87.3	36.1	75.4
KLTPLCVIL	356	77.2	29.1
KLTPLCVPL	14.6	9.6	14.8

Table 7. Conservation of EP HIV-1090 epitopes across clades, calculated as identity or immunological conservation

Protein	Sequence	Total		Clade B		Clade C	
		Identity	Imm. Cons.	Identity	Imm. Cons.	Identity	Imm. Cons.
Pol 498	ILKEPVHGV	62%	87%	77%	86%	74%	95%
Gag 386	VLAEMSQV	32%	93%	68%	91%	5%	94%
Pol 448	KLVGKLNWA	95%	96%	95%	95%	95%	98%
Env 134	KLTPLCVTL	80%	93%	90%	95%	89%	98%
Vpr 62	RILQQLFI	51%	93%	68%	91%	61%	95%
Nef 221	LTFGWCFKL	49%	74%	77%	91%	47%	81%
Gag 271	MTNNPIPV	20%	25%	91%	95%	8%	19%
Env 47	VTVYYGVPVWK	59%	87%	95%	100%	61%	92%
Pol 929	QMAVFIHNFK	84%	98%	100%	100%	94%	97%
Pol 98	VTIKIGGQLK	11%	71%	59%	91%	2%	89%
Pol 971	KIQNFRVYYR	80%	86%	91%	95%	79%	89%
Pol 347	AIFQSSMTK	53%	75%	77%	82%	44%	79%
Pol 722	KVYLAWVPAHK	14%	97%	82%	95%	3%	97%
Env 61	TTLFCASDAK	72%	89%	90%	100%	69%	92%
Nef 94	FPVRPQVPL	81%	93%	77%	95%	82%	94%
Gag 545	YPLASLRSLF	7%	29%	45%	95%	0%	0%
Rev 75	VPLQLPPL	44%	78%	68%	77%	27%	79%
Env 259	IPIHYCAPA	74%	95%	45%	95%	79%	97%
Gag 237	HPVHAGPIA	27%	54%	68%	95%	44%	94%
Pol 893	IPYNPQSQGVV	92%	96%	82%	95%	240%	97%
Env 250	CPKVSFEPI	45%	91%	77%	100%	45%	97%
Mean		54%	81%	77%	93%	59%	84%
n=		167		22		62	

Table 8. HIV Peptides predicted to be immunologically conserved

Protein	Sequence	Conserved Epitopes*	Sequence Distribution					
			All	Subtype				
				A	B	C	D	G
Pol 498	ILKEPVHGV	ILKEPVHGV	104	1	17	46	2	2
		ILREPVHGV	12			5		1
		ILKEPVHGA	10			2	1	
		ILKDPVHGV	8	5				
		KLKEPVHGV	3					
		ILKDPVHGA	2	2				
		ILKNPVHGV	2					
Gag 386	VLAEAMSQV	VLAEAMSQA	67	2	1	36	3	3
		VLAEAMSQV	54	7	15	3	1	
		VLAEAMSQT	11			9		
		VLAEAMSHA	6			4		
		ILAEAMSQV	5		3			
		ILAEAMSQA	3			2		
		VLAEAMSHV	2					
Pol 448	KLVGKLNWA	KLVGKLNWA	158	9	21	59	3	3
		KLIGKLNWA	1					
Env 134	KLTPLCVTL	KLTPLCVTL	134	8	19	55		
		QLTPLCVTL	5	2	1			
		KLTPLCVAL	3					
		RLTPLCVTL	3			3		
		KITPLCVTL	2					
Vpr 62	RILQQLLFI	RILQQLLFI	86	1	15	28	4	3
		RILQQLLFV	21	2		2		
		RTLQQLLFI	10		2	4		
		RTLQQLLFV	10			1		
		RILQQLLFT	6			2		
		RMLQQLLFI	4		1	3		
		RVLQQLLFI	3			3		
Nef 221	LTFGWCFKL	LTFGWCFKL	82	8	17	29		3
		LTFGWCYKL	31	1	2	17		
		LTLGWCFKL	4			1		

Gag 271	MTNNPPIPV	MTSNPPIPV	60	3		24	4	1
		MTNNPPIPV	33		20	5		
		MTSNPPVPV	26	1		15		1
		MTGNPPIPV	15	5		1		
		MTGNPPVPV	9			5		
		MTNNPPVPV	6			6		
		MTANPPVPV	3			2		
Env 47	VTVYYGVPVWK	VTVYYGVPVWK	99	6	21	30	3	
		VTVYYGVPVWR	40	1		18		
		VTIYYGVPVWK	2					
Pol 929	QMAVFIHNFK	QMAVFIHNFK	153	10	22	58	4	3
		QMAVHVHNFK	3			1		
		QMAVHVHNYK	2					
Pol 98	VTIKIGGQLK	VSIKVGQIK	30			30		
		VTIKIGGQLK	18		13	1		
		VTVKIGGQLK	11	1	1		1	
		VTVRIGGQLK	6	3				
		VSIKVGQIR	6			6		
		VSIRVGQIK	4			4		
		VTIRIGGQLK	3		2			
		VTVKIGGQLR	3	1				
		VTVKVGQQLK	3					
Pol 971	KIQNFRVYYR	KIQNFRVYYR	133	6	20	49	4	3
Pol 347	AIFQSSMTK	AIFQSSMTK	88	5	17	27	3	2
		AIFQCSMTK	19		2	5		
		AIFQSSMTR	13		1	11		1
		AIFQASMTK	9	1		1		
		SIFQSSMTK	9	3		6		
		AIFQYSMTK	4					
		AIFQSTMTK	2			1		
Pol 722	KVYLAWVPAHK	KVYLSWVPAHK	56	8		12	1	3
		RVYLSWVPAHK	55			41		
		KVYLAWVPAHK	23	1	18		3	
		KVYLTWVPAHK	5		2			
		KIYLSWVPAHK	5			3		
		RIYLSWVPAHK	5			4		
		KIYLAWVPAHK	2		1			
		QVYLTWVPAHK	2					

Env 61	TTLFCASDAK	TTLFCASDAK	121	9	19	41	4	1
		ATLFCASDAK	7			7		
		TILFCASDAK	6					
		PTLFCASDAK	2			1		
		TTLFCASDAR	2		2			
		TTLFCASEAK	2		1			
		ATLFCASDAR	2			2		
Nef 94	FPVRPQVPL	FPVRPQVPL	135	8	17	51	4	3
		FPVKPQVPL	9	1	3	2		
		FPVRPQVPV	4			2		
Gag 545	YPLASLRSLF	EPLTSLKSLF*	22			21		
		YPLASLKSLF*	13		5		2	
*These two would not be predicted to XR. Would choose both to get maximal population coverage.								
		YPLASLRSLF	11		10			
		YPLTSLKSLF	10		1		2	1
		YPPLASLKSL	10					
		YPLTSLRSLF	6		4			
		YPPLTSLKSL	6					
Rev 75	VPLQLPPL	VPLQLPPL	64	5	15	7	4	2
		VPLQLPPI	34	2	1	19		
		VPFQLPPI	26			23		
		VPFQLPPL	3		1			1
Env 259	IPIHYCAPA	IPIHYCAPA	124	8	10	49	3	2
		IPIHYCTPA	25	1	8	8		
		IPIHFCAPA	3		1	1	1	
Gag 237	HPVHAGPIA	HPVHAGPIA	39		15	21	1	
		HPVHAGPVA	34	1	3	27	2	
		HPVQAGPVA	12		3	6	1	
		HPIHAGPIA	2			2		
Pol 893	IPYNPQSQGVV	IPYNPQSQGVV	153	9	18	60	4	3
		IPYNPQSQGVI	5		3			
		IPYNPQSQGAV	2			1		
Env 250	CPKVSFEPI	CPKVSFEPI	50	5	17	3	2	0
		CPKVSFDPI	42			33		
		CPKVTFDPI	16			13		1
		CPKVTFEPI	13	3		1		1
		CPKISFDPI	9			5		
		CPKISFEPI	7		4		1	
		CPKVSWDPI	6					
		CPKVSFOPI	4		1			

* The preferred epitopes are shown in bold

Table 9. Predicted immunological conservation for a panel of HLA-A2 restricted HPV peptides.

Source	Parent Sequence	HPV Strain	Variant Sequences	SEQ ID NO	Predicted Immunogenicity	Measured Immunogenicity (SU)*
HPV16.E7.86	TLGIVCPI	16	TLGIVCPI		+	103.7
		18	TLSFVCPW		-	
		31	SFGIVCPN		-	
		33	TVNIVCPT		-	
		45	TLSFVCPW		-	
		52	TLQVVCPG		-	
		56	ALTVTCPL		-	
		58	TCTIVCPS		-	
HPV31.E6.11	KLHELSSAL	16	KLPQLCTEL		-	
		18	KLPDLCTEL		-	
		31	KLHELSSAL		+	26.3
		33	TLHDLQAL		-	
		45	KLPDLCTEL		-	
		52	TLHELCEVL		-	
		56	SLHHLSEVL		-	
		58	TLHDLQAL		-	
HPV18/45.E6.13	KLPDLCTEL	16	KLPQLCTEL		+	15.7
		18	KLPDLCTEL		+	212.7
		31	KLHELSSAL		-	
		33	TLHDLQAL		-	
		45	KLPDLCTEL		+	205.1
		52	TLHELCEVL		-	
		56	SLHHLSEVL		-	
		58	TLHDLQAL		-	
HPV52.E6.18	VLEESVHEI	16	ELQTTIHDI		-	
		18	ELNTSLQDI		-	
		31	ALEIPYDEL		-	
		33	ALETTIHNI		-	
		45	ELNTSLQDV		-	
		52	VLEESVHEI		+	64.1
		56	VLEIPLIDL		-	
		58	ALETSVHEI		-	
HPV18.E6.47	FAFKDLFVV	16	FAFRDLCIV		-	
		18	FAFKDLFVV		+	350.6
		31	FAFTDLTIV		-	
		33	FAFADLTVV		-	31.4
		45	FAFKDLCIV		-	176.9
		52	FLFTDLRIV		-	
		56	FACTELKLV		-	
		58	FVFADLRIV		-	7.7

HPV31.E6.45	FAFTDLTIV	16	FAFRDLCIV	-	
		18	FAFKDLFVV	-	
		31	FAFTDLTIV	+	20.7
		33	FAFADLTVV	+	11.6
		45	FAFKDLCIV	-	
		52	FLFTDLRIV	-	
		56	FACTELKLV	-	
		58	FVFADLRIV	-	
HPV52.E6.45	FLFTDLRIV	16	FAFRDLCIV	-	
		18	FAFKDLFVV	-	
		31	FAFTDLTIV	-	
		33	FAFADLTVV	-	
		45	FAFKDLCIV	-	
		52	FLFTDLRIV	+	421.4
		56	FACTELKLV	-	57.5
		58	FVFADLRIV	+	94.1
HPV58.E6.45	FVFADLRIV	16	FAFRDLCIV	-	
		18	FAFKDLFVV	-	
		31	FAFTDLTIV	-	
		33	FAFADLTVV	-	
		45	FAFKDLCIV	-	
		52	FLFTDLRIV	+	13.3
		56	FACTELKLV	-	21.0
		58	FVFADLRIV	+	62.8
HPV18.E7.7	TLQDIVLHL	16	TLHEYMLDL	-	
		18	TLQDIVLHL	+	99.0
		31	TLQDYVLDL	-	
		33	TLKEYVLDL	-	
		45	TLQEIVLHL	+	
		52	TIKDYILDL	-	
		56	TLQDVVLEL	+	38.0
		58	TLREYILDL	-	
HPV16.E7.82	LLMGTLGIV	16	LLMGTLGIV	+	518.5
		18	LFLNTLSFV	-	
		31	LLMGSPGIV	+	90.1
		33	LLMGTVNIV	-	
		45	LFLSTLSFV	+	
		52	MLLGTQVW	-	
		56	LLMGALTVT	+	
		58	LLMGCTCTIV	-	
HPV33.E7.81	LLMGTVNIV	16	LLMGTLGIV	-	
		18	LFLNTLSFV	-	
		31	LLMGSPGIV	-	
		33	LLMGTVNIV	+	179.4
		45	LFLSTLSFV	-	
		52	MLLGTQVW	+	
		56	LLMGALTVT	-	20.8
		58	LLMGCTCTIV	-	

HPV52.E7.84	MLLGTQVV	16	LLMGTGIV	-	
		18	LFLNTLSFV	-	
		31	LLMGSFGIV	-	
		33	LLMGTVNIV	+	
		45	LFLSTLSFV	-	
		52	MLLGTQVV	+	99.8
		56	LLMGALVT	-	
		58	LLMGCTIV	-	
HPV56.E7.89	LLMGALVT	16	LLMGTGIV	-	
		18	LFLNTLSFV	-	
		31	LLMGSFGIV	-	
		33	LLMGTVNIV	+	
		45	LFLSTLSFV	-	
		52	MLLGTQVV	-	
		56	LLMGALVT	+	263.5
		58	LLMGCTIV	-	43.6
* Immunogenicity was measured for all variants. Only the positive responses are shown in the table. All other responses were negative.					

Table 10. 167 HIV-1 Variants

SEQ ID NO	Sequence Designation	Name	Accession Number	SubType	Country
A.UG.92UG037_U51190		92UG037	U51190	A	UG
A.BY.97BL006_AF1932		97BL006	AF193275	A	BY
A.KE.Q23_AF004885		Q23	AF004885	A	KE
A.SE.SE6594_AF06967		SE6594	AF069672	A	SE
A.SE.SE7253_AF06967		SE7253	AF069670	A	SE
A.SE.SE7535_AF06967		SE7535	AF069671	A	SE
A.SE.SE8538_AF06966		SE8538	AF069669	A	SE
A.SE.SE8891_AF06967		SE8891	AF069673	A	SE
A.UG.U455_M62320		U455	M62320	A	UG
A.SE.UGSE8131_AF107		UGSE8131	AF107771	A	SE
A2.CY.94CY017.41_AF		94CY017.41	AF286237	A2	CY
A2.CD.97CDKTB48_AF2		97CDKTB48	AF286238	A2	CD
A2D.-97KR004_AF286		97KR004	AF286239	A2D	KR
A2G.CD.97CDKP58_AF3		97CDKP58	AF316544	A2G	CD
AC.IN.21301_AF06715		21301	AF067156	AC	IN
AC.RW.92RW009_U8882		92RW009	U88823	AC	RW
AC.SE.SE9488_AF0714		SE9488	AF071474	AC	SE
ACD.SE.SE8603_AF075		SE8603	AF075702	ACD	SE
ACG.BE.VI1035_AJ276		VI1035	AJ276595	ACG	BE
AD.SE.SE6954_AF0757		SE6954	AF075701	AD	SE
AD.SE.SE7108_AF0714		SE7108	AF071473	AD	SE
ADHK.NO.97NOGIL3_AJ		97NOGIL3	AJ237565	ADHK	NO
ADK.CD.MAL_X04415		MAL	X04415	ADK	CD
AG.NG.92NG003_U8882		92NG003	U88825	AG	NG
AG.BE.VI1197_AJ2765		VI1197	AJ276596	AG	BE
AGHU.GA.VI354_AF076		VI354	AF076474	AGHU	GA
AGU.CD.Z321_U76035		Z321	U76035	AGU	CD
AJ.BW.BW2117_AF1921		BW2117	AF192135	AJ	BW
B.NL.3202A21_U34604		3202A21	U34604	B	NL
B.US.BC_L02317		BC	L02317	B	US
B.GB.CAM1_D10112		CAM1	D10112	B	GB
B.DE.D31_U43096		D31	U43096	B	DE
B.US.DH123_AF069140		DH123	AF069140	B	US
B.GB.GB8.C1_Y13716		GB8	AJ271445	B	GB
B.DE.HAN_U43141		HAN	U43141	B	DE
B.FR.HXB2_K03455		HXB2	K03455	B	FR
B.US.JRCSF_M38429		JRCSF	M38429	B	US
B.GB.MANC_U23487		MANC	U23487	B	GB
B.US.MNCG_M17449		MNCG	M17449	B	US
B.GA.OYI_M26727		OYI	M26727	B	GA
B.US.P896_U39362		P896	M96155	B	US
B.US.RF_M17451		RF	M17451	B	US
B.CN.RL42_U71182		RL42	U71182	B	CN
B.US.SF2_K02007		SF2	K02007	B	US
B.TW.TWCYS_AF086817		TWCYS	AF086817	B	TW
B.AU.VH_AF146728		VH	AF146728	B	AU
B.US.WEAU160_U21135		WEAU160	U21135	B	US
B.KR.WK_AF224507		WK	AF224507	B	KR

B.US.WR27_U26546	WR27	U26546	B	US
B.US.YU2_M93258	YU2	M93258	B	US
BF1.BR.93BR029.4_AF	93BR029.4	AF005495	BF1	BR
C.BR.92BR025_U52953	92BR025	U52953	C	BR
C.IN.93IN101_AB0238	93IN101	AB023804	C	IN
C.IN.93IN904_AF0671	93IN904	AF067157	C	IN
C.IN.93IN999_AF0671	93IN999	AF067154	C	IN
C.IN.94IN11246_AF06	94IN11246	AF067159	C	IN
C.IN.95IN21068_AF06	95IN21068	AF067155	C	IN
C.BW.96BW0402_AF110	96BW0402	AF110962	C	BW
C.BW.96BW1210_AF110	96BW1210	AF110972	C	BW
C.BW.96BW15B03_AF11	96BW15B03	AF110973	C	BW
C.ET.ETH2220_U46016	ETH2220	U46016	C	ET
C.BW.96BW11B01_AF11	96BW11	AF110969	C	BW
C.BW.00BW0762.1_AF44	00BW0762.1	AF443088	C	BW
C.BW.00BW0768.20_AF44	00BW0768.20	AF443089	C	BW
C.BW.00BW0874.21_AF44	00BW0874.21	AF443090	C	BW
C.BW.00BW1471.27_AF44	00BW1471.27	AF443091	C	BW
C.BW.00BW1616.2_AF44	00BW1616.2	AF443092	C	BW
C.BW.00BW1686.8_AF44	00BW1686.8	AF443093	C	BW
C.BW.00BW1759.3_AF44	00BW1759.3	AF443094	C	BW
C.BW.00BW1773.2_AF44	00BW1773.2	AF443095	C	BW
C.BW.00BW1783.5_AF44	00BW1783.5	AF443096	C	BW
C.BW.00BW1795.6_AF44	00BW1795.6	AF443097	C	BW
C.BW.00BW1811.3_AF44	00BW1811.3	AF443098	C	BW
C.BW.00BW1859.5_AF44	00BW1859.5	AF443099	C	BW
C.BW.00BW1880.2_AF44	00BW1880.2	AF443100	C	BW
C.BW.00BW1921.13_AF44	00BW1921.13	AF443101	C	BW
C.BW.00BW2036.1_AF44	00BW2036.1	AF443102	C	BW
C.BW.00BW2063.6_AF44	00BW2063.6	AF443103	C	BW
C.BW.00BW2087.2_AF44	00BW2087.2	AF443104	C	BW
C.BW.00BW2127.214_AF44	00BW2127.214	AF443105	C	BW
C.BW.00BW2128.3_AF44	00BW2128.3	AF443106	C	BW
C.BW.00BW2276.7_AF44	00BW2276.7	AF443107	C	BW
C.BW.00BW3819.3_AF44	00BW3819.3	AF443108	C	BW
C.BW.00BW3842.8_AF44	00BW3842.8	AF443109	C	BW
C.BW.00BW3871.3_AF44	00BW3871.3	AF443110	C	BW
C.BW.00BW3876.9_AF44	00BW3876.9	AF443111	C	BW
C.BW.00BW3886.8_AF44	00BW3886.8	AF443112	C	BW
C.BW.00BW3891.6_AF44	00BW3891.6	AF443113	C	BW
C.BW.00BW3970.2_AF44	00BW3970.2	AF443114	C	BW
C.BW.00BW5031.1_AF44	00BW5031.1	AF443115	C	BW
C.BW.96BW01B21_AF11	96BW01B21	AF110960	C	BW
C.BW.96BW0407_AF11	96BW0407	AF110963	C	BW
C.BW.96BW0502_AF11	96BW0502	AF110967	C	BW
C.BW.96BW06.J4_AF29	96BW06.J4	AF290028	C	BW
C.BW.96BW11.06_AF11	96BW11.06	AF110970	C	BW
C.BW.96BW1210_AF11	96BW1210	AF110972	C	BW
C.BW.96BW15B03_AF11	96BW15B03	AF110973	C	BW
C.BW.96BW16.26_AF11	96BW16.26	AF110978	C	BW
C.BW.96BW17A09_AF11	96BW17A09	AF110979	C	BW
C.BW.96BWMO1.5_AF44	96BWMO1.5	AF443074	C	BW
C.BW.96BWMO3.2_AF44	96BWMO3.2	AF443075	C	BW
C.BW.98BWMC12.2_AF44	98BWMC12.2	AF443076	C	BW

C.BW.98BWMC13.4_AF44	98BWMC13.4	AF443077	C	BW
C.BW.98BWMC14.a3_AF44	98BWMC14.a3	AF443078	C	BW
C.BW.98BWMO14.10_AF44	98BWMO14.10	AF443079	C	BW
C.BW.98BWMO18.d5_AF44	98BWMO18.d5	AF443080	C	BW
C.BW.98BWMO36.a5_AF44	98BWMO36.a5	AF443081	C	BW
C.BW.98BWMO37.d5_AF44	98BWMO37.d5	AF443082	C	BW
C.BW.99BW3932.12_AF44	99BW3932.12	AF443083	C	BW
C.BW.99BW4642.4_AF44	99BW4642.4	AF443084	C	BW
C.BW.99BW4745.8_AF44	99BW4745.8	AF443085	C	BW
C.BW.99BW4754.7_AF44	99BW4754.7	AF443086	C	BW
C.BW.99BWMC16.8_AF44	99BWMC16.8	AF443087	C	BW
CRF01_AE.CF.90CF11697_	90CF11697	AF197340	CRF01_AE	CF
CRF01_AE.CF.90CF402_U5	90CF402	U51188	CRF01_AE	CF
CRF01_AE.CF.90CF4071_A	90CF4071	AF197341	CRF01_AE	CF
CRF01_AE.TH.93TH057_AF	93TH057	AF197338	CRF01_AE	TH
CRF01_AE.TH.93TH065_AF	93TH065	AF197339	CRF01_AE	TH
CRF01_AE.TH.93TH253_U5	93TH253	U51189	CRF01_AE	TH
CRF01_AE.TH.95TNIH047_	95TNIH047	AB032741	CRF01_AE	TH
CRF01_AE.TH.CM240_U547	CM240	U54771	CRF01_AE	TH
CRF01_AE.TH.TH022_AB03	TH022	AB032740	CRF01_AE	TH
CRF02_AG.SN.98SEMP1211	98SEMP1211	AJ251056	CRF02_AG	SN
CRF02_AG.FR.DJ263_AF06	DJ263	AF063223	CRF02_AG	FR
CRF02_AG.FR.DJ264_AF06	DJ264	AF063224	CRF02_AG	FR
CRF02_AG.GH.G829_AF184	G829	AF184155	CRF02_AG	GH
CRF02_AG.NG.IBNG_L3910	IBNG	L39106	CRF02_AG	NG
CRF02_AG.SE.SE7812_AF1	SE7812	AF107770	CRF02_AG	SE
CRF03_AB.RU.KAL153-2_A	KAL153-2	AF193276	CRF03_AB	RU
CRF03_AB.RU.RU98001_AF	RU98001	AF193277	CRF03_AB	RU
CRF04_cpx.CY.94CY032-3	94CY032-3	AF049337	CRF04_cpx	CY
CRF04_cpx.GR.97PVCH_AF	97PVCH	AF119820	CRF04_cpx	GR
CRF04_cpx.GR.97PVMY_AF	97PVMY	AF119819	CRF04_cpx	GR
CRF05_DF.BE.VI1310_AF1	VI1310	AF193253	CRF05_DF	BE
CRF05_DF.BE.VI961_AF07	VI961	AF076998	CRF05_DF	BE
CRF06_cpx.ML.95ML127_A	95ML127	AJ288982	CRF06_cpx	ML
CRF06_cpx.ML.95ML84_AJ	95ML84	AJ245481	CRF06_cpx	ML
CRF06_cpx.SN.97SE1078_	97SE1078	AJ288981	CRF06_cpx	SN
CRF06_cpx.AU.BFP90_AF0	BFP90	AF064699	CRF06_cpx	AU
CRF11_cpx.CM.97CM-MP81	97CM-MP818	AJ291718	CRF11_cpx	CM
CRF11_cpx.GR.GR17_AF17	GR17	AF179368	CRF11_cpx	GR
D.CD.84ZR085_U88822	84ZR085	U88822	D	CD
D.UG.94UG1141_U8882	94UG1141	U88824	D	UG
D.CD.ELI_K03454	ELI	K03454	D	CD
D.CD.NDK_M27323	NDK	M27323	D	CD
F1.BR.93BR020.1_AF0	93BR020.1	AF005494	F1	BR
F1.FI.FIN9363_AF075	FIN9363	AF075703	F1	FI
F1.FR.MP411_AJ24923	MP411	AJ249238	F1	FR
F1.BE.VI850_AF07733	VI850	AF077336	F1	BE
F2.CM.MP257_AJ24923	MP257	AJ249237	F2	CM
F2KU.BE.VI1126_AF07	VI1126	AF076475	F2KU	BE
G.NG.92NG083_U88826	92NG083	U88826	G	NG
G.BE.DRCBL_AF084936	DRCBL	AF084936	G	BE
G.SE.SE6165_AF06164	SE6165	AF061642	G	SE
H.CF.90CF056_AF0054	90CF056	AF005496	H	CF
H.BE.VI991_AF190127	VI991	AF190127	H	BE

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H.BE.VI997_AF190128	VI997	AF190128	H	BE
J.SE.SE7022_AF08239	SE7022	AF082395	J	SE
J.SE.SE7887_AF08239	SE7887	AF082394	J	SE
K.CD.EQTB11C_AJ2492	EQTB11C	AJ249235	K	CD
K.CM.MP535_AJ249239	MP535	AJ249239	K	CM
N.CM.YBF30_AJ006022	YBF30	AJ006022	N	CM
O.SN.99SE-MP1299_ZX	SEMP1299	AJ302646	O	SN
O.SN.99SE-MP1300_ZX	SEMP1300	AJ302647	O	SN
O.CM.ANT70_L20587	ANT70	L20587	O	CM
O.CM.MVP5180_L20571	MVP5180	L20571	O	CM
U.CD.-.83CD0031	83CD0031	AF286236	U	CD

Table 11. HIV Gag Sequence Alignment
 GCG Multiple Sequence File.
 Written by Omega 1.1

Name: 00BW0762_1	Len: 556	Check: 2513	Weight: 1.00
Name: 00BW0768_2	Len: 556	Check: 8965	Weight: 1.00
Name: 00BW0874_2	Len: 556	Check: 9574	Weight: 1.00
Name: 00BW1471_2	Len: 556	Check: 5395	Weight: 1.00
Name: 00BW1616_2	Len: 556	Check: 4692	Weight: 1.00
Name: 00BW1686_8	Len: 556	Check: 7822	Weight: 1.00
Name: 00BW1759_3	Len: 556	Check: 7777	Weight: 1.00
Name: 00BW1773_2	Len: 556	Check: 9727	Weight: 1.00
Name: 00BW1783_5	Len: 556	Check: 9681	Weight: 1.00
Name: 00BW1795_6	Len: 556	Check: 9667	Weight: 1.00
Name: 00BW1811_3	Len: 556	Check: 4422	Weight: 1.00
Name: 00BW1859_5	Len: 556	Check: 7320	Weight: 1.00
Name: 00BW1880_2	Len: 556	Check: 1603	Weight: 1.00
Name: 00BW1921_1	Len: 556	Check: 883	Weight: 1.00
Name: 00BW2036_1	Len: 556	Check: 2591	Weight: 1.00
Name: 00BW2063_6	Len: 556	Check: 5152	Weight: 1.00
Name: 00BW2087_2	Len: 556	Check: 5183	Weight: 1.00
Name: 00BW2127_2	Len: 556	Check: 5469	Weight: 1.00
Name: 00BW2128_3	Len: 556	Check: 9621	Weight: 1.00
Name: 00BW2276_7	Len: 556	Check: 4153	Weight: 1.00
Name: 00BW3819_3	Len: 556	Check: 4227	Weight: 1.00
Name: 00BW3842_8	Len: 556	Check: 9312	Weight: 1.00
Name: 00BW3871_3	Len: 556	Check: 501	Weight: 1.00
Name: 00BW3876_9	Len: 556	Check: 773	Weight: 1.00
Name: 00BW3886_8	Len: 556	Check: 2351	Weight: 1.00
Name: 00BW3891_6	Len: 556	Check: 129	Weight: 1.00
Name: 00BW3970_2	Len: 556	Check: 8768	Weight: 1.00
Name: 00BW5031_1	Len: 556	Check: 3966	Weight: 1.00
Name: 96BW01B21	Len: 556	Check: 602	Weight: 1.00
Name: 96BW0407	Len: 556	Check: 9836	Weight: 1.00
Name: 96BW0502	Len: 556	Check: 6402	Weight: 1.00
Name: 96BW06_J4	Len: 556	Check: 254	Weight: 1.00
Name: 96BW11_06	Len: 556	Check: 6801	Weight: 1.00
Name: 96BW1210	Len: 556	Check: 6016	Weight: 1.00
Name: 96BW15B03	Len: 556	Check: 6072	Weight: 1.00
Name: 96BW16_26	Len: 556	Check: 9409	Weight: 1.00
Name: 96BW17A09	Len: 556	Check: 2723	Weight: 1.00
Name: 96BWMO1_5	Len: 556	Check: 5051	Weight: 1.00
Name: 96BWMO3_2	Len: 556	Check: 496	Weight: 1.00
Name: 98BWMC12_2	Len: 556	Check: 1164	Weight: 1.00
Name: 98BWMC13_4	Len: 556	Check: 4961	Weight: 1.00
Name: 98BWMC14_a	Len: 556	Check: 7351	Weight: 1.00
Name: 98BWMO14_1	Len: 556	Check: 288	Weight: 1.00
Name: 98BWMO18_d	Len: 556	Check: 6836	Weight: 1.00
Name: 98BWMO36_a	Len: 556	Check: 4386	Weight: 1.00
Name: 98BWMO37_d	Len: 556	Check: 6900	Weight: 1.00
Name: 99BW3932_1	Len: 556	Check: 292	Weight: 1.00
Name: 99BW4642_4	Len: 556	Check: 1347	Weight: 1.00
Name: 99BW4745_8	Len: 556	Check: 7980	Weight: 1.00
Name: 99BW4754_7	Len: 556	Check: 9892	Weight: 1.00
Name: 99BWMC16_8	Len: 556	Check: 4279	Weight: 1.00
Name: A2_CD_97CD	Len: 556	Check: 9920	Weight: 1.00
Name: A2_CY_94CY	Len: 556	Check: 3070	Weight: 1.00
Name: A2D_97KR	Len: 556	Check: 6350	Weight: 1.00
Name: A2G_CD_97C	Len: 556	Check: 856	Weight: 1.00
Name: A_BY_97BL0	Len: 556	Check: 9315	Weight: 1.00

Name: A_KE_Q23_A	Len: 556	Check: 2442	Weight: 1.00
Name: A_SE_SE659	Len: 556	Check: 8612	Weight: 1.00
Name: A_SE_SE725	Len: 556	Check: 8315	Weight: 1.00
Name: A_SE_SE753	Len: 556	Check: 2915	Weight: 1.00
Name: A_SE_SE853	Len: 556	Check: 9112	Weight: 1.00
Name: A_SE_SE889	Len: 556	Check: 8732	Weight: 1.00
Name: A_SE_UGSE8	Len: 556	Check: 8696	Weight: 1.00
Name: A_UG_92UG0	Len: 556	Check: 6290	Weight: 1.00
Name: A_UG_U455_	Len: 556	Check: 164	Weight: 1.00
Name: AC_IN_2130	Len: 556	Check: 8482	Weight: 1.00
Name: AC_RW_92RW	Len: 556	Check: 977	Weight: 1.00
Name: AC_SE_SE94	Len: 556	Check: 8752	Weight: 1.00
Name: ACD_SE_SE8	Len: 556	Check: 9655	Weight: 1.00
Name: ACG_BE_VI1	Len: 556	Check: 3777	Weight: 1.00
Name: AD_SE_SE69	Len: 556	Check: 732	Weight: 1.00
Name: AD_SE_SE71	Len: 556	Check: 8506	Weight: 1.00
Name: ADHK_NO_97	Len: 556	Check: 5257	Weight: 1.00
Name: ADK_CD_MAL	Len: 556	Check: 5301	Weight: 1.00
Name: AG_BE_VI11	Len: 556	Check: 1610	Weight: 1.00
Name: AG_NG_92NG	Len: 556	Check: 4188	Weight: 1.00
Name: AGHU_GA_VI	Len: 556	Check: 8242	Weight: 1.00
Name: AGU_CD_Z32	Len: 556	Check: 2601	Weight: 1.00
Name: AJ_BW_BW21	Len: 556	Check: 8389	Weight: 1.00
Name: B_AU_VH_AF	Len: 556	Check: 9166	Weight: 1.00
Name: B_CN_RL42_	Len: 556	Check: 3865	Weight: 1.00
Name: B_DE_D31_U	Len: 556	Check: 9464	Weight: 1.00
Name: B_DE_IAN_U	Len: 556	Check: 6999	Weight: 1.00
Name: B_FR_HXB2_	Len: 556	Check: 141	Weight: 1.00
Name: B_GA_OYI_	Len: 556	Check: 7578	Weight: 1.00
Name: B_GB_CAM1_	Len: 556	Check: 8023	Weight: 1.00
Name: B_GB_GB8_A	Len: 556	Check: 2675	Weight: 1.00
Name: B_GB_MANC_	Len: 556	Check: 8961	Weight: 1.00
Name: B_KR_WK_AF	Len: 556	Check: 7372	Weight: 1.00
Name: B_NL_3202A	Len: 556	Check: 7117	Weight: 1.00
Name: B_TW_TWCYS	Len: 556	Check: 8767	Weight: 1.00
Name: B_US_BC_LO	Len: 556	Check: 7091	Weight: 1.00
Name: B_US_DH123	Len: 556	Check: 5049	Weight: 1.00
Name: B_US_JRCSF	Len: 556	Check: 975	Weight: 1.00
Name: B_US_MNCG_	Len: 556	Check: 688	Weight: 1.00
Name: B_US_P896_	Len: 556	Check: 8809	Weight: 1.00
Name: B_US_RF_M1	Len: 556	Check: 9306	Weight: 1.00
Name: B_US_SF2_K	Len: 556	Check: 9799	Weight: 1.00
Name: B_US_WEAU1	Len: 556	Check: 9636	Weight: 1.00
Name: B_US_WR27_	Len: 556	Check: 3349	Weight: 1.00
Name: B_US_YU2_M	Len: 556	Check: 8828	Weight: 1.00
Name: BF1_BR_93B	Len: 556	Check: 7935	Weight: 1.00
Name: C_BR_92BR0	Len: 556	Check: 4429	Weight: 1.00
Name: C_BW_96BW0	Len: 556	Check: 1550	Weight: 1.00
Name: C_BW_96BW1	Len: 556	Check: 7158	Weight: 1.00
Name: C_BW_96BW1	Len: 556	Check: 6016	Weight: 1.00
Name: C_BW_96BW1	Len: 556	Check: 6072	Weight: 1.00
Name: C_ET_ETH22	Len: 556	Check: 4314	Weight: 1.00
Name: C_IN_93IN1	Len: 556	Check: 6959	Weight: 1.00
Name: C_IN_93IN9	Len: 556	Check: 9362	Weight: 1.00
Name: C_IN_93IN9	Len: 556	Check: 3298	Weight: 1.00
Name: C_IN_94IN1	Len: 556	Check: 6744	Weight: 1.00
Name: C_IN_95IN2	Len: 556	Check: 8559	Weight: 1.00
Name: CRF01_AE_C	Len: 556	Check: 4763	Weight: 1.00
Name: CRF01_AE_C	Len: 556	Check: 4315	Weight: 1.00
Name: CRF01_AE_C	Len: 556	Check: 3920	Weight: 1.00

Name: CRF01_AE_T	Len: 556	Check: 5074	Weight: 1.00
Name: CRF01_AE_T	Len: 556	Check: 4026	Weight: 1.00
Name: CRF01_AE_T	Len: 556	Check: 2981	Weight: 1.00
Name: CRF01_AE_T	Len: 556	Check: 6648	Weight: 1.00
Name: CRF01_AE_T	Len: 556	Check: 6948	Weight: 1.00
Name: CRF01_AE_T	Len: 556	Check: 6129	Weight: 1.00
Name: CRF02_AG_F	Len: 556	Check: 8134	Weight: 1.00
Name: CRF02_AG_F	Len: 556	Check: 8925	Weight: 1.00
Name: CRF02_AG_G	Len: 556	Check: 9991	Weight: 1.00
Name: CRF02_AG_N	Len: 556	Check: 9388	Weight: 1.00
Name: CRF02_AG_S	Len: 556	Check: 9371	Weight: 1.00
Name: CRF02_AG_S	Len: 556	Check: 3289	Weight: 1.00
Name: CRF03_AB_R	Len: 556	Check: 5554	Weight: 1.00
Name: CRF03_AB_R	Len: 556	Check: 5307	Weight: 1.00
Name: CRF04_cpx_	Len: 556	Check: 5488	Weight: 1.00
Name: CRF04_cpx_	Len: 556	Check: 6046	Weight: 1.00
Name: CRF04_cpx_	Len: 556	Check: 3807	Weight: 1.00
Name: CRF05_DF_B	Len: 556	Check: 6702	Weight: 1.00
Name: CRF05_DF_B	Len: 556	Check: 5563	Weight: 1.00
Name: CRF06_cpx_	Len: 556	Check: 8164	Weight: 1.00
Name: CRF06_cpx_	Len: 556	Check: 1975	Weight: 1.00
Name: CRF06_cpx_	Len: 556	Check: 1486	Weight: 1.00
Name: CRF06_cpx_	Len: 556	Check: 4050	Weight: 1.00
Name: CRF11_cpx_	Len: 556	Check: 1515	Weight: 1.00
Name: CRF11_cpx_	Len: 556	Check: 9474	Weight: 1.00
Name: D_CD_84ZR0	Len: 556	Check: 4739	Weight: 1.00
Name: D_CD_ELI_K	Len: 556	Check: 8533	Weight: 1.00
Name: D_CD_NDK_M	Len: 556	Check: 6100	Weight: 1.00
Name: D_UG_94UG1	Len: 556	Check: 7681	Weight: 1.00
Name: F1_BE_VI85	Len: 556	Check: 8540	Weight: 1.00
Name: F1_BR_93BR	Len: 556	Check: 241	Weight: 1.00
Name: F1_FI_FIN9	Len: 556	Check: 7510	Weight: 1.00
Name: F1_FR_MP41	Len: 556	Check: 9846	Weight: 1.00
Name: F2_CM_MP25	Len: 556	Check: 1247	Weight: 1.00
Name: F2KU_BE_VI	Len: 556	Check: 2186	Weight: 1.00
Name: G_BE_DRCBL	Len: 556	Check: 8049	Weight: 1.00
Name: G_NG_92NG0	Len: 556	Check: 254	Weight: 1.00
Name: G_SE_SE616	Len: 556	Check: 6407	Weight: 1.00
Name: H_BE_VI991	Len: 556	Check: 808	Weight: 1.00
Name: H_BE_VI997	Len: 556	Check: 4749	Weight: 1.00
Name: H_CF_90CF0	Len: 556	Check: 4718	Weight: 1.00
Name: J_SE_SE702	Len: 556	Check: 2564	Weight: 1.00
Name: J_SE_SE788	Len: 556	Check: 2692	Weight: 1.00
Name: K_CD_EQTB1	Len: 556	Check: 6586	Weight: 1.00
Name: K_CM_MP535	Len: 556	Check: 3803	Weight: 1.00
Name: N_CM_YBF30	Len: 556	Check: 8603	Weight: 1.00
Name: O_CM_ANT70	Len: 556	Check: 365	Weight: 1.00
Name: O_CM_MVP51	Len: 556	Check: 9160	Weight: 1.00
Name: O_SN_99SE_	Len: 556	Check: 9380	Weight: 1.00
Name: O_SN_99SE_	Len: 556	Check: 8796	Weight: 1.00
Name: U_CD_83C	Len: 556	Check: 4633	Weight: 1.00

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00BW0762_1	MGARASILRG	.EKLDKWEKI	RLRPGGRKHY	MIKHIVWASR	ELERFALNPG
00BW0768_2	MGARASVLRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW0874_2	MGARASILRG	.GKLDTWEKI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
00BW1471_2	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW1616_2	MGARASILRG	.GKLDEWEKI	RLRPGGKKRY	MMKHLVWASR	ELERFALNPG

00BW1686_8	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
00BW1759_3	MGARASILRG	.GKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW1773_2	MGASASILRG	.GKLDKWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNSG
00BW1783_5	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MMKHLVWASR	ELERFALNPG
00BW1795_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MMKHLVWASR	ELERFALNPG
00BW1811_3	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW1859_5	MGARASVLKG	.EKLDWEKI	RLRPGGKKGY	MLKHLVWASR	ELERFALNPG
00BW1880_2	MGARASILRG	.GKLDKWERI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
00BW1921_1	MGARASILRG	.GKLDTWEKI	RLRPGGKKRY	MLKHLIWTSR	ELERFALNPD
00BW2036_1	MGARASILRG	.EKLDTWERI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW2063_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKQY	MIKHLVWASR	ELERFALNPG
00BW2087_2	MGARASILRG	.GKLDTWEKI	KLRPGGKKSY	KLKHLVWASR	ELERFALNPS
00BW2127_2	MGARASILRG	.XEKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELENFALNPG
00BW2128_3	MGARASILRG	.GQLDKWEKI	RLRPGGKKHY	MLKHLVWASG	ELEKFALNPG
00BW2276_7	MGARASVLKG	.DKLDWEKI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW3819_3	MGARASILRG	.GKLDAWERT	RLRPGGKKHY	RLKHLVWASR	ELERFALNPG
00BW3842_8	MGARASVLRG	.EKLDTWERI	KLRPGGKKHY	MLKHIVWASR	ELERFALNPG
00BW3871_3	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
00BW3876_9	MGARASILKG	.GKLDTWEKI	RLRPGGKKHY	MVXHLVWASR	ELERFALNPG
00BW3886_8	MGARASILRG	.GKLDKWEKI	RLRPGGKKCY	MIKHIIWASR	ELERFALNPG
00BW3891_6	MGARASILRG	.GKLDKWEKI	RLRPGGKKKY	MLKHLVWASR	ELERFALNSG
00BW3970_2	MGARASILRG	.GKLDAWERI	KLRPGGKKHY	MLKHLVWASR	ELERFALNPS
00BW5031_1	MGARASILRG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
96BW01B21	MGARASILRG	.GKLDQWEKI	RLRPGGKKCY	MLKHLVWASR	ELERFALNPG
96BW0407	MGARASILRG	.GKLDAWERI	RLRPGGKKCY	MMKHLVWASR	ELEKFALNPG
96BW0502	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELEGFALNPG
96BW06_J4	MGARASILRG	.GNLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
96BW11_06	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MIKHLVWASR	ELERFALNPG
96BW1210	MGARASILRG	.EKLDTWEKI	RLRPGGKKRY	MMKHLVWASR	ELENFALNPA
96BW15B03	MGARASILRG	.EKLDTWEKI	RSRPGGKKCY	MLKHIVWASR	ELERFALNPG
96BW16_26	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MLKHLVWASR	ELERFALNPG
96BW17A09	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
96BWM01_5	MGARASILRR	.GKLDKWEKI	RLRPGGKKRY	MIKHLVWASR	ELERYALNPG
96BWM03_2	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHIVWASR	ELEKFALNPG
98BWMC12_2	MGARASILRG	.EKLDTWEKI	RLRPGGKKQY	RIKHLVWASR	ELDRFALNSG
98BWMC13_4	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MMKHLVWASR	ELGRFALNPG
98BWMC14_a	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
98BWM014_1	MGARASILRG	.GKLDKWERI	RLRPGGKKQY	RLKHLVWASR	ELERFALNPG
98BWM018_d	MGARASILRG	.GKLDTWERI	KLRPGGKKHY	MMKHLVWASR	ELERFALNPS
98BWM036_a	MGARASILRG	.GKLDTWEKI	RLRPGGKKPY	MLKHLVWASR	ELERFALNPG
98BWM037_d	MGARASILRG	.GKLDWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
99BW3932_1	MGARASILRG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPE
99BW4642_4	MGARASVLKG	.EKLDTWEKI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
99BW4745_8	MGARASILRG	.GKLDGWERI	KLRPGGKKTY	MLKHLVWASR	ELERFALNPS
99BW4754_7	MGARASILRG	.EKLDWEKI	WLRPGGKNHY	MLKHLVWASR	ELERFALNPA
99BWMC16_8	MGARASILRG	.GKLDTWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
A2_CD_97CD	MGARASVLSG	.GKLEAWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPS
A2_CY_94CY	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPG
A2D_97KR	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
A2G_CD_97C	..ARASILSG	.GKLEAWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFSINPG
A_BY_97BL0	XGARASVLSG	.GKLD_A_EKI	RLRPGGKKKY	RIKHLVWASR	ELERFALNPG
A_KE_Q23_A	MGARASVLSG	.GKFDWEKI	RLRPGGKKKY	RMKHLIWASR	ELDRFALNPS
A_SE_SE659	...RASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
A_SE_SE725	...RASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPS
A_SE_SE753	MGARASVLSG	.GKLDWEKI	RLRPGGKKQY	RLKHLVWASR	ELERFALNPS
A_SE_SE853	...RASVLSG	.GRLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELDRFALNPS
A_SE_SE889	...RASVLSG	.EKKDAWEKI	RLRPGGKKKY	KLKHMVWARR	ELEKSALNPS
A_SE_UGSE8	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFALNPG
A_UG_92UG0	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
A_UG_U455	MGARASVLSG	.KKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELEKFTLNPG

AC_IN_2130	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MIKHLVWASR	ELERFALNPG
AC_RW_92RW	MGARASILRG	.GKLDAWEKI	KLKPGGKKTY	MMKHLVWASR	ELERFALNPD
AC_SE_SE94	...RASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELDRFALNPS
ACD_SE_SE8	MGARASILSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELDRFALNPS
ACG_BE_VI1	MGARASVLTG	.GKLDTWERI	RLRPAGKKKY	RMKLLVWASR	ELERFAINPG
AD_SE_SE69	MGARASVLSG	.ERLDEWEKI	QLRPGGKKRY	RLKHIVWASR	ELERFALNPG
AD_SE_SE71	...RASVLSG	.GKLDAWEKI	RLRPGGRKKY	KLKHIVWASR	ELERFALNPS
ADHK_NO_97	MGARASILSG	.GKLDKWEKI	RLRPGGKKQY	RLKHLVWASR	ELDRFALNPS
ADK_CD_MAL	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
AG_BE_VI11	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFAINPG
AG_NG_92NG	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPD
AGHU_GA_VI	MGARASILSG	.GKLDAWEKI	RLRPGGKKKY	QIKHIVWASR	ELERFALNPG
AGU_CD_Z32	MGARASVLSG	.GKLDKWEKI	RLRPGGKKQY	KLKHIVWASR	ELERFALNPG
AJ_BW_BW21	MGARASVLSG	.GKLDAWEKI	RLRPGGKKQY	RMKHLVWASR	ELERFALNPG
B_AU_VH_AF	MGARASVLSG	.GELDRWEKI	RLRPGGKKTY	KLKHIVWASR	ELERFAVNPG
B_CN_RL42	MGARASVLSG	.GQLDRWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
B_DE_D31_U	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAVNPG
B_DE_HAN_U	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	QLKHIVWASR	ELERFAVNPG
B_FR_HXB2	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
B_GA_OYI	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	QLKHIVWASR	ELERFAINPG
B_GB_CAM1	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
B_GB_GB8_A	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHVVWASR	ELERFAVNPG
B_GB_MANC	MGARASVLSG	.GKLDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFTVNLG
B_KR_WK_AF	MGARASILSG	.GELDQWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
B_NL_3202A	MGARASVLSG	.GELDKWEKI	RLRPGGKKRY	KLKHIVWASR	ELERFAVNPG
B_TW_TWCYS	MGARASILSA	.GELDKWERV	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
B_US_BC_L0	MGARASVLSG	.GKLDKWEKI	RLRPGGKKKY	KLKHLVWASR	ELERFAVNPG
B_US_DH123	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
B_US_JRCSF	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFAVNPG
B_US_MNCG	MGARASVLSG	.GELDRWENI	RLRPGGKKKY	KLKHVVWASR	ELERFAVNPG
B_US_P896	MGARASVLSG	.GELDRWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPS
B_US_RF_M1	MGARASVLSG	.GKLDKWEKI	RLRPRGKKRY	KLKHIVWASR	ELERFAVNPS
B_US_SF2_K	MGARASVLSG	.GELDKWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFAVNPG
B_US_WEAU1	MGARASVLSG	.GELDRWEKI	RLRPGGNKKY	KLKHIVWASR	ELERFAVNPG
B_US_WR27	MGARASMLSG	.GELDKWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFAVNPG
B_US_YU2_M	MGARASVLSA	.GELDKWEKI	RLRPGGKKQY	RLKHIVWASR	ELERFAVDPG
BF1_BR_93B	MGARASVISG	.GELDKWEKI	RLRPGGHKKY	RLKHIVWASR	ELERFAVNPG
C_BR_92BR0	MGARASILRG	.GKLDAWERI	KLKPGGKKHY	MMKHLVWASR	ELERFALDPG
C_BW_96BW0	MGARASILRG	.GKLDAWEKI	RLRPGGKKQY	RIKHLVWASR	ELERFALNPG
C_BW_96BW1	MGARASILRG	.GKLDTWEKI	RLRPGGKKRY	MIKHLVWASR	ELERFALNPG
C_BW_96BW1	MGARASILRG	.EKLDTWKEI	RLRPGGKKRY	MMKHLVWASR	ELENFALNPA
C_BW_96BW1	MGARASISRG	.EKLDTWKEI	RSRPGGKKCY	MLKHIVWASR	ELERFALNPG
C_ET_ETH22	MGARASILRG	.EKLDWEKI	KLKPGGKKHY	MLKHLVWASR	ELEKFALNPD
C_IN_93IN1	MGARASILRG	.GKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELERFALNPG
C_IN_93IN9	MGARASILRG	.EKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELDRFALNPG
C_IN_93IN9	MGARASILRG	.EKLDKWERI	RLRPGGKKHY	MLKHLVWASR	ELDRFALNPG
C_IN_94IN1	MGARASILRG	.GKLDKWEKI	RLRPGGKKHY	MLKHLVWASR	ELEKFALNPG
C_IN_95IN2	MGARASILRG	.GKLDKWEKI	RLRPGGKKRY	MLKHLVWASR	ELDRFAVNPG
CRF01_AE_C	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPG
CRF01_AE_C	MGARASILSG	.GKLDAWEKI	RLRPGGKKQY	RMKHLVWASR	ELERFALNPG
CRF01_AE_C	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF01_AE_T	MSARASVLSG	.EKLNAWEKI	RLRPGGRKKY	KLKHLVWASR	ELEKFALNPG
CRF01_AE_T	MGARASVLSG	..KLDLEKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
CRF01_AE_T	MGARASVLSG	.GKLDAWEKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
CRF01_AE_T	MGAKASVLSG	.GKLDAWEKI	RLRPGGRKKY	HLKHIVWASR	ELERFALNPG
CRF01_AE_T	MGARASVLSG	.GKLDAWEKI	RLRPGGRKKY	RLKHLVWASR	ELERFALNPS
CRF01_AE_T	MGARASILSG	.GKLDAWEKI	RLRPGGRKKY	RMKHLVWASR	ELERFALNPG
CRF02_AG_F	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF02_AG_F	MGARASVLSG	.GKLDSWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF02_AG_G	MGARVSVLRG	.GQLDTWEKI	RLRPGGKKKY	KMKLLVWASR	ELERFAVNPG

CRF02_AG_N	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF02_AG_S	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF02_AG_S	.GARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF03_AB_R	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RIKHLVWASR	ELERFALNPG
CRF03_AB_R	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RIKHLVWASR	ELERFALNPS
CRF04_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RIKHLVWASR	ELERFALNPS
CRF04_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF04_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF05_DF_B	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	RIKHLI WASR	ELERFALNPG
CRF05_DF_B	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
CRF06_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFALNPG
CRF06_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	KMKHLVWASR	ELERFALNPG
CRF06_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
CRF06_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFALNPG
CRF06_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELDRFALNPG
CRF11_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
CRF11_cpx	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPS
D_CD_84ZRO	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFALNPG
D_CD_ELI_K	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHIVWASR	ELERYALNPG
D_CD_NDK_M	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	ALKHLI WASR	ELERFALNPG
D_UG_94UG1	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
F1_BE_VI85	MGARASVLSG	.GKLDWEKI	QLRPGGKKRY	KMKHLI WASR	ELERFALDPG
F1_BR_93BR	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALDPG
F1_FI_FIN9	MGARASVLSG	.GKLDWEKI	RLRPGGKKQY	RIKHLVWASR	ELERFAIDPG
F1_FR_MP41	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RMKHLVWASR	ELERFAIDPG
F2_CM_MP25	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHIVWASR	ELERFALNPG
F2KU_BE_VI	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	RLKHLVWASR	ELERFALNPG
G_BE_DRCBL	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	RMKHLVWASR	ELDRFALNPG
G_NG_92NG0	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	KLKHIVWASR	ELGRFALNPG
G_SE_SE616	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	KLKHIVWASR	ELERFALNPG
H_BE_VI991	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	RLKHLVWASR	ELERFALNPG
H_BE_VI997	MGARASVLSG	.GKLDWEKI	RLRPGGKKRY	RLKHIVWASR	ELERFALNPG
H_CF_90CF0	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG
J_SE_SE702	MGARASVLSG	.GKLDWEKI	RLRPGGKKQY	RIKHLVWASR	ELDRFALNPG
J_SE_SE788	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RIKHLVWASR	ELDRFALNPG
K_CD_EQTB1	MGARASVLSG	.GKLDWEKI	QLRPGGKKKY	RLKHLVWASR	ELERFALNPG
K_CM_MP535	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	KLKHIVWASR	ELERFALNPG
N_CM_YBF30	MGARASVLSG	.GKLDWEKI	YLRPGGKKKY	RMKHLVWASR	ELERFALNPG
O_CM_ANT70	MGARASVLSG	.GKLDWEKI	RLKPGSKKKY	RLKHLVWASR	ELERFALNPG
O_CM_MVP51	MGARASVLSG	.GKLDWEKI	RLKPGSKKKY	RLKHLVWASR	ELERYACNPG
O_SN_99SE	MGARASVLSG	.GKLDWEKI	RLKPGSKKKY	RLKHLVWASR	ELDRSACNPG
O_SN_99SE	MGARASVLSG	.GKLDWEKI	RLKPGSKKKY	RLKHLVWASR	ELERFALNPG
U_CD_83C	MGARASVLSG	.GKLDWEKI	RLRPGGKKKY	RLKHLVWASR	ELERFALNPG

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00BW0762_1	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	KKIDVRDTKE
00BW0768_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIEVRDTKE
00BW0874_2	LLETAEGCRQ	IIKQLHPALQ	TGTEELRSLY	NTVATLYCVH	RGIEIRDTKE
00BW1471_2	LLETADGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIKVDQDKE
00BW1616_2	LLETSDGCKQ	IMKQLQPALQ	TGTEELKSLF	NTVATLYCVH	ANIDVRDTKE
00BW1686_8	LLETSDGCKQ	IIQQLQPALQ	TGTEELRSLF	NTVATLYCAH	KGISIQDQDKE
00BW1759_3	LLETAEGCKR	IIKQLQPALQ	TGTEELKSLH	NTVATLYCVH	KEIDVRDTKE
00BW1773_2	LLETAEGCKQ	IIKQLQPALQ	TGTEELKSLY	NTVATLYCVH	AGIEVRDTKE
00BW1783_5	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLY	NTVATLYCVH	AKIEVRDTKE
00BW1795_6	LLETSEGCKQ	IMKQLQPAIQ	TGTEELRSLF	NTVATLYCVH	EGIDVQDQDKE
00BW1811_3	LLETAAGCKQ	IIIRQLHPALQ	TGTEELRSLY	NTVATLYCVH	AEIEVRDTKE
00BW1859_5	LLETSEGCRQ	IMRQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIPVRDTKE
00BW1880_2	LLETAEGCKQ	IIIRQLHPALQ	TGTQELRSLY	NTVATLYCVH	KDIEVRDTKE
00BW1921_1	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLY	NTVATLYCVH	KGIEVQDQDKE
00BW2036_1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KKIQVQDQDKE
00BW2063_6	LLETADGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EGIDVRDTKE

00BW2087_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIEVRDTKE
00BW2127_2	LLETSEGCRQ	IIKQLQPALQ	TGTEELRSLY	NTIAVLYCAH	QRIKVQDTKE
00BW2128_3	LLETSEGCKQ	IIKQLHPALQ	TGTEELKSLY	NTVAVLYCVH	AGIAVRDTKE
00BW2276_7	LLETSEGCKQ	IMQQLQPALK	TGTEELISLY	NTVATLYCVH	EKIQVQDTKE
00BW3819_3	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	QKIEIRDTE
00BW3842_8	LMETSEGCKQ	IIQQLQPALQ	TGTEELRSLF	NTIATLYCVH	KGIKVQDTKE
00BW3871_3	LLETSDGCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIKVQDTKE
00BW3876_9	LLETSEGCEQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	ARIEVKDTKE
00BW3886_8	LLETAEGCTQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AGIDVRDTKE
00BW3891_6	LLETSDGCKQ	IIQQLQPALK	TGTEELRSLY	NTVATLYCVH	NNIEIRDTE
00BW3970_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELKSLF	NTVATLYCVH	EKIEIRDTE
00BW5031_1	LLETADGCKQ	IIKQLQPALK	TGTEELRSLY	NTVATLYCVH	RNIEVQDTKE
96BW01B21	LLETSEGCKQ	IMEQLQPALQ	TGTEELKSLY	NTVATLYCVH	ENIEVRDTKE
96BW0407	LLETSEGCKQ	IIRQLHPALQ	TGSEELKSLF	NTVATLYCVH	EKIEVRDTKE
96BW0502	LLETAEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	AGIEVRDTKE
96BW06_J4	LLETSEGCKQ	IMQQLQPALQ	TGTEELRSLF	NTVATLYCVH	KGIKVQDTKE
96BW11_06	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EGIEVQDTKE
96BW1210	LLETAEGCKQ	IMKQLQPALK	TGTEELKSLY	NTVATLYCVH	EKIEVRDTKE
96BW15B03	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIKVQDTKE
96BW16_26	LLETSEGCRQ	IMIQLQPALK	TGTEELKSLY	NTVAVLFCVH	AGIEVQDTKE
96BW17A09	LLETAEGCKQ	IIKQLQPALQ	TGTEELKSLY	NTVATLYCVH	QGIEVRDTKE
96BWM01_5	LLETSEGCKQ	IIKQLQPTIQ	TGTEELKSLY	NTVATLYCVH	KGIDVRDTKE
96BWM03_2	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EKIEVRDTKE
98BWMC12_2	LLETAEGCTQ	IMRQLQPALQ	TGTEELRSLY	NTVATLYCVL	KGIKVRDTKE
98BWMC13_4	LLETSEGCKQ	IMRQLQPAIQ	TGTEELRSLF	NTVATLYCVH	EGIDVKDTKE
98BWMC14_a	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	MGIEVRDTKE
98BWM014_1	LLETAEGCKQ	IIQQLQPALK	TGTEELRSLF	NTVATLYWVH	KNVEVRDTKE
98BWM018_d	LLETSEGCRK	IMKQLQPSIQ	TGTEELRSLY	NTIATLYCVH	EKIEVRDTKE
98BWM036_a	LLETAEGCKQ	ILQQLQPALK	TGTEELKSLY	NTVATLYCVH	QGIEVRDTKE
98BWM037_d	LLENSEGCKQ	IMKQLQPALQ	TGTEELKSLF	NTVATLYCVH	EKIEVRDTKE
99BW3932_1	LLETADGCKQ	IIKQLQPAFQ	TGTEELRSLY	NSIAVLYCVH	RRLTIQDTKE
99BW4642_4	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	ERIQVRDTKE
99BW4745_8	LLETTEGCRQ	IIRQLQPALQ	TGTEELKSLY	NTVATLYCVH	NNIEIRDTE
99BW4754_7	LLETAEGCKQ	IIKQLHPALQ	TGTEELRSLY	NTVATLYCVH	NKIEVQDTKE
99BWMC16_8	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTIATLYCVH	ESIEVRDTKE
A2_CD_97CD	LLETETGCRR	IFGQLQPALE	TGTEELRSLY	NTIAVLYFVH	QKIEVKDTKE
A2_CY_94CY	LLETPEGCRQ	IIRQLQPALQ	TGTEELKSLY	NTVVVLYWVH	QRVDVKDTKE
A2D_97KR	LLETSEGCKQ	IIGQLEPSIK	TCSEEIKSLF	NAVVTLYCVH	QRIEVRDTKE
A2G_CD_97C	LLETAAGCRQ	ILGQLQPALQ	TGTEELRSLY	NTVAVLYCVH	QKIEVKDTKE
A_BY_97BL0	LLETSEGCKQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	QRIEIKDTKE
A_KE_Q23_A	LLETADGCRQ	IMEKLQPALK	TGTEELKSLF	NTVATLYCVH	QRIDVKDTKE
A_SE_SE659	LLETTEGCRQ	IEQLQPALK	TGTEELKSLF	NTVATLYCVH	QRIDVKDTKE
A_SE_SE725	LLETTEGCRQ	IMEQLQSALK	TGTEELRSLF	NTVAVLYCVH	QRIEIKDTKE
A_SE_SE753	LLETAEGCQ	IMKQLQPALK	TGTEELRSLY	NTVATLYCVH	QRINVTDTKE
A_SE_SE853	LLETTEGCRQ	IIGQLQPAFK	TGTEELKSLY	NTVATLWCVH	QRIDVKDTKE
A_SE_SE889	LLETTEGCRQ	IMDKLQPALK	TGTEELRSLY	NTVATLYCVH	QKIAVKDTKE
A_SE_UGSE8	LLETAEGCQ	IEQLQSAPK	TGTEELRSLY	NTVATLYCVH	QRIDVKDTKE
A_UG_92UG0	LLETTEGCRQ	IMEQLQSALK	TGTEELRSLY	NTVATLYCVH	QRIEIKDTKE
A_UG_U455_	LLETAEGCQ	ILGQLQPALQ	TGTEELRSLY	NTVAVLYCVH	QRIDVKDTKE
AC_IN_2130	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	AGIEIRDTE
AC_RW_92RW	LLETPEGCKQ	IMRQLQPALQ	TGTEELRSLY	NTVATLYCVH	QKIDVKDTKE
AC_SE_SE94	LLETSEGCRQ	ILEQLQPALK	TGTEELKSLF	NTVATLYCVH	QRIEIKDTKE
ACD_SE_SE8	LLETTEGCRQ	IMDKLQPALK	TGTEELRSLY	NTVATLWCVH	KRIDVKDTKE
ACG_BE_VI1	LLETAEGCQ	IEQLQSTLK	TGSEELKSLF	NTVATLWCVH	LRIEIKDTKE
AD_SE_SE69	LLETPEGCKQ	IMGQLQPAIQ	TGSEELKSLF	NTVATLYCVH	AKIKVDTKE
AD_SE_SE71	LLETTKGCRQ	IMEQLQPAFK	TGTEELKSLY	NTVATLYCVH	QQIEVKDTKE
ADHK_NO_97	LLETSEGCRQ	VMEQLQPALK	TGSEELKSLF	NLVAVLWCVH	QRIDVRDTKE
ADK_CD_MAL	LLETGEGCRQ	IMEQLQSTLK	TGSEELKSLY	NTVATLYCVH	QRIDVKDTKE
AG_BE_VI11	LLETAEGCQ	IEQLQSTLR	TGSEELKSLY	NTLATLWCVH	KKIEVRDTKE
AG_NG_92NG	LLETTEGCRQ	IMRQLQPSLQ	TGTEELKSLF	NTVATLYCVH	QRIEIKDTKE

AGHU_GA_VI	LLETAEGCQQ	IMEQLQSALK	TGSEELKSLF	NTVATLYCVH	QKIDVKDTKE
AGU_CD_Z32	LLETTEGCQQ	ILSQFQPALK	TGTEEIISLY	NTVATLYCVH	QNIEVKDTKE
AJ_BW_BW21	LLETAEGCQQ	IMEQLQSALK	TGSEELRSLY	NTVATLYCVH	QRIEVKDTKE
B_AU_VH_AF	LLETSEGCRQ	ILVQLQPSLP	TGSEELKSLF	NTVATLYCVH	QKIEIRDTKE
B_CN_RL42	LLETSEGCRQ	ILEQLQPALQ	TGSEELRSLF	NTVATLYCVH	LRIEIKDTKE
B_DE_D31_U	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIEVKDTKE
B_DE_HAN_U	LLETSEGCRQ	IMGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE
B_FR_HXB2	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QRIEIKDTKE
B_GA_OYI	LLETSEGCRQ	ILGQLQPSLK	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE
B_GB_CAM1	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIDVKDTKE
B_GB_GB8_A	LLETSEGCRQ	ILEQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIDVKDTKE
B_GB_MANC	LLETSEGCRQ	ILVQLQPSLQ	TGSEELKSLY	NTVAVLYCVH	QGIEVKDTKE
B_KR_WK_AF	LLETSEGCRQ	ILGQLQPSLQ	TGSEELKSLF	NTVAVLYCVH	QRIEIKDTKE
B_NL_3202A	LLETAEGCRC	ILGQLQPALQ	TGSEELRSLF	NTVAVLYCVH	QRIEVKDTKE
B_TW_TWCYS	LLETSEGCRQ	ILGQLQSSLQ	TGSEELRSLY	NTVATLYCIH	QKIEIKDTKD
B_US_BC_L0	LLETAEGCRC	ILGQLQPSLQ	TGSEELKSLY	NTIATLYCVH	QMIDVKDTKE
B_US_DH123	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	ERIEVKDTKE
B_US_JRCSE	LLETSEGCRQ	ILGQLQPSLK	TGSEELTSLY	NTVATLYCVH	QRIEIKDTKE
B_US_MNCG	LLETSEGCRQ	ILGQLQPSLQ	TGSEELKSLY	NTVATLYCVH	QKIEIKDTKE
B_US_P896	LLETSEGCRQ	ILGQLQSSLQ	TGSEELKSLY	NTVATLYCVH	QRIEVKDTKE
B_US_RF_M1	LLETAEGCRC	ILGQLQPALQ	TGSEELKSLY	NTVATLYCVH	QNIEVRDTKE
B_US_SF2_K	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QRIDVKDTKE
B_US_WEAU1	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVAVLYCVH	QKIEVKDTKE
B_US_WR27	LLETAEGCRC	ILRQLQPSLQ	TGSEELRSLF	NTVATLYCVH	QRIGVKDTKE
B_US_YU2_M	LLETSEGCRQ	ILGQLQPSLQ	TGSEELRSLY	NTVATLYCVH	QKIEVKDTKE
BF1_BR_93B	LLETSEGCRQ	ILEQLQPALK	TGSEELRSLY	NTVATLYCVH	QKIDVKDTKE
C_BR_92BR0	LLETSEGCKQ	IMKQLQPALQ	TGTEELISLH	NTVATLYCVH	EKIDVRDTKE
C_BW_96BW0	LLETSEGCKQ	IIQQLQPALQ	TGTEELRSLF	NTVATLYCVH	KKIEVRDTKE
C_BW_96BW1	LLGTSEGCKQ	IMKQLQPALQ	TGTEELRSLY	NTVATLYCVH	EGIEVQDTKE
C_BW_96BW1	LLETAEGCCKQ	IMKQLQPALK	TGTEELKSLY	NTVATLYCVH	EKIEVRDTKE
C_BW_96BW1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	EKIKVKDTKE
C_ET_ETH22	LLDTSAGCKQ	IIKQLQPALQ	TGTEELKSLF	NTVATLYCVH	QKIEIKDTKE
C_IN_93IN1	LLETAEGCCKQ	IIKQLQPALQ	TGTEELKSLH	NTVATLYCVH	AGIEVRDTKE
C_IN_93IN9	LLETSEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	AGIEVRDTKE
C_IN_93IN9	LLBAAEGCKQ	IIKQLQPALQ	TGTEELRSLH	NTVATLYCVH	EGIEVRDTKE
C_IN_94IN1	LLETSEGCKQ	IMKQLQPALQ	TGTEELRSLF	NTVATLYCVH	ABIEVRDTKE
C_IN_95IN2	LLETAEGCCKQ	IIKQLQPALQ	TGTEELRSLF	NTVATLYCVH	AGIEVRDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSNLK	TGSEELKSLF	NTIATLWCVH	QRIDVKDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSTIK	TGSEELKSLF	NTIATLWCVH	QRIDVKDTKE
CRF01_AE_C	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLF	NTIATLWCVH	QRINVTDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLF	NTIATLWCVH	QKIEVKDTKK
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLY	NTVATLWCVH	QRIDVKDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLY	NTIATLWCVH	QRIEIKDTKE
CRF01_AE_T	LLETAEGCQQ	LIEQLQSTLK	TGSEELRSLF	NTIATLWCVH	QRIEIKDTKE
CRF01_AE_T	FLETAEGCQQ	LIEQLQSTLK	TGLEELKSLF	NTVATLWCVH	QRIEIKDTKE
CRF01_AE_T	LLETAEGCQQ	LIGQLQSNLK	TGSEELRSLF	NTVATLWCVH	QRIEIKDTKE
CRF02_AG_F	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLY	NTIATLWCVH	KRIDIKDTKE
CRF02_AG_F	LLETAEGCQQ	LMKQLQSALG	TGSEELKSLY	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_G	LLETTEGCQQ	ILEQLQPALK	AGSEELKSLY	NTVATLYCVH	QKIDVRDTKE
CRF02_AG_N	LLETAEGCQQ	LMEQLQSALR	TGSEELKSLF	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_S	LLETAEGCQQ	LMEQLQSTLR	TGSEELKSLF	NTIATLWCVH	QRIDIKDTKE
CRF02_AG_S	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLF	NTVATLYCVH	QRIEIKDTKE
CRF03_AB_R	LLETSEGCRQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	QRIEIKDTKE
CRF03_AB_R	LLETSEGCRQ	ILEQLQPTLK	TGSEELKSLY	NTVATLYCVH	RRIEIKDTKE
CRF04_cpx	LLETAEGCQQ	LMEQLQSTLK	TGSEELRSLY	NTIATLWCVH	QRIDVQDTKE
CRF04_cpx	LLETAEGCQQ	LMEQLQPTLR	TGSEELKSLF	NTLATLWCVH	QRIDVKDTKE
CRF04_cpx	LLETAEGCQQ	LMEQLQSTLK	TGSEELKSLF	NLIATLWCVH	QRIEIKDTKE
CRF05_DF_B	LLETSEGCKQ	IIISQLQPAIQ	TGTEELKSLY	NTVATLYCVH	ERIEVKDTKE
CRF05_DF_B	LLETSEGCKQ	IIAQQLQPAIQ	TGSEELRSLY	NTVATLYCVH	EKIEVKDTKE
CRF06_cpx	LLETAEGCQQ	LIEQLQSTLK	TGSEELKSLF	NTVATLYCVH	QRIKVTDTKE

CRF06_cpx_	LLETAEGCQQ	IMEQLQSALR	TGSEELKSLY	NTVATLYCVH	QRIKVTDTKE
CRF06_cpx_	LLETPEGCQQ	IMEQLQSTLR	TGSEELKSLY	NTVATLYCVH	QRIKVTDTKE
CRF06_cpx_	LLETAEGCQQ	IIEQLQSALK	TGSEELRSLF	NTVATLYCVH	QRIKVQDTKE
CRF11_cpx_	LLETGEGCQQ	LMGQLQPALG	TGTEELRSLY	NTLATLYCVH	HRIEIKDTKE
CRF11_cpx_	LLETGEGCCKQ	IMGQLQPALG	TGTEELRSLY	NTVAALYCVH	LRIEVKDTKE
D_CD_84ZR0	LLETSEGCKQ	IMEQLQPALK	TGSEELRSIY	NTVATLYCVH	KRIEIKDTKE
D_CD_ELI_K	LLETSEGCKQ	IIGQLQPAIQ	TGTEELRSLY	NTVATLYCVH	KGIDVKDTKE
D_CD_NDK_M	LLETSEGCKQ	IIGQLQPSIQ	TGSEEIRSLY	NTVATLYCVH	ERIEVKDTKE
D_UG_94UG1	LLETSEGCRQ	IIRQLQPSIQ	TGSEEIKSLY	NTVVTLYCVH	ERIKVASTKE
F1_BE_VI85	LLETSEGCKQ	IIRQLQPSLQ	TGSEELKSLF	NTVAVLYYVH	QRAGVTDTK
F1_BR_93BR	LLETSEGCRK	IIGQLQPSLQ	TGSEELKSLY	NTIAVLYYVH	QKVEVKDTKE
F1_FI_FIN9	LLETSEGCKQ	IIAQIQPSIQ	TGSEELRSLY	NTIAVLYFVH	QKIEVKDTKE
F1_FR_MP41	LLETPEGCKQ	IIRQLQPSLQ	TGSEELRSLF	NTVAVLYCVH	QKIEIKDTKE
F2_CM_MP25	LLETTEGCKK	IIGQLQPSLQ	TGSEELKSLF	NTIVVLYYVH	QKIEVRDTKE
F2KU_BE_VI	LLESANGCRQ	IIEQIQPALQ	TGSEELRSLF	NTVVTLYWVH	QRIEVKDTKE
G_BE_DRCBL	LLETAEGCQK	IMAQLQPALQ	TGTEEIKSLF	NTVATLYCVH	QKIEVRDTKE
G_NG_92NG0	LLETAEGCVQ	IMKQLQP.AL	TGTEELRSLF	NTVATLYCVH	QKIEVKDTKE
G_SE_SE616	LLETAEGCQQ	IMRQLQPSLQ	TGTEEIKSLY	NAVATLYCVH	QRIEVKDTKE
H_BE_VI991	LLETADGCQQ	ILGQLQPALK	TGTEDLQSLY	NTIAVLYCVH	QRIDVKDTKE
H_BE_VI997	LLESAGCCLQ	IIEQLRPSIK	TGTEELXSLF	NTVATLYCVL	QRIEVKDTKE
H_CF_90CF0	LLETPEGCLQ	IIEQIQPAIK	TGTEELKSLF	NLVAVLYCVH	RKIDVKDTKE
J_SE_SE702	LLESAGCQK	ILVQLQPALQ	TGTEEIKSLY	NTVATLYCVH	QRIEIKDTKE
J_SE_SE788	LLESAGCQQ	ILVQLQPALQ	TGTQEIKSLY	NTVATLYCVH	QRIEIKDTKE
K_CD_EQTB1	LLETVEGCRQ	IIRQLQPSLQ	TGSEELRSLF	NTVATLYWVH	QSIQVRDTKE
K_CM_MP535	LLETTEGCRQ	IITQIQPSIQ	TGSEEIKSLY	NTIAVLYFVH	QKIEVKDTKE
N_CM_YBF30	LMDTADGCAK	LLNQLEPALK	TGSEELRSLY	NALAVLYCVH	SRIQIHNTQE
O_CM_ANT70	LLETAEGNEK	LLQQLEPALK	TCSDSLQSLW	NAIVVLWCVH	NRYKIGDTQQ
O_CM_MVP51	LLETAEGTEQ	LLQQLEPALK	TGSEDLKSLW	NAIAVLWCVH	NRFDIRDTQQ
O_SN_99SE	LLETAEGNEK	LLQQLEPALK	TGSESLSQSLW	NTIAVLWCVH	NRIKVEDTQQ
O_SN_99SE	LLETAEGNEE	LLQQLEPALK	TGSESLSQSLW	NTIAVLWCVH	KRFKVEDTQQ
U_CD_83C	LLETAEGCQQ	IIGQLQPALQ	TGSEELKSIY	NLVATLYCVH	QRIEVKDTKE

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00BW0762_1	ALDQIEKEQN	QSQQK.....	.TQQAETADK	K.....	VSQNYPIVQN
00BW0768_2	ALDKMEEEQN	KSQQK.....	TQQAEEAA.AG	K.....	VSQNYPIVQN
00BW0874_2	ALDKIEKEQNESQQ	KTQQAACAADG	K.....	VSQNYPIVQN
00BW1471_2	ALDKIEEEQN	K.....	CQQQAKAAEG	K.....	VSQNYPIVQN
00BW1616_2	ALDKLEEEQN	KSQQE.....	TQQQTKAADG	KIS.....	..HNYPIVQN
00BW1686_8	ALDKIEEEQN	KSQQ.....	KTQQVAAAAG	Q.....	VSQNYPIVQN
00BW1759_3	ALDKIEEEQK	KSQQK.....	.LQEEEAADR	KV.....S	..QNYPIVQN
00BW1773_2	ALDKIEEEQN	KCQK.....	.TQAKEADG	K.....	VSQNYPIVQN
00BW1783_5	ALDKIEEEQN	KCQK.....	.TQQAETQQ	AGAA...GGK	VSQNYPIVQN
00BW1795_6	ALDKVEEEQN	KSQQ.....	KMQQAEEAADK	KVS.....	..QNYPIVQN
00BW1811_3	ALDKIEEEQN	KSQQK.....	.TQQAQEATA	TG.....K	VSQNYPIVQN
00BW1859_5	ALDKIEEEQN	KCQQ.....	KTQQTEAAAG	K.....	VSQNYPIVQN
00BW1880_2	ALDKIEEEQN	KSQQK.....	.AQQAEEAADK	Q.....	VSQNYPIVQN
00BW1921_1	ALDKIEEEQN	KSQQ.....	KTQQAEEAAAG	K.....	VSQNYPIVQN
00BW2036_1	ALDKIEEEQN	TCQQ.....	KTQQAEEAAAG	K.....	ISQNYPIVQN
00BW2063_6	ALDKIEEBEQ	KSQQ.....	KTQQAEEAADK	KVS.....	..QNYPIVQN
00BW2087_2	ALDKIEEEQN	KCQK.....	.TQQAACAADK	G.....E	VSQNYPIVQN
00BW2127_2	ALDEIEEBEQ	KCQK.....	.AQQEKATDGK	VSQNYPIVQN
00BW2128_3	ALDKIEEEQN	KIQK.....	.TQAKEADKK	VSQNYPIVQN
00BW2276_7	ALDKIEEBEQ	KSQQKSQQ..	KTQQAQAADG	K.....	VSQNYPIVQN
00BW3819_3	ALDKIEEBEQ	KCQK.....	.TQQKAADKK	ISQNYPIVQN
00BW3842_8	ALDKIEEBEQ	KSQQKTQQQQ	KTQQTEAAAG	K.....	VSQNYPIVQN
00BW3871_3	ALDKIEEBEQ	KSQQ.....	KTQQAEEAAAE	K.....	VSQNYPIVRN
00BW3876_9	ALDKIEEBEQ	KRQK.....	.AQQEKAADGK	VSQNYPIVQN
00BW3886_8	ALDKIEEBEQ	KSQQK.....	.TQQAQAADKK	VSQNYPIVQN
00BW3891_6	ALDRIEEBEQ	KCQK.TQQQ	KTQQVEAADG	K.....	VSQNYPIVQN
00BW3970_2	ALDKIEEBEQ	KSQQK.....	.TQQAACAADG	KI.....S	..QNYPIVQN

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00BW5031_1 ALDKVEEEQN NCQOK.....TQQAEEAAGG.....K ISQNYPIVQN
96BW01B21 ALDKIEEEQN KSQOK.....TQOAKTDD..G.....K ISPNYPIVQN
96BW0407 ALDKIEEEQN KCQOK.....IQQAEEAADK G.....K VSQNYPIVQN
96BW0502 ALDKIEEEQN KSQOK.....TQQAKEADG K.....K VSQNYPIVQN
96BW06_J4 ALDKIEEEQN KSQK.....KTQQAEEAAG K.....K VSQNYPIVQN
96BW11_06 AVDKIEEEQN KSQK.....KTQQAEEAADK KVS.....K VSQNYPIVQN
96BW1210 ALDKIEEEQN KCQOK.....EQQAEEAAK G.....K VSQNYPIVQN
96BW15B03 ALDKIEEEQN KSQE.....KTQQAEEAAG K.....K ISQNYPIVQN
96BW16_26 ALDKIEEEQN KSQOK.....TQQAKEATG K.....K VSQNYPIVQN
96BW17A09 ALDKIEEEQN K.....FQQAKAADG K.....K VSQNYPIVQN
96BWMO1_5 ALDKIEEEQN KIQQ.....KMQQAEEADK KISQ...DKK ISQNYPIVQN
96BWMO3_2 ALDRIEEEQN KCQOK.....AQQEEA.AA K.....K VSQNYPIVQN
98BWMC12_2 ALDKIEEEQN .....KSKQ KTQQAKAADK K.....K VSQNYPIVQN
98BWMC13_4 ALDKVEEEQN KIQQ.....KMQQAESADK KVS.....K VSQNYPIVQN
98BWMC14_a ALDKIEEEQN KVQQ.....KTQQAEEAAG K.....K VSQNYPIVQN
98BWMO14_1 ALDKIEEEQN KSQOK.....TQQAEEAADK G.....K VSQNYPIVQN
98BWMO18_d ALDKVEEEQN KCQOK.....TQQAEEAADK G.....K VSQNYPIVQN
98BWMO36_a ALDKIEEEQN KIQQ.....TQKATAADK G.....K VSQNYPIVQN
98BWMO37_d ALDKIEEEQN KSQK.....K.TQQADG KV.....S ..QNYPIVQN
99BW3932_1 ALDKIEEEQN KCQOK.....TQQEKMAEG .....K VSQNYPIVQN
99BW4642_4 ALDKIEEEQN KCQS.....KTQQAEEAAE K.....K VSQNYPIVQN
99BW4745_8 ALDRIEEEQN .....KSKQ KAQQAKAAG K.....K VSQNYPIVQN
99BW4754_7 ALDKIEEEQN KSQOK.....TTQAEEAADK K.....K VSQNYPIVQN
99BWMC16_8 ALDKIEEEQN KCQOK.....TQQAEEAADK G.....K VSQNYPIVQN
A2_CD_97CD ALDKIEEEQN KCKQK.....TQQAADTG SSSSQNYRGS SSQNYPIVQN
A2_CY_94CY ALDKIEEEQN ..KQK.....TQHAAADTG NS.....S S.QNYPIVQN
A2D_97KR ALDKLEEEQN KHKQK.....TQPAAADTG SS.....S GSQNYPIVQN
A2G_CD_97C ALDKIEEEQN TCKQR.....TQHAAADTG SSRSQDYRGS SSQNYPIVQN
A_BY_97BL0 ALDKIEEIQN XSKQ.....KTQQAATGTG S.....SS.K VSQNYPIVQN
A_KE_Q23_A ALDKIEEIQN KSKQ.....KTQQAADTG N.....SS.N VSQNYPIVQN
A_SE_SE659 ALDKIEEMQK KSKQ.....KTSQATADTG S.....SS.K VSQNYPIVQN
A_SE_SE725 ALDKIEEIQN KSKQ.....KAQQAADTG N.....SS.K VSQNYPIVQN
A_SE_SE753 ALDKIEEIQN KSEQ.....KTQQAADTG N.....S..K VSQNYPIVQN
A_SE_SE853 ALDKLEEIQN KSKQ.....KTQQAVADTG S.....SS.K VSHNYPVVQN
A_SE_SE889 ALDKIEEIQN KNKQ.....KTQQAADTG N.....SS.N VSRNYPVVQN
A_SE_UGSE8 ALDKIEEIQN KSKQ.....KKEQAAADTG N.....SS.K VSQNYPIVQN
A_UG_92UG0 ALDKIEEIQN KSKQ.....KTQQAADTG S.....SS.K VSQNYPIVQN
A_UG_U455_ ALNKIEEMQN KNKQR.....TQQAANTG SS.....S ..QNYPIVQN
AC_IN_2130 ALDKIEEEQN KSQOK.....TQQAKEADG K.....K VSQNYPIVQN
AC_RW_92RW ALDKIEEEQN KSQOK.....TQQAEEAADK G.....K VSQNYPIVQN
AC_SE_SE94 ALDKIEEIQN KSKQ.....KAQQAADTG N.....SG.K VSQNYPIVQN
ACD_SE_SE8 ALDKIEEIQN KSKQ.....KAQQAADTG N.....SS.N VSQNYPIVQN
ACG_BE_VI1 ALDKLEEVQN KSKQR.....TQQAADTG .....S GSQNFPIVQN
AD_SE_SE69 ALDKIEEEQN KSK.....K KAQQATADTK N.....SS.Q VSQNYPIVQN
AD_SE_SE71 ALDKIEEMQN RSKQ.....KTQQAADTG N.....NS.K VSQNYPIVQN
ADHK_NO_97 ALDKIEEIQN KSKQ.....KTQQAADTG N.....GS.N ISQNYPIVQN
ADK_CD_MAL ALDKIEEIQN KSRQKTQQA AQAQAAAATK N.....SS.S VSQNYPIVQN
AG_BE_VI11 AVDKIEEMQN KSKQ.....KTQQAADTG G.....S SSQNYPIVQN
AG_NG_92NG ALEEVEKIQN NSQOE.....TQKAAMGKG N.....SS.Q VSQNYPIVQN
AGHU_GA_VI ALDKIEEIQN KSKQ.....KTQQAADTG N.....SS.K VSQNYPIVQN
AGU_CD_Z32 ALDEVEKAQK SSQOK.....TQKATMAEE N.....SSNQ VSKNFPVVQN
AJ_BW_BW21 ALDKIEEIQN KSKQ.....KAQQAADTG N.....SS.S VSQNYPIVQN
B_AU_VH_AF ALEKIEEEQN KSKKKAQQA AADAAAADAG N.....SS.K VSQNYPIVQN
B_CN_RL42_ ALEKIEEEQN KSKK.....KAQQTAAAGT NNS.....Q ASQNYPIVQN
B_DE_D31_U ALDKIEEEQN KSKK.....KAQPAARDAG N.....NS.Q VSQNYPIVQN
B_DE_HAN_U ALDKVEEEQN NSKK.....KAQQAADAG N.....RN.Q VSQNYPIVQN
B_FR_HXB2_ ALDKIEEEQN KSKK.....KAQQAADTG H.....SN.Q VSQNYPIVQN
B_GA_OYI_ ALDKIEEEQN KSKK.....KAQQTAAADTG NSS.....Q VSQNYPIVQN
B_GB_CAM1_ ALEKIEEEQN KSKK.....KAQQAAGTG N.....SS.Q VSQNYPIVQN
B_GB_GB8_A ALDKIEEEQN KSKK.....KAQQAADK NSNS...N.Q VSQNYPIVQN

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B_GB_MANC	ALDKIEEEQN	KSKK.....	KAQPAAADTG	N.....SS.Q	VSHNYPVQN
B_KR_WK_AF	ALEKIEEEQS	KSKK.....	KAQQATADTG	S.....SS.Q	VSQNYPIVQN
B_NL_3202A	ALDKIEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_TW_TWCYS	ALEKIEEEQN	KSKK.....	KAQQAATGTG	NNS.....P	VSQNYPIVQN
B_US_BC_L0	ALEKIEEEQN	NSKK.....	KAQQAADTG	N.....SS.Q	VSRNYPVQN
B_US_DH123	ALDKVEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_US_JRCSF	ALEKIEEEQT	KSMK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_US_MNCG	ALEKIEEEQN	KSKK.....	KAQQAADTG	NRG.N.SS.Q	VSQNYPIVQN
B_US_P896	ALDKIEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
B_US_RF_M1	ALDKIEEEQN	KSKK.....	KAQQAADTG	N.....GS.Q	VSQNYPIVQN
B_US_SF2_K	ALEKIEEEQN	KSKK.....	KAQQAADTG	TG..N.SS.Q	VSQNYPIVQN
B_US_WEAU1	ALDKIEEEQN	KSKK.....	KAQQAADTE	N.....RN.Q	VSQNYPIVQN
B_US_WR27	ALEKIEEEQN	KSKK.....	KAQQAADTG	N.....NS.K	VSQNYPIVQN
B_US_YU2_M	ALEKIEEEQN	KSKK.....	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
BF1_BR_93B	ALEKIEEEQN	.SKK.....	KAQQAADTG	NNS.....Q	VSQNYPIVQN
C_BR_92BR0	ALDKIEEEQN	KSQK.....	.TQQAADK	G.....K	VSQNYPIVQN
C_BW_96BW0	ALDKIEEEQN	KSQK.....	.IQQAADK	G.....K	VSQNYPIVQN
C_BW_96BW1	AVDKIEEEQN	KSQK.....	KTQQAADK	RVS.....	..QNYPIVQN
C_BW_96BW1	ALDKIEEEQN	KSQK.....	.EQQAADK	G.....K	VSQNYPIVQN
C_BW_96BW1	ALDKIEEEQN	KSQK.....	KTQQAADK	K.....	ISQNYPIVQN
C_ET_ETH22	ALDKIEEEQN	ESQK.....	.TQQAADR	G.....K	DSQNYPIVQN
C_IN_93IN1	ALDKIEEEQN	KIQK.....	.TQQAADG	K.....	VSQNYPIVQN
C_IN_93IN9	ALDKIEEEQN	KNQK.....	.TQQAADG	K.....	VSQNYPIVQN
C_IN_93IN9	ALDKIEEEQN	KSQK.....	.TQQAADG	K.....	VSQNYPIVQN
C_IN_94IN1	ALDKIEEEQN	KSQK.....	.TQQAADSQNYPIVQN
C_IN_95IN2	ALDKIEEEQN	KIKK.....	.TQQAADDG	K.....	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KNKQ.....	KTQQAADTG	S.....NS.K	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KSKQ.....	KAQQAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_C	ALDKIEEVQN	KNKQ.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAADTG	S.....SS.T	VSHNYPVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
CRF01_AE_T	ALDKIEEVQN	KSQK.....	KTQQAADTG	S.....SS.K	VSQNYPIVQN
CRF02_AG_F	ALEKIEEVQN	KSKQ.....	KTQQAADTGS	SSQNYPIVQN
CRF02_AG_F	ALDKIEEVQN	KSKQ.....	KTQQAADTGS	SSQNYPIVQN
CRF02_AG_G	ALDKLEEIQN	KSKQ.....	.TQQAANSQ	VSQNYPIVQN
CRF02_AG_N	ALDKMEEIQN	KSKQ.....	KVQQTAAATGS	SSQNYPIVQN
CRF02_AG_S	ALDKVEEVQN	KSKQ.....	KTQQAADTGS	SSQNYPIVQN
CRF02_AG_S	ALDKLEEIQN	KSKQ.....	KTQQAADTGS	SSQNYPIVQN
CRF03_AB_R	ALDKIEEIQN	KSKQ.....	KTQQAADTGSS.K	VSQNYPIVQN
CRF03_AB_R	ALDKIEEIQN	KSKQ.....	KTQQAADTGSS.K	VSQNYPIVQN
CRF04_cpx	ALDKIEEIQN	KSKQ.....	KTQQAADTG	G.....SS.N	VSQNYPIVQN
CRF04_cpx	ALDKVEEVQN	KSKQ.....	KTQQAADTG	G.....SS.K	VSQNYPIVQN
CRF04_cpx	ALDKVEEVQN	KSKQ.....	KTQQAADTGSS.N	VSQNYPIVQN
CRF05_DF_B	ALEKIEEEQN	KSKR.....K	KAQQAADTG	N.....SS.Q	ASQNYPIVQN
CRF05_DF_B	ALEKIEEEQN	KSKS.....K	RAQQAADTG	N.....SS.P	VSQNYPIVQN
CRF06_cpx	AIDKIEEIQN	KSKQ.....	.AHQAADTG	N.....SS.N	LSQNYPIVQN
CRF06_cpx	ALDKIEEIQN	KSKQ.....	.AQQAADTG	N.....SS.N	LSQNYPIVQN
CRF06_cpx	ALHKIEEIQN	KSKQ.....	.VQQAADTG	N.....SS.Q	LSQNYPIVQN
CRF06_cpx	AVDKVEEIQN	KSKQ.....	.TQQTAAATG	N.....SS.N	LSQNYPIVQN
CRF11_cpx	ALDKIEEIQN	KSKQ.....	KKQQAADTG	N.....SS.N	VSQNYPIVQN
CRF11_cpx	ALDKVEEIQN	KSK.....	.KQQAADTG	N.....SS.N	VSQNYPIVQN
D_CD_842R0	ALDKIEEEQN	NSKK.....	RAQQAADTG	N.....SS.Q	VSQNYPIVQN
D_CD_ELI_K	ALEKMEEEQN	KSK.....K	KAQQAADTG	N.....NS.Q	VSQNYPIVQN
D_CD_NDK_M	AVEKMEEEQN	KSK.....K	KTQQAADTGS.Q	VSQNYPIVQN
D_UG_94UG1	ALDKIEEEQA	KSK.....K	KAQQAADTG	N.....SS.Q	VSQNYPIVQN
F1_BE_VI85	ALDKLEEEQN	KSQK.....	.KTQQAADKG	VSQNYPIVQN
F1_BR_93BR	ALEKLEEEQN	KGRQ.....	.KTQQAADKG	VSQNYPIVQN

F1_FI_FIN9	ALDKLEEEQN	KSQOKT....	.QAAAAADKG	VSQNYPIVQN
F1_FR_MP41	ALEKLEEEQN	KGQQ.....	.KTQAAAADKG	VSQNYPIVQN
F2_CM_MP25	ALDKLQEEQD	KHQQ.....	.KTQQATADK	GVSK.....G	VSQNYPIVQN
F2KU_BE_VI	ALDKLEEEQK	TOKQQ.....	.KTQQAAGKG	VSQNYPIVQN
G_BE_DRCBL	ALEEVEKIQK	KSQQ.....KEN	S.....SS.Q	VSQNYPIVQN
G_NG_92NG0	APEEVEKIQK	NSQQE.....	.IQQAANKNEG	N.....SN.P	VSQNYPIVQN
G_SE_SE616	ALEEVEKIQK	KSQEK.....	.IQQAAMDKG	N.....SN.Q	VSQNYPIVQN
H_BE_VI991	ALGKIEEIQN	KNKQR.....	.TOQAPAAAD	K.EK...DSK	ISQNYPIVQN
H_BE_VI997	ALGKIEEIQN	KRQQK.....	.TOQATANK.	..ER...DNK	VSQNYPIVQN
H_CF_90CF0	ALDKIEEIQN	KSQQK.....	.TOQAAAADK.	..EK...DNK	VSQNYPIVQN
J_SE_SE702	ALDKIEEIQN	KNKQQ.....	.TQKAETDKK	DNS.....Q	VSQNYPIVQN
J_SE_SE788	ALEKIEEIQN	KNKQQ.....	.AQKAETDKK	DNS.....Q	VSQNYPIVQN
K_CD_BQTB1	ALDKLEEEQ.	NRTQQ.....	.KTQQKGADKG	VSQNYPIVQN
K_CM_MP535	ALDKLEEEQ.	NKSQR.....	.KTQQAADKG	VSQNYPIVQN
N_CM_YBF30	ALDKIKEKQE	QHKPE....P	KNPEAGAAAA	TDS.....N	ISRNYPVQT
O_CM_ANT70	AIQKLKEVMG	SRKS.....	.ADAAKEDTS	A....R..Q	AGQNYPIVSN
O_CM_MVP51	AIQKLKEVMA	SRKS.....	.AEAAKEETS	P....R..Q	TSQNYPIVTN
O_SN_99SE_	AIQKLKEVMG	SRKS.....	.AGTAKEDTS	A....R..Q	TGQNYPIVTN
O_SN_99SE_	AIQKLKEVMG	SRKS.....	.AGAAKEDTS	A....R..Q	TGQNYPPVAN
U_CD___83C	ALDKIEEVQN	KGKQK.....	.AQQAADK.	..GS...NSQ	VSQNYPIVQN

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00BW0762_1	IQQQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW0768_2	LQQQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW0874_2	LQQQMVHNPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1471_2	AQQQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPSDLNTM
00BW1616_2	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1686_8	LQQQMVHQAI	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLHTM
00BW1759_3	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPSDLNTM
00BW1773_2	LQQQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1783_5	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPGDLNTM
00BW1795_6	LQQQMVHQAI	SPRTLNAWVK	VIEDKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1811_3	AQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALPE	GATPQDLNTM
00BW1859_5	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1880_2	LQQQMVHQPL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW1921_1	LQQQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2036_1	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
00BW2063_6	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2087_2	AQQQMVHQTI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2127_2	LQQQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2128_3	LQQQMVHQPL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW2276_7	IQQQMVHQPL	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDSNTM
00BW3819_3	LQQQMVHQNI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3842_8	LQQQMVHQAI	SPRTLNAWVK	VVEEKGFNPE	VIPMFTALSE	GATPQDLNTM
00BW3871_3	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GAAPQDLNTM
00BW3876_9	LQQQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3886_8	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
00BW3891_6	LQQQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
00BW3970_2	LQQQMVHQPI	APRTLNAWVK	VIEEKNFSPE	VIPMFTALSE	GATPQDLNSM
00BW5031_1	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFNPE	IIPIFTALSE	GATPRDLNTM
96BW01B21	LQQQMVHQPL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW0407	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW0502	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW06_J4	LQQQMVHQPI	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLNTM
96BW11_06	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW1210	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	IIPMFTALSE	GATPQDLNTM
96BW15B03	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW16_26	LQQQMVHQAI	SPRTSNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BW17A09	AQQQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
96BWM01_5	LQQQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQILNTM

96BWM03_2	LQGQMVHQAI	SPRTLNAWVK	VVQEKGFNPE	VIPMFTALSE	GATPQDLNTM
98BWM012_2	VQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM013_4	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM014_a	LQGQMVHQAI	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLNTM
98BWM014_1	IQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM018_d	LQGQVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM036_a	LQGQMVHQAP	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
98BWM037_d	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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99BW4745_8	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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A2_CD_97CD	AQGQMVHQAV	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
A2_CY_94CY	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
A2D_97KR	AQGQMTYQNL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
A2G_CD_97C	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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AC_IN_2130	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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AC_SE_SE94	PQGQMVHQPI	SPRTLNAWVK	VIEDKAFSPE	VIPMFTALSE	GATPQDLNTM
ACD_SE_SE8	AQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
ACG_BE_VI1	AQEQMVHQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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AD_SE_SE71	AQGQMIHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
ADHK_NO_97	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
ADK_CD_MAL	AQGQMIHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
AG_BE_VI11	AQGQMVHQSM	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLNTM
AG_NG_92NG	AQGQVHQPI	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLNTM
AGHU_GA_VI	AQGQMVHQAM	SPRTLNAWVK	VIEEKGFNPE	VIPMFTALSE	GATPQDLNTM
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AJ_BW_BW21	AQGQMVHQAV	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_AU_VH_AF	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_CN_RL42	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_DE_D31_U	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_DE_HAN_U	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_FR_HXB2	IQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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B_GB_CAM1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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B_GB_MANC	LQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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B_NL_3202A	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_TW_TWCYS	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_US_BC_L0	IQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_US_DH123	IQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
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B_US_P896	IQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_US_RF_M1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
B_US_SF2_K	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM

B_US_WEAU1	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_WR27	LQGQMVHQAL	SPRTLFAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
B_US_YU2_M	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
BF1_BR_93B	LQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
C_BR_92BR0	LQGQMVHQPI	SARTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW0	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_BW_96BW1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_ET_ETH22	MQGQMVHQPI	SARTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN9	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_93IN9	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_94IN1	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
C_IN_95IN2	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
CRF01_AE_C	AQGQMVHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_C	AQGQMVHQAL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_C	AQGQMIHQAL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPV	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
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CRF01_AE_T	AQGQMVHQPI	SPRTLNAWVK	VIEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMAHQPL	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF01_AE_T	AQGQMVHQPV	SPRTLNAWVK	VVEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_F	AQGQMT HQPM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_F	AQGQMT HQPM	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_G	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF02_AG_N	AKGQMT HQSM	SPRTLNAWVK	VIEEKGFNPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_S	AQGQMT HQSI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF02_AG_S	AQGQMVHQSI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF03_AB_R	AQGQMT HQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF03_AB_R	AQGQMT HQSM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
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CRF04_cpx	AQGQMVHQAM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
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CRF05_DF_B	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
CRF05_DF_B	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
CRF06_cpx	AQGQMVHQAM	SPRTLNAWVK	VIEDKAFSPE	VIPMFTALSE	GATPQDLNMM
CRF06_cpx	AQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF06_cpx	AQGQMIHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF06_cpx	AQGQMVHQAI	SPRTLNAWVK	AIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF11_cpx	AQGQMVHQPV	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNMM
CRF11_cpx	AQGQMVHQAM	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNMM
D_CD_84ZR0	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFNPE	VIPMFSALSE	GATPQDLNTM
D_CD_ELI_K	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
D_CD_NDK_M	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
D_UG_94UG1	LQGQMVHHPL	SPRTLNAWVK	VIEEKAFNPE	VIPMFSALSE	GATPQDLNTM
F1_BE_VI85	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
F1_BR_93BR	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
F1_FI_FIN9	LQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
F1_FR_MP41	LQGQMVHQPI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
F2_CM_MP25	LQGQMVHQSL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
F2KU_BE_VI	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
G_BE_DRCBL	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFTALSE	GATPQDLNTM
G_NG_92NG0	AQGQMIHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNTM
G_SE_SE616	AQGQMVHQAI	TPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNLM
H_BE_VI991	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
H_BE_VI997	AQGQMVHQPI	SXRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
H_CF_90CF0	AQGQMVHQAI	SPRTLNAWVK	VVEEKAFSPE	VIPMFSALSE	GATPQDLNAM
J_SE_SE702	LQGQPVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM

J_SE_SE788	LQGQPVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
K_CD_EQTB1	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM
K_CM_MP535	LQGQMVHQAL	SPRTLNAWVK	VIEEKAFSPE	VIPMFTALSE	GATPQDLNTM
N_CM_YBF30	AQQQMVHQPL	TPRTLNAWVK	VIEEKAFSPE	VIPMFMAISE	GATPSDLNTM
O_CM_ANT70	AQQQMVHQAI	SPRTLNAWVK	AVEEKAFNPE	IIPMFMAISE	GAISYDINTM
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U_CD_83C	MQGQMVHQAI	SPRTLNAWVK	VIEEKAFSPE	VIPMFSALSE	GATPQDLNTM

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00BW1471_2	LNTVGGHQ.A	AMQMLKDTIN	EEVAEWDR LH	PVQAGPIAPG	QMRDPRGSDI
00BW1616_2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR MH	PVQAGPVAPG	QMRDPRGSDI
00BW1686_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW1759_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
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00BW2128_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
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00BW3819_3	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW3842_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVQAGPVAPG	QIREPRGSDI
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00BW3876_9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVHAGPVAPG	QMRDPRGSDI
00BW3886_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
00BW3891_6	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
00BW3970_2	LNAVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QLREPRGSDI
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96BW0407	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
96BW0502	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QMRDPRGSDI
96BW06_J4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPVAPG	QMRDPRGSDI
96BW11_06	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
96BW1210	LNTVGGHQ.A	AMQMLKDTIN	EEAAGWDR LH	PVHAGPVAPG	QMREPRGSDI
96BW15B03	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
96BW16_26	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QMREPRGSDI
96BW17A09	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
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99BW4642_4	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
99BW4745_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR IH	PVHAGPVAPG	QMREPRGSDI

99BW4754_7	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIAPG	QIREPRGSDI
99BWM16_8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRTH	PVHAGPIAPG	QMREPRGSDI
A2_CD_97CD	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRTH	PVQAGPIPPG	QMREPRGSDI
A2_CY_94CY	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A2D_97KR	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A2G_CD_97C	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_BY_97BL0	LNTVGGHQ.A	AMQMLKDTIN	EEAAXDXRLH	PAQAGPFPFG	QMREPRGSDI
A_KE_Q23_A	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE659	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE725	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE753	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PAHAGPVAPG	QMREPRGSDI
A_SE_SE853	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_SE_SE889	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_SE_UGSE8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
A_UG_92UG0	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PIHAGPVAPG	QMREPRGSDI
A_UG_U455	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPVAPG	QMREPRGSDI
AC_IN_2130	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGPIPPG	QMREPRGSDI
AC_RW_92RW	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PAQAGPIAPG	QMREPRGSDI
AC_SE_SE94	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVQAGPVAPG	QIREPRGSDI
ACD_SE_SE8	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PAQAGPVAPG	QMREPRGSDI
ACG_BE_VII	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDRVH	PVHAGLIAPG	QMREPRGSDI
AD_SE_SE69	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPNPPG	QMREPRGSDI
AD_SE_SE71	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPNAPG	QMREPRGSDI
ADHK_NO_97	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
ADK_CD_MAL	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
AG_BE_VII1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
AG_NG_92NG	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
AGHU_GA_VI	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
AGU_CD_Z32	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
AJ_BW_BW21	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_AU_VH_AF	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_CN_RL42	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_DE_D31_U	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_DE_HAN_U	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_FR_HXB2	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_GA_OYI	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_GB_CAM1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_GB_GB8_A	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_GB_MANC	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_KR_WK_AF	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_NL_3202A	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_TW_TWCYS	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_BC_L0	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_DH123	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_JRCSF	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_MNCG	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_P896	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_RF_M1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_SF2_K	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_WEAU1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_WR27	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
B_US_YU2_M	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
BF1_BR_93B	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_BR_92BR0	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_BW_96BW0	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_BW_96BW1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_BT_ETH22	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PVHAGPIPPG	QMREPRGSDI
C_IN_93IN1	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDRTH	PIHAGPIAPG	QMREPRGSDI

C_IN_93IN9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PIHAGPIAPG	QMREPRGSDI
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C_IN_94IN1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
C_IN_95IN2	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVPAGPIAPG	QLREPRGSDI
CRF01_AE_C	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_C	LNIVGGHQ.A	AMQILKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGADI
CRF01_AE_C	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGEHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PVHAGPIPPG	QIREPRGSDI
CRF01_AE_T	LNIVGGHQ.A	AMQMLKETIN	EEPAEWDR VH	PVHAGPIPPG	QMREPRGSDI
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CRF02_AG_F	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_F	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
CRF02_AG_G	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR TH	PIHAGPNPPG	QMREPRGSDI
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CRF03_AB_R	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAQAGPFP PG	QMREPRGSDI
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CRF04_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAADWDR TH	PVHAGPIPPG	QMREPRGSDI
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CRF05_DF_B	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVQAGPVAPG	QMRDPRGSDI
CRF05_DF_B	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR VH	PAQAGPIAPG	QIREPRGSDI
CRF06_cpx_	LNIVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QIREPRGSDI
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D_CD_ELI_K	LNTVGGHQ.A	AMQMLKETIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
D_CD_NDK_M	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PVHAGPVAPG	QMREPRGSDI
D_UG_94UG1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPVAPG	QLREPRGSDI
F1_BE_VI85	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPAPPG	QMREPRGSDI
F1_BR_93BR	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PTQAGPIPPG	QIREPRGSDI
F1_FI_FIN9	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
F1_FR_MP41	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PAHAGPIPPG	QMREPRGSDI
F2_CM_MP25	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
F2KU_BE_VI	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIAPG	QMREPRGSDI
G_BE_DRCBL	LNTVGGHQ.A	AMQMLKETIN	DEAAEWDR LH	PQAGPIAPG	QIRDPTGSDI
G_NG_92NG0	LNTVGGHQ.A	AMQMLKDTIN	DEAAEWDR LH	PQAGPIPPG	QIREPSGSDI
G_SE_SE616	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PQAGPFP PG	QIREPRGSDI
H_BE_VI991	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
H_BE_VI997	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
H_CF_90CF0	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIPPG	QMREPRGSDI
J_SE_SE702	LNTIGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPVAPG	QVREPRGSDI
J_SE_SE788	LNTIGGHQ.A	AMQMLKDTIN	EEAAEWDR VH	PVHAGPIAPG	QVREPRGSDI
K_CD_EQTB1	LNTVGGHQ.A	AMQMLKDTIN	EEAAEWDR LH	PVQAGPIPPG	QIREPRGSDI
K_CM_MP535	LNTVGGHQ.A	AMQMLKDTIN	DEAAEWDR LH	PVHAGPIPPG	QMREPRGSDI
N_CM_YBF30	LNTVGGHQ.A	AMQMLKEVIN	EEAADWDR TH	PVPVGPLPPG	QLRDPRGSDI
O_CM_ANT70	LNAIGGHQ.G	ALQVLKEVIN	EEAVEWDR TH	PPVGPLPPG	QIREPTGSDI
O_CM_MVP51	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDR TH	PPAMGPLPPG	QIREPTGSDI
O_SN_99SE_	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDR TH	PPAAGPLPVG	QIREPTGSDI
O_SN_99SE_	LNAIGGHQ.G	ALQVLKEVIN	EEAAEWDR TH	PQAAGPLPPG	QIREPTGSDI
U_CD_83C	LNTVGGHQ.A	AMQMLKDTIN	EEAADWDR LH	PVHAGPIPPG	QMREPRGSDI

	251		300
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00BW0874_2	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1471_2	AGTTSTLQEQ	VAWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1616_2	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW IILGLNKIVR MYSPVSILDI
00BW1686_8	AGTTSNLQEQ	VAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1759_3	AGTTSTLQEQ	IAWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1773_2	AGTTSTLQEQ	ITWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1783_5	AGTTSTLQEQ	ITWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1795_6	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1811_3	AGTTSTLQEQ	IAWMTN.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
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00BW1880_2	AGTTSTLQEQ	ITWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW1921_1	AGTTSTLQEQ	IAWMTN.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW2036_1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW2063_6	AGTTSTLAEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW2087_2	AGTTSTLQEQ	IAWMTN.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW2127_2	AGTTTTLQEQ	INWMTS.NPP	IPVGEIYKRW IILGLNKIVR MYSPVSILDI
00BW2128_3	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW2276_7	AGTTSTLQEQ	IAWMTS.NPA	IPVGDYKRW IILGLDKIVR MYSPVSILDI
00BW3819_3	AGTTSTLQEQ	VAWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW3842_8	AGTTSNLQEQ	ITWMTS.NPP	IPVGEIYKRW IILGLNKIVR MYSPVSILDI
00BW3871_3	AGTTSTLQEQ	IDWMTN.NPP	IPVGEIYKRW IILGLNKIVR MYSPVSILDI
00BW3876_9	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW IILGLNKIVR MYSPVSILDI
00BW3886_8	AGTTSTLQEQ	IAWMTN.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW3891_6	AGTTSNLQEQ	INWMTA.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW3970_2	AGTTSTLQEQ	IAWMTN.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
00BW5031_1	AGTTSTLQEQ	IAWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW01B21	AGTTSNLQEQ	IAWMTA.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW0407	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW0502	AGATSTLQEQ	IAWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW06_J4	AGTTSTLQEQ	IGWMTH.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW11_06	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW1210	AGTTSNLQEQ	INWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW15B03	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
96BW16_26	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW IILGLNKIVR MYSPVSILDI
96BW17A09	AGTTSTLQEQ	IAWMTN.NPP	IPVGDYKRW ITMGLNKIVR MYSPVSILDI
96BWM01_5	AGTTSTLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
96BWM03_2	AGSTSTLQEQ	IAWMTS.NPP	VPVGDYKRW IILGLNKIVR MYSPVSILDI
98BWMC12_2	AGSTSNLQEQ	IAWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
98BWMC13_4	AGTTSTLQEQ	IAWMTR.NPP	VPVGEIYKRW IILGLNKIVR MYSPVSILDI
98BWMC14_a	AGTTSTLQEQ	VGWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
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99BW3932_1	AGTTSTLQEQ	IQWMTS.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
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99BW4745_8	AGTTSTLQEQ	INWMTG.NPP	IPVGDYKRW IIMGLNKIVR MYSPVSILDI
99BW4754_7	AGTTSTLQEQ	ITWMTN.NPP	IPVGEIYKRW IILGLNKIVR MYSPVSILDI
99BWMC16_8	AGTTSTLQEQ	IAWMTS.NPP	VPVGEIYKRW IILGLNKIVR MYSPVSILDI
A2_CD_97CD	AGATSNLQEQ	IGWMTS.NPP	IPVGEIYKRW IILGLNKIVR MYSPVSILDI
A2_CY_94CY	AGTTSTLQEQ	IGWMTS.DPP	IPVGEIYKRW IILGLNKIVR MYSPVSILDI
A2D_97KR	AGTTSTLQEQ	IGWMTS.NPP	VPVGEIYKRW IILGLNKIVR MYSPVSILDI
A2G_CD_97C
A_BY_97BL0	AGTTSTLQEQ	IGXMTS.NPP	IPXGDYKRX IILGLNKIVR MYSPVSILDI
A_KE_Q23_A	AGTTSTPQEQ	IGWMTG.NPP	IPVGDYKRW IILGLNKIVR MYSPVSILDI
A_SE_SE659
A_SE_SE725

A_SE_SE753	AGTTSTPQEQ	IGWMTG.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	AGTTSTLQEQ	IAWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
A_UG_92UG0	AGTTSTPQEQ	IAWMTG.NPP	IPVGDIYKRW	MILGLNKIVR	MYSPPVSILDI
A_UG_U455	AGTTSTVQEQ	IGWMTG.NPP	IPVGDIYRRW	IILGLNKIVR	MYSPPVSILDI
AC_IN_2130	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AC_RW_92RW	AGTTSTLQEQ	IAWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AC_SE_SE94
ACD_SE_SE8	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
ACG_BE_VI1	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AD_SE_SE69	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AD_SE_SE71
ADHK_NO_97	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
ADK_CD_MAL	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AG_BE_VI11	AGTTSTLQEQ	VGWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AG_NG_92NG	AGTTSTLQEQ	ITWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AGHU_GA_VI	AGTTSTTQEQ	IGWMTG.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AGU_CD_Z32	AGTTSTLQEQ	IRWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
AJ_BW_BW21	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_AU_VH_AF	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_CN_RL42	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_DE_D31_U	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_DE_HAN_U	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_FR_HXB2	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_GA_OYI	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_GB_CAM1	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_GB_GB8_A	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_GB_MANC	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_KR_WK_AF	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_NL_3202A	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_TW_TWCYS	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_BC_L0	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_DH123	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_JRCSF	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_MNCG	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_P896	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_RF_M1	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_SF2_K	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_WEAU1	AGTTSTLQEQ	IAWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_WR27	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
B_US_YU2_M	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
BF1_BR_93B	AGTTSTLQEQ	IQWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BR_92BR0	AGTTSTLQEQ	ITWMTN.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW0	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	INWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_BW_96BW1	AGTTSTLQEQ	IAWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_ET_ETH22	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN1	AGTTSSLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN9	AGTTSSLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_93IN9	AGTTSTLQEQ	IAWMTG.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_94IN1	AGTTSTLQEQ	IAWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
C_IN_95IN2	AGTTSTLQEQ	IAWMTN.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	XGTTSNLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	AGTTSTLQEQ	IGWMTS.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_C	AGTTSTLQEQ	IGWMTS.NPP	VPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYSPPVSILDI
CRF01_AE_T	AGTTSTLQEQ	IGWMTN.NPP	IPVGDIYKRW	IILGLNKIVR	MYQPVSILDI

CRF01_AE_T AGTTTTLQEQ IGWMTN.NPP IPVGSIIYKRW IILGLNKIVR MYSPVSILDI
 CRF01_AE_T AGTTSTLQEQ IGWMTN.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF01_AE_T AGTTSTLQEQ IGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF02_AG_F AGTTSTPQEQ IGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF02_AG_F AGTTSTLQEQ IGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF02_AG_G AGTTSNLQEQ IAWMTG.NPP IPVGEIYKRW IVLGLNKIVR MYSPVGILDI
 CRF02_AG_N AGTTSTLQEQ IGWMTS.NPP IPVGEIYKRW IVLGLNKIVR MYSPVSILDI
 CRF02_AG_S AGTTSTLQEQ IGWMTS.NPP IPVGEIYKRW IVLGLNKIVR MYSPVSILDI
 CRF02_AG_S AGTTSTLQEQ IGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF03_AB_R AGSSSTLQEQ IGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF03_AB_R AGTTSTLQEQ IGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF04_cpx_ AGTTSTLQEQ IGWMTS.NPP VPVGEIYKRW IILGLNKIVR TYSPIILDI
 CRF04_cpx_ AGTTSTLQEQ IGWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 CRF04_cpx_ AGTTSTLQEQ VGWMTS.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 CRF05_DF_B AGTTSTLQEQ IAWMTN.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 CRF05_DF_B AGTTSTLQEQ ITWMTN.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 CRF06_cpx_ AGTTSTLQEQ IGWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVGILDI
 CRF06_cpx_ AGTTSTLQEQ IGWMTG.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 CRF06_cpx_ AGTTSTLLQEQ IGWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 CRF06_cpx_ AGTTSTLQEQ IRWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 CRF11_cpx_ AGTTSTLQEQ IGWMTG.NPP IPVGDIYRRW IILGLNKIVR MYSPVSILDI
 CRF11_cpx_ AGTTGNLQEQ IGWMTG.NPP IPVGEIYRRW IILGLNKIVR MYSPVSILDI
 D_CD_84ZR0 AGTTSTLQEQ IGWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 D_CD_ELI_K AGTTSTLQEQ IAWMTS.NPP IPVGEIYKRW IIVGLNKIVR MYSPVSILDI
 D_CD_NDK_M AGTTSTLQEQ IAWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 D_UG_94UG1 AGTTSNLQEQ IGWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 F1_BE_VI85 AGTTSTLQEQ IQWMTG.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 F1_BR_93BR AGTTSTLQEQ IQWMTG.NPP VPVGEMYKRW IILGLNKIVR MYSPVGILDI
 F1_FI_FIN9 AGTTSTLQEQ IQWMTS.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 F1_FR_MP41 AGTTSTLQEQ IQWMTS.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 F2_CM_MP25 AGTTSTLQEQ IAWMTS.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 F2KU_BE_VI AGATSNLQEQ IAWMTS.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 G_BE_DRCBL AGATSTLQEQ IRWMTS.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 G_NG_92NG0 AGTTSTLQEQ IRWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 G_SE_SE616 AGTTSSLQEQ ITWMTG.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 H_BE_VI991 AGTTSTLQEQ VAWMTG.NPP IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 H_BE_VI997 AGTTSTLQEQ IAWMTG.NPS IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 H_CF_90CF0 AGTTSTLQEQ IAWMTG.NPA IPVGDIYKRW IILGLNKIVR MYSPVSILDI
 J_SE_SE702 AGTTSNLQEQ IGWMTG.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 J_SE_SE788 AGTTSTLQEQ IGWMTG.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 K_CD_EQTB1 AGTTSTLQEQ ITWMTS.NPP IPVGEIYKRW IILGLNKIVR MYSPVSILDI
 K_CM_MP535 AGTTSTLQEQ IAWMTS.NPP VPVGEIYKRW IILGLNKIVR MYSPVSILDI
 N_CM_YBF30 AGTTSTLAEQ VAWMTA.NPP VPVGEIYRRW IVLGLNRIVR MYSPVSILEI
 O_CM_ANT70 AGTTSTQEQ IHWTTRPNQP IPVGDIYKRW IVLGLNKMKV MYSPVSILDI
 O_CM_MVP51 AGTTSTQEQ IIWTRGANS IPVGDIYKRW IVLGLNKMKV MYSPVSILDI
 O_SN_99SE AGTTSTQEQ VHWITRPNQP IPVGDIYKRW IVLGLNKVVK MYSPVSILDI
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301

350

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00BW1811_3	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
00BW1859_5	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW1880_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW1921_1	KQGPKEPFRD	YVDRFFKTLR	AEQSSQEVKN	WMTDTLLVQN	ANPDCKTILR
00BW2036_1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW2063_6	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILR
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00BW2128_3	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW2276_7	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW3819_3	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
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00BW3876_9	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
00BW3886_8	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
00BW3891_6	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
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00BW5031_1	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	GNPDCKNILR
96BW01B21	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW0407	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILR
96BW0502	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
96BW06_J4	KQGPKEPFRD	YVDRFFKTLR	AEQCTQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW11_06	KQGPKEPFRD	YVDRFFKTLR	AEQSSQEVKN	WMTDTLLVQN	ANPDCKTILK
96BW1210	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW15B03	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKPILR
96BW16_26	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BW17A09	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
96BWM01_5	KQGPKEPFRD	YVDRFFKTLR	AEQSSQEVKN	WMTDTLLVQN	ANPDCKTILR
96BWM03_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
98BWM012_2	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
98BWM013_4	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
98BWM014_a	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
98BWM014_1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
98BWM018_d	KQGPKEPFRD	YVDRFFKTLR	AEQSTQEVKN	WMTDTLLVQN	ANPDCKTILR
98BWM036_a	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
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99BW3932_1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
99BW4642_4	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
99BW4745_8	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
99BW4754_7	KQGPKEPFRD	YVDRFFKTLR	AEQSTQDVKN	WMTDTLLVQN	ANPDCKTILR
99BWM016_8	KQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTDTLLVQN	ANPDCKTILR
A2_CD_97CD	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKSILR
A2_CY_94CY	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKSILR
A2D_97KR	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILR
A2G_CD_97C
A_BY_97BL0	RQGPKEPFRD	YVDRFFKTLX	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
A_KE_Q23_A	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKAILR
A_SE_SE659
A_SE_SE725
A_SE_SE753	KQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKSILR
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKSILR
A_UG_92UG0	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILR
A_UG_U455_	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKSILR
AC_IN_2130	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR
AC_RW_92RW	KQGPKEPFRD	YVDRFFKTLR	AEQASQDVKN	WMTDTLLVQN	ANPDCKTILR
AC_SE_SE94
ACD_SE_SE8	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK
ACG_BE_VI1	RQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILR

[illegible]

CRF04_cpx_	RQGPKEPFRD	YVDRFFKCLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILK
CRF04_cpx_	RQGPKEPFRD	YVDRFFKCLR	AEQATQEVKN	WMTETLLVQN	ANPDCKSILK
CRF04_cpx_	RQGTKEPFRD	YVDRFFKCLR	AEQATQDVKN	WMTETLLVQN	ANPDCKSILK
CRF05_DF_B	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK
CRF05_DF_B	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
CRF06_cpx_	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
CRF06_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
CRF06_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
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CRF06_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
CRF11_cpx_	KQGPKEPFRD	YVDRFFKALR	AEQATQEVKG	WMTDTLLIQN	ANPDCKSILR
CRF11_cpx_	RQGPKEPFRD	YVDRFFKTLR	AEQASQEVKN	WMTETLLVQN	ANPDCKSILR
D_CD_84ZR0	RQGPKEPFRD	YVDRFYKTLR	AEQASQEVKN	WMTETLLVQN	ANPDCKTILK
D_CD_ELI_K	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
D_CD_NDK_M	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
D_UG_94UG1	RQGPKEPFRD	YVDRFYKTLR	AEQASQDVKN	WMTETLLVQN	ANPDCKTILK
F1_BE_VI85	KQGPKEPFRD	YVDRFFKVLK	AEQASQDVKG	WMTDTLLVQN	ANPDCKTILK
F1_BR_93BR	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTDTLLVQN	ANPDCKTILK
F1_FI_FIN9	RQGPKEPFRD	YVDRFFKALR	AEQATQEVKG	WMTDTLLVQN	ANPDCKIILK
F1_FR_MP41	RQGPKEPFRD	YVDRFFKTLR	AEQASQEVKN	WMTESLLVQN	SNPDCKTILK
F2_CM_MP25	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTETLLVQN	ANPDCKTILK
F2KU_BE_VI	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLIQN	ANPDCKTILK
G_BE_DRCBL	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKS	WMTDTLLIQN	ANPDCKIILK
G_NG_92NG0	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKG	WMTDTLLVQN	ANPDCKTILR
G_SE_SE616	RQGPKEPFRD	YVDRFFKCLR	AEQASQDVKG	WMTDTLLVQN	ANPDCKTILR
H_BE_VI991	KQGPKEPFRD	YVDRFFRVLR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
H_BE_VI997	KQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILR
H_CF_90CF0	KQGPKEPFRD	YVDRFFKTLR	AEQATQDVKN	WMTETLLVQN	ANPDCKTILR
J_SE_SE702	RQGPKEPFRD	YVDRFFKALR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
J_SE_SE788	RQGPKEPFRD	YVDRFFKALR	AEQATQDVKN	WMTDTLLVQN	ANPDCKTILK
K_CD_EQTB1	RQGPKEPFRD	YVDRFFRVLR	AEQATQEVKN	WMTETLLVQN	ANPDCKTILK
K_CM_MP535	RQGPKEPFRD	YVDRFFKTLR	AEQATQEVKN	WMTDTLLVQN	ANPDCKTILK
N_CM_YBF30	KQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQLLK
O_CM_ANT70	KQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQILK
O_CM_MVP51	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	SNPDCKQILK
O_SN_99SE	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQILK
O_SN_99SE	RQGPKEPFRD	YVDRFYKTLR	AEQATQEVKN	WMTETLLVQN	ANPDCKQILK
U_CD_83C	KQGPKEPFRD	YVDRFFKVLK	AEQSSQEVKN	WMTDTLLIQN	ANPDCKTILK

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400

00BW0762_1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TNIMLQK
00BW0768_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQHN...	...TSIMMQK
00BW0874_2	GLGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQSN...	...S.IMMQR
00BW1471_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TNVMMQK
00BW1616_2	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAGN...	...ATIMMQK
00BW1686_8	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...PNILMQR
00BW1759_3	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSKANN...	...ANILMQR
00BW1773_2	ALGPAASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANT...	...TNIMMQK
00BW1783_5	ALGQASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVGN...	...PQVMMQR
00BW1795_6	ALGSGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...VQIMMQK
00BW1811_3	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQTTS...	...MQIMMQR
00BW1859_5	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...ANIMMQR
00BW1880_2	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...TSIMMQK
00BW1921_1	ALGPGATLEE	MMTACQGVGG	PSHKARALAE	AMSQANN...	...TNIMMQK
00BW2036_1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVNG...	...SNVLMQR
00BW2063_6	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INVMMQK
00BW2087_2	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANS...	...TNIMIQR
00BW2127_2	ALGSGVTLLEE	MMSACRGVGG	PSHKARVLAE	AMSQANN...	...TNIMMQR
00BW2128_3	ALGPAATLVE	MMTACQGVGG	PSHKARVLAE	AMSQTAS...	...TNILMQR
00BW2276_7	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN...	...SNIMMQR
00BW3819_3	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INVMMQR

00BW3842_8	ALPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANS...	...TNIMMQR
00BW3871_3	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...SNIMMQR
00BW3876_9	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAGS...	...VNILMQR
00BW3886_8	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INVMMQR
00BW3891_6	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN...	...SNIMMQR
00BW3970_2	AIGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTH...	...SNIMMQR
00BW5031_1	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INIMMQR
96BW01B21	ALPGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...MNIMMQR
96BW0407	ALPGASLEE	MMTACQGVGG	PSHKARVLGE	AMSQA.N...	...TNVMMQR
96BW0502	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANS...	...VNIMMQR
96BW06_J4	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...TSILMQR
96BW11_06	TLGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQANN...	...PNIMMQR
96BW1210	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHAGN...	...AGIMMQR
96BW15B03	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATS...	...ANILMQR
96BW16_26	ASGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...TNIMMQR
96BW17A09	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHANN...	...TSIMMQR
96BWM01_5	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...IQVMMQR
96BWM03_2	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN...	...TNIMMQR
98BWMC12_2	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHTN...	...S.IMMQR
98BWMC13_4	ALPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...INIMMQR
98BWMC14_a	SLGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAN...	...TSIMMQR
98BWM014_1	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANS...	...TNILMQR
98BWM018_d	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQAGN...	...ANIMMQR
98BWM036_a	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQANN...	...ANIMMQR
98BWM037_d	ALPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN...	...SNIMMQR
99BW3932_1	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...ASVMMQR
99BW4642_4	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMGQVNS...	...TNIMMQR
99BW4745_8	GLGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN...	...SNIMMQR
99BW4754_7	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...PNIMMQR
99BWMC16_8	ALPGASIEE	MMTACQGVGG	PSHKARVSAE	AMSQANQ...	...ANIMMQR
A2_CD_97CD	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQNT...	...NIMMQR
A2_CY_94CY	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHVQSTN...	...T.NIMMQR
A2D_97KR	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQNTN...	...SNIMMMQR
A2G_CD_97C
A_BY_97BLO	ALGSEATLEE	MMTACQGVGG	PGHKAXVXAE	AMSQVQN...	...ANIMMQR
A_KE_Q23_A	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...TNIMMQR
A_SE_SE659
A_SE_SE725
A_SE_SE753	ALGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...PNIMMQR
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	GLGAGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQQ...	...TNIMMQR
A_UG_92UG0	ALGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQH...	...TNIMMQR
A_UG_U455_	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQQT...	...SIMMQR
AC_IN_2130	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN...	...NSILMQR
AC_RW_92RW	ALPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQQ...	...PNIMMQR
AC_SE_SE94
ACD_SE_SE8	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN...	...ANTAIMMQR
ACG_BE_VI1	ALPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQANN...	...TVMMQR
AD_SE_SE69	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATNN...	...INAAIMMQR
AD_SE_SE71
ADHK_NO_97	ALPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQN...	...VSVMMQR
ADK_CD_MAL	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...STAAIMMQR
AG_BE_VI11	ALGTGATLEE	MVTACQGVGG	PGHKARVLAE	AMSQVH...	...QTNIMMQR
AG_NG_92NG	ALGAGATLEE	MLTACQGVGG	PSHKARVLAE	AMSRAT.G...	...TSAAIMMQR
AGHU_GA_VI	GLGAGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVHN...	...TSIMMQR
AGU_CD_Z32	ALPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.S...	...TAAAIMMQR
AJ_BW_BW21	ALGAGATLEE	MMTACQGVGG	PGHKARILAE	AMSQVQN...	...TNIMMQR
B_AU_VH_AF	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT...	...NSATIMMQR
B_CN_RL42_	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVTNSAI	TNSATIMMQR

B_DE_D31_U	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATVMMQR
B_DE_HAN_U	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.GSAAIMMQR
B_FR_HXB2_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_GA_OYI_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVN....	.SVTVMMQK
B_GB_CAM1_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_GB_GB8_A	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVN....	.SATIMMQK
B_GB_MANC_	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVT....	.NSATIMMQR
B_KR_WK_AF	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAT....	.NSATIMMQR
B_NL_3202A	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_TW_TWCYS	ALGPAATLEE	MMTACQGVGG	PSHKARVLAE	AMSRVP....	.NSTNIMMQR
B_US_BC_L0	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_DH123	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQITN...	.TSATIMMQG
B_US_JRCSF	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NPATIMMQR
B_US_MNCG_	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_P896_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
B_US_RF_M1	ALGPAATLEE	MMTACQGVGG	PSHKARILAE	AMSQVT....	.NSATIMLQK
B_US_SF2_K	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NPANIMMQR
B_US_WEAU1	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NTATIMMQR
B_US_WR27_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.GSNAIMMQK
B_US_YU2_M	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSATIMMQR
BF1_BR_93B	ALGPAATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVT....	.NSGTIMMQR
C_BR_92BR0	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSKVNN...	.TNIMMQR
C_BW_96BW0	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQT.N...	.TNVMMQR
C_BW_96BW1	ALGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQANN...	.SNIMMQK
C_BW_96BW1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSHAGN...	.AGIMMQR
C_ET_ETH22	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATS...	.ANILMQR
C_IN_93IN1	ALGPGASLEE	MMTACQGVGG	PAHKARVLAE	AMSQVNN...	.TTIMMQK
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	.STILMQR
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	.SAILMQK
C_IN_93IN9	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQAN....	.SNILMQR
C_IN_94IN1	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	.SAILMQR
C_IN_95IN2	ALGPGASLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	.SAILMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	.HANIMMQR
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVH....	.HTNIMMQK
CRF01_AE_C	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	.HANIMMQR
CRF01_AE_T	SLGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	.HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQ....	.HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQ....	.HANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	.QANIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHAQ....	.HATIMMQR
CRF01_AE_T	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSHVQ....	.QANIMMQR
CRF02_AG_F	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	.QSNIMMQR
CRF02_AG_F	ALGPGASLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	.QSNIMMQR
CRF02_AG_G	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQSP..	.NILMQR
CRF02_AG_N	ALGTGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQ....	.QANVMMQR
CRF02_AG_S	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQ....	.QPNIMMQR
CRF02_AG_S	ALGPGATLEE	MMSACQGVGG	PGHKARVLAE	AMSQAQ....	.QSNIMMQR
CRF03_AB_R	ALGSGATLEE	MMTVQGVGG	PGHKARVLAE	AMSQVQN...	.ANIMMQK
CRF03_AB_R	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVQN...	.ANIMMQK
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASN...	.AAAAIMMQK
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PAHKARVLAE	AMSQASN...	.AAAAIMMQK
CRF04_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASS...	.AAAAIMMQK
CRF05_DF_B	ALGQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	.SAATAMMQR
CRF05_DF_B	ALGPQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATG...	.SPAVMMQ.R
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQAS...	.VGAIMMQ.K
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQASGT..	.LTAIMMQ.K
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQASGT..	.VAAAIMMQK
CRF06_cpx_	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVSGA..	.TAAIMMQ.K
CRF11_cpx_	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQVQQ...	.TNVMMQR
CRF11_cpx_	ALGVGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAQH...	.TNIMMQR

D_CD_84ZR0	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATS...	.ASAAIMMQK
D_CD_ELI_K	ALGPQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	.SVTTAMMQR
D_CD_NDK_M	ALGPQATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTG...	.SATAVMMQR
D_UG_94UG1	ALGPAATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	.ANTAIMMQR
F1_BE_VI85	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAN....	...SAIMMQK
F1_BR_93BR	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQATN...	...TAIMMQK
F1_FI_FIN9	GLGIGATLEE	MMTACRQVGG	PGHKARILAE	AMSQAN....	...TTIMMQK
F1_FR_MP41	ALGPGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQATN...	...AAIMMQK
F2_CM_MP25	ALGPGATLEE	MMTACQGVGG	PSHKARILAE	AMSKATG...	...AAIMMQK
F2KU_BE_VI	ALGPGASLEE	MMTACQGVGG	PAHKARVLAE	AMSQATN...	...TAIMMQK
G_BE_DRCBL	GLGQATLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.G..	.AAAAIMMQK
G_NG_92NG0	ALGPGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQASGA..	.AAAAIMMQK
G_SE_SE616	ALGQASLEE	MMTACQGVGG	PSHKARVLAE	AMSQAS.G..	.AAAAIMMQR
H_BE_VI991	ALGRGASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNAS.	...AAIMMQK
H_BE_VI997	ALGQASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNAN.	...AAIMMQK
H_CF_90CF0	ALGQASIEE	MMTACQGVGG	PSHKARVLAE	AMSQVTNTN.	...TAIMMQK
J_SE_SE702	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...TNIMMQR
J_SE_SE788	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...TNIMMQR
K_CD_EQTB1	ALGSGATLEE	MMTACQGVGG	PGHKARVLAE	AMSQVTN...	...SAVMMQR
K_CM_MP535	ALGPGASLEE	MMTACQGVGG	PSHKARILAE	AMSQVTN...	...PVVMMQK
N_CM_YBF30	ALGPGATLEE	MMTACQGVGG	PAHKARVLAE	AMSQVQQP..	...TTSVFAQR
O_CM_ANT70	SLGPGATLEE	MMVACQGVGG	PTHKARVLAE	AMATAQQDLK	GGYTAVFMQR
O_CM_MVP51	ALGPEATLEE	MMVACQGVGG	PTHKAKILAE	AMASAQQDLK	GGYTAVFMQR
O_SN_99SE_	SLGPGATLEE	MMIACQGVGG	PTHKARVLAE	AMA.AAQDLK	GGYTAVFMQR
O_SN_99SE_	SLGPGATLEE	MMIACQGVGG	PTHKARVLAE	AMS.AAQDLK	GGYSVFMQR
U_CD___83C	ALGTGATLEE	MMTACQGVGG	PSHKARVLAE	AMSQTN....	...TAIMMQR

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450

00BW0762_1	NNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW0768_2	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW0874_2	SNFKGHKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1471_2	GNFKGPRRVI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKECT..E
00BW1616_2	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1686_8	SNFKGSK.RV	KCFNCGKEGH	IARNCRAPRK	RGCWKCGKEG	HQMKDCT..E
00BW1759_3	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1773_2	SNFKGPRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1783_5	NNLKGTTRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGREG	HQMKDCT..E
00BW1795_6	NNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1811_3	SNFKGSKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKDG	HQMKDCT..E
00BW1859_5	SNFKGPRKII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1880_2	SNFKGPRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW1921_1	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW2036_1	GNFKGPKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW2063_6	NNFKGPRRLV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW2087_2	SNFKGSKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGREG	HQMKDCT..E
00BW2127_2	GNFRGAKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW2128_3	SNFKGSKRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW2276_7	SNFKGPRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW3819_3	SNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW3842_8	GNFKGPKRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGREG	HQMKDCT..E
00BW3871_3	SNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	RGCWKCGKEG	HQMKDCT..E
00BW3876_9	GNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW3886_8	GNFKGAKRIV	KCFNCGREGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW3891_6	SNFKGSRRIV	KCFNCGKVGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
00BW3970_2	SNFKGPKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGQEG	HQMKDCT..E
00BW5031_1	NNFKGPKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
96BW01B21	SNFKNPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
96BW0407	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
96BW0502	SNFKGPRRNV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
96BW06_J4	GNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E

96BW11_06	NNFKGPRRIV	KCFNCGKEGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCT..E
96BW1210	GNFKGPRKIP	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCS..E
96BW15B03	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW16_26	SNFKGPRRSV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BW17A09	GNFKGPRRTI	KCFNCGKEGH	LAKNCRAPRK	XGCWKCCKEG	HQMKECT..E
96BWM01_5	NNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
96BWM03_2	GNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCNN..E
98BWMC12_2	SNFKGPKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCN..B
98BWMC13_4	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWMC14_a	GNFKGPRRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM014_1	SHFKGSKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM018_d	GNFKGPRRII	KCSNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM036_a	SNFKGPKRTV	KCFNCGKEGH	VARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
98BWM037_d	GNFKGSKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW3932_1	SNFKGPKRII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4642_4	SNFKGPKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4745_8	SNFKGPRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BW4754_7	XNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
99BWMC16_8	SNFKGPKRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2_CD_97CD	GNFKGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2_CY_94CY	GNFRGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2D_97KR	GNFRGQK..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
A2G_CD_97C
A_BY_97BL0	SNFRGPKR..I	KCXNCGKEGH	LARNCRAPRK	XGCWKCCKEG	HQMKDCTE..
A_KE_Q23_A	GNFKGQKR..I	KCFNCGKEGH	LARNCRALRK	KGCWKCCKEG	HQMKDCTE..
A_SE_SE659
A_SE_SE725
A_SE_SE753	GNFRGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	GNFRGQKK..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
A_UG_92UG0	GNFKGQKR..I	KCFNCGKEGH	LAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
A_UG_U455	GNFRGPRR..I	KCFNCGKEGH	LAKNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_IN_2130	SNFKGPKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_RW_92RW	GNFKGQRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCT..E
AC_SE_SE94
ACD_SE_SE8	GNFKGPKKII	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
ACG_BE_VI1	GNFKGPKRII	KCFNCGKEGH	VARNCRAPRK	KGCWKCCKEG	HQMKDCTT..E
AD_SE_SE69	GNFKGQKR..I	KCFNCGKLGH	IARNCKAPRK	KGCWKCCKEG	HQMKDCTE..
AD_SE_SE71
ADHK_NO_97	GNFKGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
ADK_CD_MAL	GNFKGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AG_BE_VI11	GNFRGQKT..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AG_NG_92NG	NNFKGPRRGI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AGHU_GA_VI	GNFKGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
AGU_CD_Z32	SNFKGPKRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDC..E..
AJ_BW_BW21	SNFKGQKR..I	KCFNCGKEGH	LARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_AU_VH_AF	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	RGCWKCCKEG	HQMKDCTE..
B_CN_RL42	GNFRNQRKIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HLMKDCTE..
B_DE_D31_U	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRR	KGCWKCCKEG	HQMKDCTE..
B_DE_HAN_U	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_FR_HXB2	GNFRNQRKIV	KCFNCGKEGH	TARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_GA_OYI	GNFKNQRKTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_GB_CAM1	GNFRNQRKTV	KCFNCGKVGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCNE..
B_GB_GB8_A	GNFRSQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKECTE..
B_GB_MANC	GNFRNQRKTV	KCFNCGKEGH	IAKNCRAPRR	KGCWKCCKEG	HQMKDCTE..
B_KR_WK_AF	GNFRNQRRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_NL_3202A	GNFRNQRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_TW_TWCYS	GNFRNQRKTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCCKEG	HQMKDCTE..
B_US_BC_LO	GNFRNQRKTV	KCFNCGKEGH	IARNCKAPRK	RGCWKCCKEG	HQMKDCTE..

B_US_DH123	GNFRNQRK.I	KCFNCGKEGH	ISKNCRAPRK	KGCWKCGKEG	HQMKDCTE..
B_US_JRCSF	GNFRNQKKNV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKECTE..
B_US_MNCG	GNFRNQRKII	KCFNCGKEGH	IAKNCRAPRK	RGCWKCGKEG	HQMKDCTE..
B_US_P896	GNFRNQKRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCTE..
B_US_RF_M1	GNFRDQKIV	KCFNCGKVGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCTNEG
B_US_SF2_K	GNFRNQKRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWRCGREG	HQMKDCTE..
B_US_WEAU1	GNFRSPRKTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCGQEG	HQMKDCTE..
B_US_WR27	GNFRNQKRTV	KCXXCAGEGH	XARXCKAPRK	RGCWKCGKEG	HQMXDXXE..
B_US_YU2_M	GNFRNQKRTV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCTE..
BF1_BR_93B	GNFRNQKRTI	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCTE..
C_BR_92BR0	SNCKGPKRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_BW_96BW0	SNFKGPRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_BW_96BW1	NNFKGPTRIV	KCFNCGKEGH	IARNCKAPRK	KGCWKCGKEG	HQMKDCT..E
C_BW_96BW1	GNFKGPRKIP	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCS..E
C_BW_96BW1	SNFKGPKRII	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_ET_ETH22	SNFKGPKRAI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_IN_93IN1	SNFKGSKRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_IN_93IN9	SNFKGSKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_IN_93IN9	SNFKGSKRTV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_IN_94IN1	SNFKGSKRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
C_IN_95IN2	SNFKGSKRIV	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	RGCWKCGQEG	HQMKDCTE..
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGREG	HQMKDCTE..
CRF01_AE_C	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF01_AE_T	GNFKGPRR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQTR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRALRK	KGCWKCGKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	QGCWKCGKEG	HQMKDCTE..
CRF01_AE_T	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF02_AG_F	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCGKEG	HQMKDCTE..
CRF02_AG_F	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCGKEG	HQMKDCTE..
CRF02_AG_G	GNFKGQK.RI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
CRF02_AG_N	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	RGCWKCGKEG	HQMKDCTE..
CRF02_AG_S	GNFRGQRP.I	KCFNCGKEGH	LARNCKAPRK	KGCWKCGKEG	HQMKDCTE..
CRF02_AG_S	GNFRGQRT.I	KCFNCGKEGH	LARNCKAPRK	RGCWKCGKEG	HQMKDCTE..
CRF03_AB_R	SNFRGPKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF03_AB_R	SNFRGPKR.I	KCFNCGKDGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCNE..
CRF04_cpx_	SKFKGQRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF04_cpx_	SNFRGQKRII	KCFNCGKEGH	LARNCRAPRK	RGRWKCGKEG	HQMKDCTE..
CRF04_cpx_	SNFKGPRRSI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCPE..
CRF05_DF_B	GNFKGPRKII	KCFNCGKEGH	IAKNCRAPGK	KGCWKCGREG	HQMKDCTE..
CRF05_DF_B	GNFKGPRKSI	KCFNCGKEGH	TAKNCRAPRK	RGCWKCGREG	HQMKDCIE..
CRF06_cpx_	SNFKGPKRSI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF06_cpx_	SNYKGPKRSI	KCFNCGREGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF06_cpx_	SNFKGP.RKI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF06_cpx_	SNFKGQKRII	KCFNCGKEGH	TARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
CRF11_cpx_	SNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	KGCWKCGREG	HQMKDCTE..
CRF11_cpx_	GNFKGQKR.I	KCFNCGKEGH	LARNCRAPRK	K.GCKCGKEG	HQMKDCTE..
D_CD_84ZR0	SNFKGTRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
D_CD_ELI_K	GNFKGPRKII	KCFNCGKEGH	IAKNCRAPRK	KGCWRCGKEG	HQLKDCTE..
D_CD_NDK_M	GNFKGPRKSI	KCFNCGKEGH	TAKNCRAPRK	KGCWKCGREG	HQMKDCTE..
D_UG_94UG1	GNFKGPKKII	KCFNCGKEGH	TAKNCRAPRK	KGCWKCGREG	HQMKDCTE..
F1_BE_VI85	SNFKGQRRVV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGREG	HQMKDCT..E
F1_BR_93BR	SNFKGQRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGREG	HQMKDCT..E
F1_FI_FIN9	SNFRGQRRIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGQEG	HQMKDCT..E
F1_FR_MP41	SNYKGPRRFI	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
F2_CM_MP25	SNFKGQRRIV	KCFNCGKEGH	IARNCRAPRK	RGCWKCGQEG	HQMKDCT..E
F2KU_BE_VI	GNFKGPRRDV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
G_BE_DRCBL	SNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKECTE..

G_NG_92NG0	SNFKGPRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKECTE..
G_SE_SE616	SNFKGPRRTI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCTE..
H_BE_VI991	GNFKGPRRTV	KCSNCGKEGH	IARNCRAPRK	KGCWKCGQEG	HQMKDCT..G
H_BE_VI997	SNFKGPRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGREG	HQMKDCT..E
H_CF_90CF0	GNFKGQRKFV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGREG	HQMKDCT..E
J_SE_SE702	GNFRDHRKIV	KCFNCGKQGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
J_SE_SE788	GNFRDHRKIV	KCFNCGKQGH	IAKNCRAPRK	KGCWKCGKEG	HQMKDCT..E
K_CD_EQTB1	GNFKGQRRII	KCFNCGKEGH	LARNCRAPRK	KGCWKCGKEG	HQMKDCS..E
K_CM_MP535	GNFKGHRKIV	KCFNCGKEGH	IARNCRAPRK	KGCWKCGKEG	HQMKDCT..E
N_CM_YBF30	GNFKGIRKPI	KCFNCGKEGH	LARNCKAPRR	GGCWKCGQEG	HQMKDCKNEG
O_CM_ANT70	GQNPIRKGTI	KCFNCGKEGH	IARNCRAPRK	KGCWKCGQEG	HQMKDCRN..G
O_CM_MVP51	GQNPNRKGPI	KCFNCGKEGH	IAKNCRAPRK	RGCWKCGQEG	HQMKDCKN..G
O_SN_99SE	GQNPSRKGP	KCFNCGKEGH	LARNCRAPRK	KGCWKCGQEG	HQMKDCKN..G
O_SN_99SE	GQNPGRKGPI	KCFNCGKEGH	LARNCRAPRK	KGCWKCGQEG	HQMKDCRN..G
U_CD__83C	GNFKGPRRIV	KCFNCGKEGH	IAKNCRAPRK	KGCWKCGREG	HQMKDCT..E

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500

00BW0762_1	RQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	TAPPAESFK.
00BW0768_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	TAPPAESFK.
00BW0874_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPSA	PPAESLRPEP	SAPPAESLR.
00BW1471_2	RQANFLGKIW	PSQKG.RPGN	FLQNRPEP..	SAPPAESFR.
00BW1616_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPEPTA	PP....APVP	TAPPAESFR.
00BW1686_8	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	SAPPAESFK.
00BW1759_3	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPLESFK.
00BW1773_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
00BW1783_5	RQANFLGKIW	PSQKGGPRGN	FLQNRPA...ESRLEP	TAPPAESFR.
00BW1795_6	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...P	TAPPAESFR.
00BW1811_3	RQANFLGRIW	PSHKG.RPGN	FLQNRPEPTA	P.....LEP	TAPPAESFR.
00BW1859_5	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	TAPPAESFR.
00BW1880_2	RQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	TAPPAESFK.
00BW1921_1	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	TAPPAESFR.
00BW2036_1	RQANFLGKIW	PSNKG.RPGN	FLQNRTPAPPVEP	TAPPAESFR.
00BW2063_6	RQANFLGKIW	PSHKG.RPGN	FLQSRLE...P	TAPPAESF..
00BW2087_2	RQANFLGKIW	PSHKGGRPGN	FLQSRPEPTA	P....PAEP	TAPPAESFR.
00BW2127_2	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	P....RPEP	SAPPAESFR.
00BW2128_3	RQANFLGRIW	PSNKG.RPGN	FLQNRPEPTA	PPAE.NRPEP	TAPPAESFR.
00BW2276_7	RQANFLGKIW	PSNKG.RPGN	FLQNRTEPTA	P.....LEP	TAPPADSFK.
00BW3819_3	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...	P.....TAP	TAPPAESFR.
00BW3842_8	RQANFLGKIW	PSRGG.RPGN	FLQNRTEPTA	P.....PEP	TAPPAESFR.
00BW3871_3	RQANFLGKIW	PSHKG.RPGN	FLQNRPEP..	TAPPAESFR.
00BW3876_9	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...P	TAPPAESFR.
00BW3886_8	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	P....PAEP	TAPPAESFR.
00BW3891_6	RQANFLGRIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
00BW3970_2	RQANFLGRFW	PSQKG.RPGN	FLQ.....SRSEP	TAPPAESFR.
00BW5031_1	RQANFLGKIW	PSNKG.RPGN	FLQSRPEPTA	P.....PMP	TAPPAESFR.
96BW01B21	RQANFLGKIW	PSHKG.RPGN	FLQNR.....LEP	SAPPAESFR.
96BW0407	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
96BW0502	RQANFLGKIW	PSHKG.RPGN	FLQNRSEPA.APTVP	TAPPAESFR.
96BW06_J4	RQANFLGKIW	PSHKGGRPGN	FLQSRPEP..	TAPPAESFR.
96BW11_06	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESL..
96BW1210	RQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	SAPPAESFR.
96BW15B03	RQANFLGKIW	PSHKG.RPGN	FLQNRTEP..	TAPPAESFK.
96BW16_26	RQADFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
96BW17A09	RQANFLGKIW	PSHKGGRPGN	FLQNRPEP..	TAPPAESFR.
96BWM01_5	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAEIL..
96BWM03_2	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	TAPPAERFR.
98BWM12_2	RQANFLGRLW	PSHKG.RPGN	FPQNR.....VEP	TAPPAESLR.
98BWM13_4	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESL..
98BWM14_a	RQANFLGKIW	PSHKG.RPGN	FLQSRPEP..	SAPPAESFR.
98BWM14_1	RQANFLGKIW	PSHKGGRPGN	FLQRRPEP..	TAPPAESFR.

98BWM018_d	RQANFLGKIW	PSHKG.RPGN	FIQNRPAPT.APPVEP	TAPPAESFR.
98BWM036_a	RQANFLGRIW	PSHKG.RPGN	FLQSRPEPTA	P.....PAEP	TAPPAESFR.
98BWM037_d	RQANFLGKIW	PSHKG.RPGN	FLQ.....KRPEP	TAPPAESFR.
99BW3932_1	RQVNFLGKIW	PSNKG.RPGN	FLQNRTPVTA	PPAESFRIEP	TAPPAESFR.
99BW4642_4	RQANFLGKIW	PSHKG.RPGN	FFQNRTEP..	TAPPAESFR.
99BW4745_8	RQANFLGKIW	PSNKG.RPGN	FLQNRPEPTA	P.....LEP	TAPPAESFR.
99BW4754_7	RQANFLGKIW	PSNKG.RPGN	FLQSR.....PEP	TAPPAESFK.
99BWMC16_8	RQANFLGKIW	PSNKG.RPGN	FLQNRPEPT.APLEP	TAPPAESFR.
A2_CD_97CD	RQANFLGKIW	PSNKG.RPGN	FPQSRTE...P	TAPPMME....
A2_CY_94CY	RQANFLGKIW	PSNKG.RPGN	FPQSRTE...P	TAPPAENLR.
A2D___97KR	RQANFLGKIW	PSHSG.RPGN	FPQSRTE...P	TAPPAEDFG.
A2G_CD_97C
A_BY_97BL0	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...PS	APP.AENFR.
A_KE_Q23_A	RQANFLGKIW	PSRKG.RPGN	FPQNRLE...PT	APP.AETCG.
A_SE_SE659
A_SE_SE725
A_SE_SE753	RQANFLGRIW	PSSKG.RPGN	FPQSRLE...PT	APP.AEIFG.
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	RQANFLGKIW	PSHKG.RPGN	FPQSRPE...PS	APP...AEM.
A_UG_92UG0	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPAAEIFG.
A_UG_U455_	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...P	TAPPAEIFG.
AC_IN_2130	RQANFLGKIW	PSHKG.RPGN	FLQ.....NRPEP	TAPPAESFR.
AC_RW_92RW	RQANFLGKIW	PSNKG.RPGN	FPQSRLE...EP	TAPPA.....
AC_SE_SE94
ACD_SE_SE8	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...PT	APPA.ESFG.
ACG_BE_VI1	RQANFLGKIW	PSNKG.RPGN	FPQSRPEPTA	PP.....AEP	TAPPAESFG.
AD_SE_SE69	RQANFLGKIW	PSSKG.RPGN	FLQSRP....EP	TAPPAESFG.
AD_SE_SE71
ADHK_NO_97	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PS	APPA.ESFG.
ADK_CD_MAL	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...PT	APPA.ESFG.
AG_BE_VI11	RQANFLGKIW	PSSKG.RPGN	FPQSRLE...PT	APPA.ESLG.
AG_NG_92NG	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
AGHU_GA_VI	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...PT	APPA.ESFG.
AGU_CD_Z32	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFE.
AJ_BW_BW21	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...PT	APPA.ESFG.
B_AU_VH_AP	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_CN_RL42_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_DE_D31_U	RQANFLGKIW	PSYKG.RPGN	FLQRRPE...P	TAPPEESFR.
B_DE_HAN_U	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_FR_HXB2_	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_GA_OYI_	RQANFLGKIW	PSHKG.RPGN	FLQNRPE...P	TAPPAESFG.
B_GB_CAM1_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_GB_GB8_A	RQANFLGKIW	PSHKG.RPGN	FLQSRPEPIA	PP.....EP	TAPPEESFR.
B_GB_MANC	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_KR_WK_AF	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	SAPPEESFR.
B_NL_3202A	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_TW_TWCYS	RQANFLGKIW	PSHKE.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_BC_L0	RQANFLGKIW	PSHKG.RPGN	FPQSRLE...P	TAPPEESFR.
B_US_DH123	RQANFLGKIW	PSHKE.RPGN	FLQSRPE...P	SAPPEESFR.
B_US_JRCSP	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_MNCG_	RQANFLGKIW	PSCKG.R.RN	FPQSRTE...P	TAPPEESFR.
B_US_P896_	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_RF_M1	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_SF2_K	RQANFLGKIW	PSYKG.RPGN	FLQSRPE...P	TAPPEESFR.
B_US_WEAU1	RQANFLGKIW	SSQKG.RPGN	FPQSRLE...P	TAPPEESFR.
B_US_WR27_	RQAXFLGXIR	PSHXG.RPGX	FLQNRPE...P	SAPPAESFR.
B_US_YU2_M	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPSEESVR.
BF1_BR_93B	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFR.
C_BR_92BR0	RQANFLGKIW	PSHRG.RPGN	LLQNRRT....EP	TAPPE.....

C_BW_96BW0	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_BW_96BW1	RRANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESF..
C_BW_96BW1	GQANFLGKIW	PSHKG.RPGN	FLQSR.....PEP	SAPPAESFR.
C_BW_96BW1	RQANFLGKIW	PSHKG.RPGN	FLQNRTEP..	TAPPAESFK.
C_ET_ETH22	RQANFLGRLW	PSNKG.RPGN	FLQSRP....EP	TAPPESLRPE
C_IN_93IN1	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_IN_93IN9	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_IN_93IN9	RQANFLGKIW	PSHKG.RPGN	FLQNRPEPTA	PP...ARPEP	TAPPAESFR.
C_IN_94IN1	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
C_IN_95IN2	RQANFLGKIW	PSHKG.RPGN	FLQ.....SRPEP	TAPPAESFR.
CRF01_AE_C	RQANFLGKIW	PLNKG.RPGN	FPQSRLE...PT	APPA.ESLG.
CRF01_AE_C	RQANFLCKIW	PSSKG.RPGN	FPQSRPE...PT	APPM.ESLG.
CRF01_AE_C	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESLG.
CRF01_AE_T	RQANFLGKFW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APP..AEWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF01_AE_T	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...PT	APPA.ENWG.
CRF02_AG_F	GQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESLG.
CRF02_AG_F	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESFG.
CRF02_AG_G	RQANFLGKIW	PSNKG.RPGN	FPQSRPE...	P.....	SAPPAESFG.
CRF02_AG_N	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESFG.
CRF02_AG_S	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESLG.
CRF02_AG_S	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PT	APPA.ESFG.
CRF03_AB_R	RQANFLGRIW	PSSKG.RPGN	FPQSRPE...PS	APP.AENFG.
CRF03_AB_R	RQANFLGKIW	PSSKG.RPGN	FPQSRPE...PS	APP.AENFG.
CRF04_cpx	RQANFLGRMW	PSSKG.RPGN	FLQNRPE...PT	APPA.ECLE.
CRF04_cpx	RQANFLGRMW	PSSKG.RPGN	FLQSRPE...PT	APPA.ESLE.
CRF04_cpx	RQANSLGRMW	PSSKG.RPGN	FLQSRTE...PT	APPA.ESFE.
CRF05_DF_B	RQANFLGKVV	PSHKG.RPGN	FLQSRP....EP	SAPPAESFR.
CRF05_DF_B	GQANFLGRVW	LSHKG.RPGN	FLQSRP....EP	SAPPAESFG.
CRF06_cpx	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPIESFG.
CRF06_cpx	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
CRF06_cpx	RQANFLGRIW	PSSKG.RPGN	FLQNRPE...P	TAPPAESFG.
CRF06_cpx	RQANFLGKIW	PSHKG.RPGN	FLQNRPEQNR	P.....EP	SAPPAESFG.
CRF11_cpx	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...PT	APPA.ESFG.
CRF11_cpx	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...PT	APPA.ESFG.
D_CD_84ZR0	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAE.FG.
D_CD_ELI_K	RQANFLGRIW	PSHKG.RPGN	FLQSRP....EP	TAPPAESFG.
D_CD_NDK_M	RQANFLGKIW	PSHKG.RPGN	FLQSRP....EP	TAPPAESFG.
D_UG_94UG1	RQANFLGKIW	PSHKG.RPGN	FLQSRPPA..EP	TAPPAEIFG.
F1_BE_VI85	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...P	TAPPAESFG.
F1_BR_93BR	RQANFLGKIW	PSNKG.RPGN	FIQNRPE...P	SAPPAESFR.
F1_FI_FIN9	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...P	TAPPAESLG.
F1_FR_MP41	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
F2_CM_MP25	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.
F2KU_BE_VI	RQANFLGKIW	PSNKG.RPGN	FLQSRPE...P	TAPPAESFG.
G_BE_DRCHL	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAENFG.
G_NG_92NG0	RQANFLGKIW	PSNKG.RPGN	FLQNRTE...P	TAPPAESFG.
G_SE_SE616	RQANFLGKIW	PSNKG.RPGN	FLQNRTE...P	TAPPAESLG.
H_BE_VI991	RQANFLGKIW	PSSKG.RPGN	FPQKRLE...P	TAPPAESFG.
H_BE_VI997	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESFG.
H_CF_90CF0	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESFG.
J_SE_SE702	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESLG.
J_SE_SE788	RQANFLGKIW	PSSKG.RPGN	FLQSRPE...P	TAPPAESLG.
K_CD_EQTB1	RQANFLGKFW	PLNKE.RPGN	FLQNRPE...P	TAPPAESFG.
K_CM_MP535	RQANFLGKIW	PSHKG.RPGN	FLQSRPE...P	TAPPAESFG.
N_CM_YBF30	RQANFLGKSW	SPFKG.RPGN	FPQTTTRK..EP	TAPPLESYG.
O_CM_ANT70	RQANFLGKYW	PP.GGTRPGN	YVQRPAAH...P	SAPPMEEEVK

O_CM_MVP51	RQANFLGKYW	PP.GGTRPGN	YVQKQVS...P	SAPPMEEAVK
O_SN_99SE_	RQANFLGKYW	PP.GGTRPGN	YAQRQVS...P	SAPPMTEEMK
O_SN_99SE_	KQANFLGKYW	PP.GGTRPGN	YAQRQVS...P	SAPPMTEEMK
U_CD_83C	RQANFLGKIW	PSNKG.RPGN	FLQNRPE...P	TAPPAESFG.

501

550

00BW0762_1FE...	..ETNPTP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW0768_2FE...	..ETTPAP..	...KQE....	LKDR.....E	PLTALKSLFG
00BW0874_2FE...	..ETTPAL..	...KRE....	LKER.....E	PLISLKSLFG
00BW1471_2FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW1616_2F....	..GETTPSP..	...RQE....	AKDRE.....	PLISLKSLFG
00BW1686_8FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW1759_3FE...	..ETTPAP..	...KQE....	PKDRE.....	TLTSLRSLFG
00BW1773_2FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW1783_5FE...	..ETTPVQ..	...KQE....	TKDRE.....	PLTSLKSLFG
00BW1795_6F....	..EETTPSP..	...KQE....	LKDKE.....	PLTSLKSLFG
00BW1811_3FE...	..ETTPAS..	...KQE....	KKDRE.....	TLTSLRSLFG
00BW1859_5FE...	..ETTPAP..	...KQE....	QKDR.....E	PLTSLKSLFG
00BW1880_2FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLKSLFG
00BW1921_1FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW2036_1FE...	..ETTPAP..	...KQE....	LKDR.....E	PLISLKSLFG
00BW2063_6F....	..EETTPAP..	...KQE....	MKDKE.....	PLISLKSLFG
00BW2087_2FE...	..ETTPAS..	...KQD....	LKDRE.....	PLTSLKSLFG
00BW2127_2FE...	..ETTHAP..	...KQE....	LKDRE.....	ALTSKSLFG
00BW2128_3FE...	..ETTPAP..	...KQE....	PKNRE.....	PLTSLKSLFG
00BW2276_7FE...	..ETTPEL..	...KQG....	PKDR.....E	PLTSLKSLFG
00BW3819_3FE...	..EITPAP..	...KQE....	TKDRE.....	PLTSLKSLFG
00BW3842_8FE...	..ETTPAP..	...KQE....	PKDRGPY.RE	PLISLKSLFG
00BW3871_3FE...	..ETTPVP..	...KQE....	PTDR.....E	PLTSLKSLFG
00BW3876_9FE...	..ETTPTL..	...KQE....	LKDRE.....	PLTSLKSLFG
00BW3886_8FE...	..ETTPVP..	...KQE....	QKDRE.....	ALTSKSLFG
00BW3891_6FE...	..EITPVP..	...KQE....	PKDR.....E	PLTSLKSLFG
00BW3970_2FE...	..ETTPAP..	...KQE....	PKDRE.....	PLISLKSLFG
00BW5031_1FG...	..ETTPAP..	...KQE....	MKERE.....	PLISLKSLFG
96BW01B21FE...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLRSLFG
96BW0407FE...	..ETTPGQ..	...KQE....	SKDRE.....	TLTSLKSLFG
96BW0502FE...	..ETTPAP..	...KQE....	PKDREPY.RE	PLTALRSLFG
96BW06_J4FE...	..ETTPAL..	...KQE....	PKDK.....E	PLTSLKSPFG
96BW11_06F....	..EETTPAP..	...KQE....	TKDRE.....	PLISLKSLFG
96BW1210FE...	..ETTPAQ..	...KQE....	PKDREP....	PLASLKSLFG
96BW15B03FE...	..ETTPAP..	...KQE....	PKDR.....E	PLISLKSLFG
96BW16_26FG...	..ETTPAP..	...KQE....	PKDRE.....	PLTSLRSLFG
96BW17A09FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSFKSLFG
96BWM01_5F....	..EETTPAP..	...KQE....	MKDKEPY.KE	PLISLRSLFG
96BWM03_2PE...	..PTAPPAE..	...RQE....	SKDR.....E	PLISLKSLFG
98BWMC12_2LE...	..ETTPAS..	...KQE....	MKDR.....E	PLISLKSLFG
98BWMC13_4F....	..EETTPAP..	...KQE....	PKDKE.....	PLISLKSLFG
98BWMC14_aFE...	..ETTPAP..	...KQE....	QKDR.....E	PLTSLKSLFG
98BWM014_1FESRP	EPTAPPAES.	..FRQE....	PKDR.....E	PLTALKSLFG
98BWM018_dFE...	..ETTPAL..	...KQE....	PKDREA....	PLTSLKSLFG
98BWM036_aFE...	..ETNLAP..	...KQE....	PKDRE.....	PLTSLKSLFG
98BWM037_dFE...	..ETTPAP..	...RQE....	AKDKE.....	PLNSLKSLFG
99BW3932_1FE...	..ETTPAP..	...KQE....	LKDRE.....	ALTSKSLFG
99BW4642_4FE...	..ETTPAP..	...KQE....	PKDR.....E	PLTSLKSLFG
99BW4745_8FE...	..GATPTP..	...KQE....	PRDR.....E	PLTSLKSLFG
99BW4754_7FE...	..ETTPAQ..	...KQE....	SKDRE.....	PLTSLKSLFG
99BWMC16_8FE...	..ETNPAP..	...KQE....	LKNRE.....	TLTSLRSLFG
A2_CD_97CDF....	..EETSSSL..	...KQE....	NREPS....T	PAISLKSLFG
A2_CY_94CYF....	..MGEEITSSL..	...KQEL...E	TREPY....N	PAISLKSLFG
A2D_97KRF....	..MGEEETPLQ..	...KQEL...K	NREQH....T	PAISLKSLFG

A2G_CD_97C
A_BY_97BL0	MGEET	PSLK.Q...E	QKDRE...QYP	PSISLKSFLG
A_KB_Q23_A	MGEETV	SPLK.Q...E	QKDRE...QAQ	PLVSLKSFLG
A_SE_SE659
A_SE_SE725
A_SE_SE753	MREEIA	SPPK.Q...E	Q...KG...QDP	PLVSLKSFLG
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	MGEET	SPPK.Q...E	Q...NNP	PSVSLKSFLG
A_UG_92UG0	MREEIV	SPPK.Q...E	QNDRD...QNP	PSVSLKSFLG
A_UG_U455	MGEKMTSPA	..KQEL...K	DREQ...T	PLVSLKSFLG
AC_IN_2130FE...	..ETTPAL	..KQE...	QKDRE...	PLTSLKSFLG
AC_RW_92RWENFG	MGEETASPL	..K.QE...	QKDRE...	PLISLKSFLG
AC_SE_SE94
ACD_SE_SE8	FGEEITP	S.QK.Q...E	QKDKE...LY	PLASLKSFLG
ACG_BE_VI1	KEDAIDSS	..PKQE...	PRDKG...LYP	PLTSLKSFLG
AD_SE_SE69	FGEEIAP	..SQKQE...Q	KDK...ELY	PLASLKSFLG
AD_SE_SE71
ADHK_NO_97	IGEEIT	SYQK.Q...E	QKDRE...PPP	PLVSLKSFLG
ADK_CD_MAL	FGEEIK	PSQK.Q...E	QKDKE...L.Y	PLASLKSFLG
AG_BE_VI11	MEEET	PSQK.Q...E	PRDTG...LYP	PLTSLKSFLG
AG_NG_92NG	FGEEIAP	S.LK.Q...E	PREKE...SPP	L.TSLKSFLG
AGHU_GA_VI	FGEEIA	PSPR.P...E	PREKE...R.Y	PLTSLKSFLG
AGU_CD_Z32	TKEETS	S.PK.Q...E	PRDKG...LYP	PLASLKSFLG
AJ_BW_BW21	FGEEAT	PSPK.Q...E	GKDKE...L.Y	PLTSLKSFLG
B_AU_VH_AF	FGEEETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_CN_RL42	FGEEETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_DE_D31_U	FGEEATAP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_DE_HAN_U	SGVETTP	..PQKQE...	PIDK...ELY	PLTSLKSFLG
B_FR_HXB2	FGEEETTP	..PQKQE...	PIDK...GLY	PLTSLKSFLG
B_GA_OYI	FGEEKTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_GB_CAM1	FGGETTP	..SQKQE...	PINK...EPY	PLASLKSFLG
B_GB_GB8_A	FGEEETTP	..AQKQE...	PIDK...ELY	PLASLKSFLG
B_GB_MANC	FGEEETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_KR_WK_AF	FGEEETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_NL_3202A	FGEEETTP	..SQKQE...	PRDK...ELY	PLASLKSFLG
B_TW_TWYS	FGEEETTP	..SQKQE...	PIDK...DLY	PLASLKSFLG
B_US_BC_L0	FGEEETTP	..PQKQERE...	..DK...EMY	PLASLKSFLG
B_US_DH123	FGEEATP	..SQKQE...	..PK...ELY	PLASLKSFLG
B_US_JRCSF	FGEEATP	..SQKQE...	PIDK...ELY	PLTSLKSFLG
B_US_MNCG	FGEEETTP	..YQKQEKQKQ	TIDK...DLY	PLASLKSFLG
B_US_P896	FGEEETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_US_RF_M1	FGEEETTP	..SQKQE...	KIDK...ELY	PLASLKSFLG
B_US_SF2_K	FGEEKTP	..SQKQE...	PIDK...ELY	PLTSLKSFLG
B_US_WEAU1	FREETTP	..SQKQE...	PIDK...ELY	PLTSLKSFLG
B_US_WR27	FGXETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
B_US_YU2_M	FGEEETTP	..SQKQE...	PIDK...ELY	PLASLKSFLG
BF1_BR_93B	FGEEVTP	..SQKQE...	PIDK...EMY	PLASLKSFLG
C_BR_92BR0ESFR	FGEEETTPS	..RKQE...	TIDKEL...	PLTSLKSFLG
C_BW_96BW0FE...	..ETTPVP	..KQE...	PKDRE...	PLTSLKSFLG
C_BW_96BW1EETTPAP	..KQE...	TKDRE...	PLISLKSFLG
C_BW_96BW1FE...	..ETTPAQ	..KQE...	PKDREP...	PLASLKSFLG
C_BW_96BW1FE...	..ETTPAP	..KQE...	PKDR...E	PLISLKSFLG
C_ET_ETH22	PTAPPESFR	FEEATPSPK	..Q...E	LKDRE...	ALTSLSLFG
C_IN_93IN1FE...	..ETTPAP	..KQE...	PKDRE...	PLTSLKSFLG
C_IN_93IN9FE...	..ETTPAP	..KQE...	PKDRE...	PLTSLKSFLG
C_IN_93IN9FE...	..ETTPAL	..KQE...	PKDRE...	PLTSLKSFLG
C_IN_94IN1FE...	..ETTPAP	..KQE...	PKERE...	PLTSLKSFLG
C_IN_95IN2FE...	..ETTPAP	..KQE...	PKDRE...	PLTSLKSFLG
CRF01_AE_C	MGEET	SPPK.Q...E	QKDKE...HPS	PLVSLKSFLG

CRF01_AE_C	MGEEIT....	SFPK.Q...	E	QKDKK..QPP	PLVSLKSLFG
CRF01_AE_C	MGEEIT....	SFSR.Q...	E	QKORE..HPP	PLVSLKSLFG
CRF01_AE_T	MGEETT....	.SLLKQ...	E	QKDKE..HHP	PLVSLKSLFG
CRF01_AE_T	MGEEIT....	SLPK.Q...	E	QKDKD..PPP	.LVSLKSLFG
CRF01_AE_T	MGEE.....	QKDKB..HPP	PSVSLKSLFG
CRF01_AE_T	MGEETT....	SSLK.Q...	E	QKDKE..PPP	PLISLKSLFG
CRF01_AE_T	MGEEITGEEI	TSLPKQ...	E	QKDKB..HPP	PLVSLKSLFG
CRF01_AE_T	MGEEIT....	SFLK.Q...	E	QKDKE..HPP	PSVSLKSLFG
CRF02_AG_F	MGEEIT....	SPPK.Q...	E	ARDQG..LYP	PLASLKSLFG
CRF02_AG_F	MGEEIT....	SPPK.Q...	E	PRDQG..LYP	PLASLKSLFG
CRF02_AG_G	TREEITSS..	..PQQE....	PRDKG..LYP	PLTSLKSLFG
CRF02_AG_N	MGEEIP....	PSPQ.Q...	E	PRDKG..LYP	PLTSLKSLFG
CRF02_AG_S	IGEEIT....	SSQK.Q...	E	PGDKG..LYP	PLASLKSLFG
CRF02_AG_S	MGEEIT....	SSPK.Q...	E	PGDKG..LYP	PLTSLKSLFG
CRF03_AB_R	MGEEIT....	PSLK.Q...	E	QKDRE..QHP	PSISLKSLFG
CRF03_AB_R	MGEEIT....	PSLK.Q...	E	QKDRG..QHP	PSISLKSLFG
CRF04_cpx_	RKEETTS...	S.LK.Q...	E	PRDKE..LYP	.LTSLKSLFG
CRF04_cpx_	MKEETTS...	S.PK.Q...	E	PRDKE..LYP	.LTSLKSLFG
CRF04_cpx_	MKEETTS...	S.PK.Q...	E	QRDKE..LYP	.ITSLKSLFG
CRF05_DF_B	FGEEIAS...	.SPKQE...Q	KDEG...LYP	PLASLKSLFG	
CRF05_DF_B	FGEEITP...	.SPKQE...Q	KDEG...LYP	PLASLKSLFG	
CRF06_cpx_	FGEEIAP...	S.PK.Q...	E	SKEKEEKGLY	PLASLKSLFG
CRF06_cpx_	FGEEIAP...	S.PE.Q...	K	PKEKE...LY	PLTSLRSLFG
CRF06_cpx_	FGEEIAP...	S.LK.Q...	E	PKEKEKE.LY	PLASLKSLFG
CRF06_cpx_	FGEEIAP...	S.PK.Q...	E	PKEKE...LY	PLASLKSLFG
CRF11_cpx_	FGEEIAP...	.SPK.Q...	E	PKEKEK.ELY	PLTSLKSLFG
CRF11_cpx_	FGEEITP...	.SPK.Q...	E	PKEK...ELY	PITSLKSLFG
D_CD_84ZR0	FGEEITP...	.SQKQEQK..	DKDK...ELY	PLASLKSLFG	
D_CD_ELI_K	FGEEITP...	.SQKQEQ...Q	KDK...ELY	PLTSLKSLFG	
D_CD_NDK_M	FGEEITP...	.SQKQEQ...Q	KDK...ELY	PLASLKSLFG	
D_UG_94UG1	LGEEITP...	.PQKQE...Q	KDK...ELY	PLTSLKSLFG	
F1_BE_VI85FR...	.EEITPSP...	...KQE....	QKDGEL..YP	PLASLKSLFG	
F1_BR_93BRFG...	.EETTPSP...	...KQE....	QKDEGL..YP	PLASLKSLFG	
F1_FI_FIN9IR...	.EEVTPSP...	...RQE....	QKEEGQ..YP	PLASLKSLFG	
F1_FR_MP41FK...	.EEITPSP...	...KQE....	QKDEGQGLYP	PLASLKSLFG	
F2_CM_MP25FG...	.EEIAPSP...	...KQE....	QKDKEQ..VP	PLISLKSLFG	
F2KU_BE_VIFG...	.EEINPSP...	...RQE....	TKDKGQ..EP	PLTSLKSLFG	
G_BE_DRCBL	FGEEIAP...	S.PK.Q...	E	QKEKE..LYP	L.SSLKSLFG
G_NG_92NG0	FGEEIAP...	S.PK.Q...	E	PKEKE..LYP	L.TSLKSLFG
G_SE_SE616	FGEEIAP...	S.PK.Q...	E	MKEKE..LYP	...SLKSLFG
H_BE_VI991FG...	.EEITPSP...	...RQE....	LKEQE...P	PLTSLRSLFG	
H_BE_VI997FG...	.EEMTSSP...	...KQE....	LKDKE...P	PFASLKSLFG	
H_CF_90CF0FG...	.EEMTPSP...	...KQEQ...	LKDKE...P	PLASLRSFLG	
J_SE_SE702FG...	.EEIPSP...	...KQE....	PKDKE...LY	PLTSLRSLFG	
J_SE_SE788LG...	.EEIPSP...	...KQE....	PKDKE...LY	PLTSLKSLFG	
K_CD_EQTB1FG...	.EKITPSL...	...RQE....	MKDQEQ..GP	PLTSLKSLFG	
K_CM_MP535FG...	.EEITPSP...	...RQE....	TKDKEQ..SP	PLTSLKSLFG	
N_CM_YBF30FQ...	.EEKSTQ...	GKEMQE...N	QERTENSLYP	PLTSLRSLFG	
O_CM_ANT70QENQEQ...	...KGG....	PNE....LY	PFASLKSLFG	
O_CM_MVP51EQENQSQ...	...KGD....	QBE....LY	PFASLKSLFG	
O_SN_99SE_QENQEQ...	...KED....	QNE....LY	PFASLRSFLG	
O_SN_99SE_QENQEQ...	...KGD....	QNE....LY	PFASLKSLFG	
U_CD_83CFG...	.EETTPSP...	...KQE....	PRDKESL.YP	PLTSLKSLFG	

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00BW0762_1	SDPLSQ
00BW0768_2	SDPLSQ
00BW0874_2	NDPLSQ
00BW1471_2	SDPLSQ
00BW1616_2	SDPLSQ

00BW1686_8	SDPLSQ
00BW1759_3	SDPLSQ
00BW1773_2	SDPLSQ
00BW1783_5	SDPLSQ
00BW1795_6	SDPLSQ
00BW1811_3	SDPLSQ
00BW1859_5	SDPLSQ
00BW1880_2	NDPLSQ
00BW1921_1	SDPLSQ
00BW2036_1	SDPLSQ
00BW2063_6	NDPLSQ
00BW2087_2	SDPLSQ
00BW2127_2	SDPLSQ
00BW2128_3	SDPWSQ
00BW2276_7	SDPLSQ
00BW3819_3	SDPLSQ
00BW3842_8	SDPLSQ
00BW3871_3	SDPLSQ
00BW3876_9	SDPLSQ
00BW3886_8	SDPLSQ
00BW3891_6	SDPLSQ
00BW3970_2	SDPLSQ
00BW5031_1	SDPLSQ
96BW01B21	SDPLSQ
96BW0407	NDPLSQ
96BW0502	SGPLSQ
96BW06_J4	SDPLSQ
96BW11_06	SDPLSQ
96BW1210	NDPLSQ
96BW15B03	SDPLSQ
96BW16_26	NDPLSQ
96BW17A09	SDPLSQ
96BWM01_5	SDPLSQ
96BWM03_2	SDPLSQ
98BWM012_2	NDPLSQ
98BWM013_4	SDPLSQ
98BWM014_a	NDPLSQ
98BWM014_1	SDPLSQ
98BWM018_d	SDPLSQ
98BWM036_a	SDPLSQ
98BWM037_d	SDPLSQ
99BW3932_1	SDPLSQ
99BW4642_4	SDPLSQ
99BW4745_8	SDPLSQ
99BW4754_7	NDPLSQ
99BWM016_8	GDPLSQ
A2_CD_97CD	NDLLSQ
A2_CY_94CY	NDPLLQ
A2D_97KR	NDPLLQ
A2G_CD_97C
A_BY_97BL0	NDPLSQ
A_KE_Q23_A	NDLLSQ
A_SE_SE659
A_SE_SE725
A_SE_SE753	NDLLSQ
A_SE_SE853
A_SE_SE889
A_SE_UGSE8	NDLLSQ
A_UG_92UG0	NDLLSQ
A_UG_U455_	NDPLSQ

AC_IN_2130	SDPLSQ
AC_RW_92RW	NDPLSQ
AC_SE_SE94
ACD_SE_SE8	NDP...
ACG_BE_VI1	NDP...
AD_SE_SE69	NDP...
AD_SE_SE71
ADHK_NO_97	NDPLSQ
ADK_CD_MAL	NDQLSQ
AG_BE_VI11	NDP...
AG_NG_92NG	NDP...
AGHU_GA_VI	SDP...
AGU_CD_Z32	SDP...
AJ_BW_BW21	SDP...
B_AU_VH_AF	NDPSSQ
B_CN_RL42	NDPSSQ
B_DE_D31_U	NDPSSQ
B_DE_HAN_U	SDPSSQ
B_FR_HXB2	NDPSSQ
B_GA_OYI	NDPSSQ
B_GB_CAM1	NDPSSQ
B_GB_GB8_A	NDPSSQ
B_GB_MANC	NDPSSQ
B_KR_WK_AF	NDPSSQ
B_NL_3202A	NDPSSQ
B_TW_TWCYS	NDPSSQ
B_US_BC_L0	NDPSSQ
B_US_DH123	NDP...
B_US_JRCSE	NDPSSQ
B_US_MNCG	NDPLSQ
B_US_P896	NDPSSQ
B_US_RF_M1	NDPSSQ
B_US_SF2_K	NDPSSQ
B_US_WEAU1	NDPSSQ
B_US_WR27	NDPSSQ
B_US_YU2_M	SDPSSQ
BF1_BR_93B	NDPSSQ
C_BR_92BR0	SDPLST
C_BW_96BW0	SDPLSQ
C_BW_96BW1	SDPLSQ
C_BW_96BW1	NDPLSQ
C_BW_96BW1	SDPLSQ
C_ET_ETH22	NDHLLQ
C_IN_93IN1	SDLLSQ
C_IN_93IN9	SDPLSQ
C_IN_93IN9	SDPLSQ
C_IN_94IN1	SDPLSQ
C_IN_95IN2	SDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_C	NDPLSQ
CRF01_AE_T	NDPSSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF01_AE_T	NDPLSQ
CRF02_AG_F	NDP...
CRF02_AC_F	NDP...
CRF02_AG_G	NDP...

CRF02_AG_N	NDP...
CRF02_AG_S	NDP...
CRF02_AG_S	NDPYSQ
CRF03_AB_R	DDPLSQ
CRF03_AB_R	NDPLSQ
CRF04_cpx	SDPLSQ
CRF04_cpx	NHPLSQ
CRF04_cpx	SDPLSR
CRF05_DF_B	NDPLSQ
CRF05_DF_B	NDPLSQ
CRF06_cpx	SDP...
CRF06_cpx	NDP...
CRF06_cpx	NDP...
CRF06_cpx	SDP...
CRF11_cpx	SDP...
CRF11_cpx	SDPLSQ
D_CD_84ZR0	NDPLSQ
D_CD_ELI_K	NDPLSQ
D_CD_NDK_M	NDPSSQ
D_UG_94UG1	NDPLSQ
F1_BE_VI85	NDP...
F1_BR_93BR	NDP...
F1_FI_FIN9	NDP...
F1_FR_MP41	SDP...
F2_CM_MP25	SDQ...
F2KU_BE_VI	SDPLLQ
G_BE_DRCBL	NDQ...
G_NG_92NG0	SDP...
G_SE_SE616	SDP...
H_BE_VI991	NDQ...
H_BE_VI997	NDPLSQ
H_CF_90CF0	SDPLLQ
J_SE_SE702	SDPLSQ
J_SE_SE788	SDPLSQ
K_CD_EQTB1	SDPLSQ
K_CM_MP535	NDPLSQ
N_CM_YBF30	NDPSSQ
O_CM_ANT70	TDQ...
O_CM_MVP51	TDQ...
O_SN_99SE	TDQ...
O_SN_99SE	TDQ...
U_CD_83C	SDPSLQ

Table 12. HIV Env Sequence Alignment
GCG Multiple Sequence File.
Written by Omega 1.1

Name: 00BW0762_1	Len: 962	Check: 4645	Weight: 1.00
Name: 00BW0768_2	Len: 962	Check: 9565	Weight: 1.00
Name: 00BW0874_2	Len: 962	Check: 7745	Weight: 1.00
Name: 00BW1471_2	Len: 962	Check: 9593	Weight: 1.00
Name: 00BW1616_2	Len: 962	Check: 792	Weight: 1.00
Name: 00BW1686_8	Len: 962	Check: 3744	Weight: 1.00
Name: 00BW1759_3	Len: 962	Check: 9808	Weight: 1.00
Name: 00BW1773_2	Len: 962	Check: 3500	Weight: 1.00
Name: 00BW1783_5	Len: 962	Check: 9684	Weight: 1.00
Name: 00BW1795_6	Len: 962	Check: 8410	Weight: 1.00
Name: 00BW1811_3	Len: 962	Check: 2068	Weight: 1.00
Name: 00BW1859_5	Len: 962	Check: 5692	Weight: 1.00
Name: 00BW1880_2	Len: 962	Check: 1901	Weight: 1.00
Name: 00BW1921_1	Len: 962	Check: 5923	Weight: 1.00
Name: 00BW2036_1	Len: 962	Check: 7035	Weight: 1.00
Name: 00BW2063_6	Len: 962	Check: 4853	Weight: 1.00
Name: 00BW2087_2	Len: 962	Check: 2085	Weight: 1.00
Name: 00BW2127_2	Len: 962	Check: 4015	Weight: 1.00
Name: 00BW2128_3	Len: 962	Check: 5884	Weight: 1.00
Name: 00BW2276_7	Len: 962	Check: 8913	Weight: 1.00
Name: 00BW3819_3	Len: 962	Check: 9390	Weight: 1.00
Name: 00BW3842_8	Len: 962	Check: 8867	Weight: 1.00
Name: 00BW3871_3	Len: 962	Check: 7069	Weight: 1.00
Name: 00BW3876_9	Len: 962	Check: 4761	Weight: 1.00
Name: 00BW3886_8	Len: 962	Check: 7681	Weight: 1.00
Name: 00BW3891_6	Len: 962	Check: 379	Weight: 1.00
Name: 00BW3970_2	Len: 962	Check: 8001	Weight: 1.00
Name: 00BW5031_1	Len: 962	Check: 4902	Weight: 1.00
Name: 96BW01B21	Len: 962	Check: 5774	Weight: 1.00
Name: 96BW0407	Len: 962	Check: 4260	Weight: 1.00
Name: 96BW0502	Len: 962	Check: 4658	Weight: 1.00
Name: 96BW06_J4	Len: 962	Check: 9749	Weight: 1.00
Name: 96BW11_06	Len: 962	Check: 4328	Weight: 1.00
Name: 96BW1210	Len: 962	Check: 3855	Weight: 1.00
Name: 96BW15B03	Len: 962	Check: 9133	Weight: 1.00
Name: 96BW16_26	Len: 962	Check: 5	Weight: 1.00
Name: 96BW17A09	Len: 962	Check: 6458	Weight: 1.00
Name: 96BWM01_5	Len: 962	Check: 9487	Weight: 1.00
Name: 96BWM03_2	Len: 962	Check: 8766	Weight: 1.00
Name: 98BWMC12_2	Len: 962	Check: 2722	Weight: 1.00
Name: 98BWMC13_4	Len: 962	Check: 2526	Weight: 1.00
Name: 98BWMC14_a	Len: 962	Check: 7761	Weight: 1.00
Name: 98BWM014_1	Len: 962	Check: 93	Weight: 1.00
Name: 98BWM018_d	Len: 962	Check: 279	Weight: 1.00
Name: 98BWM036_a	Len: 962	Check: 134	Weight: 1.00
Name: 98BWM037_d	Len: 962	Check: 9669	Weight: 1.00
Name: 99BW3932_1	Len: 962	Check: 3527	Weight: 1.00
Name: 99BW4642_4	Len: 962	Check: 1175	Weight: 1.00
Name: 99BW4745_8	Len: 962	Check: 8117	Weight: 1.00
Name: 99BW4754_7	Len: 962	Check: 5709	Weight: 1.00
Name: 99BWMC16_8	Len: 962	Check: 285	Weight: 1.00
Name: A2_CD_97CD	Len: 962	Check: 2892	Weight: 1.00
Name: A2_CY_94CY	Len: 962	Check: 8628	Weight: 1.00
Name: A2D_97KR	Len: 962	Check: 471	Weight: 1.00
Name: A2G_CD_97C	Len: 962	Check: 939	Weight: 1.00
Name: A_BY_97BL0	Len: 962	Check: 4291	Weight: 1.00

Name: A_KE_Q23_A	Len: 962	Check: 1190	Weight: 1.00
Name: A_SE_SE659	Len: 962	Check: 6674	Weight: 1.00
Name: A_SE_SE725	Len: 962	Check: 4925	Weight: 1.00
Name: A_SE_SE753	Len: 962	Check: 2482	Weight: 1.00
Name: A_SE_SE853	Len: 962	Check: 1860	Weight: 1.00
Name: A_SE_SE889	Len: 962	Check: 2102	Weight: 1.00
Name: A_SE_UGSE8	Len: 962	Check: 5063	Weight: 1.00
Name: A_UG_92UG0	Len: 962	Check: 6685	Weight: 1.00
Name: A_UG_U455_	Len: 962	Check: 8657	Weight: 1.00
Name: AC_IN_2130	Len: 962	Check: 7784	Weight: 1.00
Name: AC_RW_92RW	Len: 962	Check: 4676	Weight: 1.00
Name: AC_SE_SE94	Len: 962	Check: 2949	Weight: 1.00
Name: ACD_SE_SE8	Len: 962	Check: 1464	Weight: 1.00
Name: ACG_BE_VI1	Len: 962	Check: 2980	Weight: 1.00
Name: AD_SE_SE69	Len: 962	Check: 8959	Weight: 1.00
Name: AD_SE_SE71	Len: 962	Check: 7056	Weight: 1.00
Name: ADHK_NO_97	Len: 962	Check: 487	Weight: 1.00
Name: ADK_CD_MAL	Len: 962	Check: 2555	Weight: 1.00
Name: AG_BE_VI11	Len: 962	Check: 6342	Weight: 1.00
Name: AG_NG_92NG	Len: 962	Check: 1272	Weight: 1.00
Name: AGHU_GA_VI	Len: 962	Check: 1974	Weight: 1.00
Name: AGU_CD_Z32	Len: 962	Check: 4356	Weight: 1.00
Name: AJ_BW_BW21	Len: 962	Check: 9995	Weight: 1.00
Name: B_AU_VH_AF	Len: 962	Check: 5833	Weight: 1.00
Name: B_CN_RL42_	Len: 962	Check: 4092	Weight: 1.00
Name: B_DE_D31_U	Len: 962	Check: 5486	Weight: 1.00
Name: B_DE_HAN_U	Len: 962	Check: 3480	Weight: 1.00
Name: B_FR_HXB2_	Len: 962	Check: 6939	Weight: 1.00
Name: B_GA_OYI_	Len: 962	Check: 9780	Weight: 1.00
Name: B_GB_CAM1_	Len: 962	Check: 9716	Weight: 1.00
Name: B_GB_GB8_C	Len: 962	Check: 4180	Weight: 1.00
Name: B_GB_MANC	Len: 962	Check: 9762	Weight: 1.00
Name: B_KR_WK_AF	Len: 962	Check: 6641	Weight: 1.00
Name: B_NL_3202A	Len: 962	Check: 7168	Weight: 1.00
Name: B_TW_TWCYS	Len: 962	Check: 3591	Weight: 1.00
Name: B_US_BC_LO	Len: 962	Check: 7266	Weight: 1.00
Name: B_US_DH123	Len: 962	Check: 6905	Weight: 1.00
Name: B_US_JRCSF	Len: 962	Check: 9381	Weight: 1.00
Name: B_US_MNCG_	Len: 962	Check: 9951	Weight: 1.00
Name: B_US_P896_	Len: 962	Check: 5855	Weight: 1.00
Name: B_US_RF_M1	Len: 962	Check: 6075	Weight: 1.00
Name: B_US_SF2_K	Len: 962	Check: 1434	Weight: 1.00
Name: B_US_WEAU1	Len: 962	Check: 5451	Weight: 1.00
Name: B_US_WR27_	Len: 962	Check: 4262	Weight: 1.00
Name: B_US_YU2_M	Len: 962	Check: 5841	Weight: 1.00
Name: BF1_BR_93B	Len: 962	Check: 5506	Weight: 1.00
Name: C_BR_92BR0	Len: 962	Check: 8769	Weight: 1.00
Name: C_BW_96BW0	Len: 962	Check: 6197	Weight: 1.00
Name: C_BW_96BW1	Len: 962	Check: 8144	Weight: 1.00
Name: C_BW_96BW1	Len: 962	Check: 1160	Weight: 1.00
Name: C_BW_96BW1	Len: 962	Check: 2736	Weight: 1.00
Name: C_ET_ETH22	Len: 962	Check: 8219	Weight: 1.00
Name: C_IN_93IN1	Len: 962	Check: 4068	Weight: 1.00
Name: C_IN_93IN9	Len: 962	Check: 3674	Weight: 1.00
Name: C_IN_93IN9	Len: 962	Check: 1581	Weight: 1.00
Name: C_IN_94IN1	Len: 962	Check: 9352	Weight: 1.00
Name: C_IN_95IN2	Len: 962	Check: 6988	Weight: 1.00
Name: CRF01_AE_C	Len: 962	Check: 8684	Weight: 1.00
Name: CRF01_AE_C	Len: 962	Check: 3342	Weight: 1.00
Name: CRF01_AE_C	Len: 962	Check: 5017	Weight: 1.00

Name: CRF01_AE_T	Len: 962	Check: 9124	Weight: 1.00
Name: CRF01_AE_T	Len: 962	Check: 2718	Weight: 1.00
Name: CRF01_AE_T	Len: 962	Check: 2104	Weight: 1.00
Name: CRF01_AE_T	Len: 962	Check: 8495	Weight: 1.00
Name: CRF01_AE_T	Len: 962	Check: 4076	Weight: 1.00
Name: CRF01_AE_T	Len: 962	Check: 948	Weight: 1.00
Name: CRF02_AG_F	Len: 962	Check: 9298	Weight: 1.00
Name: CRF02_AG_F	Len: 962	Check: 9278	Weight: 1.00
Name: CRF02_AG_G	Len: 962	Check: 4373	Weight: 1.00
Name: CRF02_AG_N	Len: 962	Check: 8955	Weight: 1.00
Name: CRF02_AG_S	Len: 962	Check: 252	Weight: 1.00
Name: CRF02_AG_S	Len: 962	Check: 5147	Weight: 1.00
Name: CRF03_AB_R	Len: 962	Check: 2239	Weight: 1.00
Name: CRF03_AB_R	Len: 962	Check: 2671	Weight: 1.00
Name: CRF04_cpx_	Len: 962	Check: 4892	Weight: 1.00
Name: CRF04_cpx_	Len: 962	Check: 8070	Weight: 1.00
Name: CRF04_cpx_	Len: 962	Check: 5453	Weight: 1.00
Name: CRF05_DF_B	Len: 962	Check: 174	Weight: 1.00
Name: CRF05_DF_B	Len: 962	Check: 2694	Weight: 1.00
Name: CRF06_cpx_	Len: 962	Check: 7351	Weight: 1.00
Name: CRF06_cpx_	Len: 962	Check: 5073	Weight: 1.00
Name: CRF06_cpx_	Len: 962	Check: 661	Weight: 1.00
Name: CRF06_cpx_	Len: 962	Check: 8440	Weight: 1.00
Name: CRF11_cpx_	Len: 962	Check: 2217	Weight: 1.00
Name: CRF11_cpx_	Len: 962	Check: 8216	Weight: 1.00
Name: D_CD_84ZR0	Len: 962	Check: 4843	Weight: 1.00
Name: D_CD_ELI_K	Len: 962	Check: 8403	Weight: 1.00
Name: D_CD_NDK_M	Len: 962	Check: 5813	Weight: 1.00
Name: D_UG_94UG1	Len: 962	Check: 9407	Weight: 1.00
Name: F1_BE_VI85	Len: 962	Check: 2982	Weight: 1.00
Name: F1_BR_93BR	Len: 962	Check: 8919	Weight: 1.00
Name: F1_FI_FIN9	Len: 962	Check: 6761	Weight: 1.00
Name: F1_FR_MP41	Len: 962	Check: 478	Weight: 1.00
Name: F2_CM_MP25	Len: 962	Check: 9292	Weight: 1.00
Name: F2KU_BE_VI	Len: 962	Check: 567	Weight: 1.00
Name: G_BE_DRCBL	Len: 962	Check: 6261	Weight: 1.00
Name: G_NG_92NG0	Len: 962	Check: 4508	Weight: 1.00
Name: G_SE_SE616	Len: 962	Check: 6733	Weight: 1.00
Name: H_BE_VI991	Len: 962	Check: 7498	Weight: 1.00
Name: H_BE_VI997	Len: 962	Check: 8345	Weight: 1.00
Name: H_CF_90CF0	Len: 962	Check: 2490	Weight: 1.00
Name: J_SE_SE702	Len: 962	Check: 4446	Weight: 1.00
Name: J_SE_SE788	Len: 962	Check: 1662	Weight: 1.00
Name: K_CD_EQTB1	Len: 962	Check: 7406	Weight: 1.00
Name: K_CM_MP535	Len: 962	Check: 512	Weight: 1.00
Name: N_CM_YBF30	Len: 962	Check: 1733	Weight: 1.00
Name: O_CM_ANT70	Len: 962	Check: 75	Weight: 1.00
Name: O_CM_MVP51	Len: 962	Check: 3290	Weight: 1.00
Name: O_SN_99SE_	Len: 962	Check: 6963	Weight: 1.00
Name: O_SN_99SE_	Len: 962	Check: 6278	Weight: 1.00
Name: U_CD_83C	Len: 962	Check: 9044	Weight: 1.00

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00BW0762_1	...MRVMGI	MRNC.QQWWI	WV.ILGFWML	MVCN.VIGNL	WVTVYYGVPV
00BW0768_2	...MRVREI	LRNC.QQWWT	WG.SLGFWMV	MIYS.VVGEL	WVTVYYGVPV
00BW0874_2	...MRAMGT	QRNC.RQWWI	WG.ILGFWML	MTCS.GVG.E	MVTVYYGVPV
00BW1471_2	...MRVMGI	LRSC.QQWWI	WG.ILGFWML	MICS.VLGNL	WVTVYYGVPV
00BW1616_2	...MRVMGI	QRNC.QRWWI	WG.ILGFWMI	Y.N.VVGNL	WVTVYYGVPV
00BW1686_8	...MRVKGI	QRNW.PQWWI	WG.SLGFWML	MFYS.VMGNL	WVTVYYGVPV
00BW1759_3	...MRVRGI	PRNW.QQWWI	WG.ILGFCMI	ITCK.VVGNL	WVTVYYGVPV


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00BW1773_2 ....MRVREI LRSY.QHWW WS.ILGLWIL IISN.VVGNL WVTVYYGVPV
00BW1783_5 ....MRVMGI KRNC.PPWWI WG.ILGFWM MLICN.VMGNL WVTVYYGVPV
00BW1795_6 ....TRVMGI RRNW.QQWWI WG.ILGFWM MLICN.VMGNL WVTVYYGVPV
00BW1811_3 ....MRVRGT LKNY.QRWWI WG.ILGLWIL LINI.VVGNL WVTVYYGVPV
00BW1859_5 ....MRVRGI PRNW.QQWWI WG.ILGFWM MLICN.VVGNL WVTVYYGVPV
00BW1880_2 ....MRVTGI MRNC.QQWWI WV.ILGFWM MLICN.VIGNL WVTVYYGVPV
00BW1921_1 ....MRVRGI QRNW.QQWWI WG.SLGFWM A.CS.VVGNL WVTVYYGVPV
00BW2036_1 ....MRVRGI SRNW.QQWWI WG.ILGFWM MICS.VLGNL WVTVYYGVPV
00BW2063_6 ....MRVMGI MRNW.PPWWI WG.ILGFWM MLICN.VMGNL WVTVYYGVPV
00BW2087_2 ....MRVTGM WKNC.QQWWI WG.ILGFWM MICS.VLGNL WVTVYYGVPV
00BW2127_2 ....MRVRGI PRNW.QQWWI WG.ILGFWM MIYS.MMGNL WVTVYYGVPV
00BW2128_3 ....MRVRGI LKNC.QQWWI WI.ILGFWM IITN.VVGKL WVTVYYGVPV
00BW2276_7 ....MRVRGI LRNW.QQWWI WG.ILGFWM MICS.VMGNL WVTVYYGVPV
00BW3819_3 ....MRVRGI LRNW.QQWWI WG.ILSFWVL MICS.RGEDR WVTVYYGVPV
00BW3842_8 ....MRVRGI LRNW.QQWWI WV.ILGFWM .IYS.VAGNL WVTVYYGVPV
00BW3871_3 ....MRVRGI QRNW.QQWWI WG.SLGFWM MIYN.VMGSL WVTVYYGVPV
00BW3876_9 ....MRVREI LRNW.KQLWT WG.ILGFWM IICS.AGGNL WVTVYYGVPV
00BW3886_8 ....MRVRGI LRIW.QWWWI WA.SLGFWM IICN.EKGKL WVTVYYGVPV
00BW3891_6 ....MRVRGI LRNY.QQWWI WG.ILGFWM MMCN.VMGDL WVTVYYGVPV
00BW3970_2 ....MRVKGI MRNC.QQWWI WG.ILGFWM LICN.GEGNL WVTVYYGVPV
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96BW0407 ....MRVMGI QRNC.QQWWI WG.ILGFWM FNGM.GSW..VT.VYGVVPV
96BW0502 ....MRVMGI LKNY.QQWWI WG.ILGFWM IISS.VVGNL WVTVYYGVPV
96BW06_J4 ....MRVKGI PRNW.QQWWI WG.SLGFWM C..S.VMGNL WVTVYYGVPV
96BW11_06 ....MRVMEI MRNC.QQWWI WG.ILGFWM MICN.VMGKS WVTVYYGVPV
96BW1210 ....MRVRGI LRNY.LQWWI WG.ILGFWM MVCS.K.ENM WVTVYG.VPV
96BW15B03 ....MRVRGI LRSW.QQWWI WG.TLGFWM .ICS.GLGNL WVTVYDGVVPV
96BW16_26 ....MIVRGI LKTC.QQWWI WI.ILGFWM IINN.VVGH L WVTVYDGVVPV
96BW17A09 ....MRVMGI LRNC.QQWWI WG.ILGFWM MICS.VLGNL WVTVYYGVPV
96BWM01_5 ....MRVMGI KKNW.QPWWI WG.VLGFWM MICS.VMGNL WVTVYYGVPV
96BWM03_2 ....MRVRGT QRNW.QRWWI WS.ILAFWM INCN.GEEKL WVTVYYGVPV
98BWM012_2 ....MRVMGI QKNC.QRWWI WG.ILGFWM MSYS.VLGNL WVTVYYGVPV
98BWM013_4 ....MRVMGI KMNW.QQWWI WG.ILGFWM MICS.VMGNL WVTVYYGVPV
98BWM014_a ....MRVKGI LRNW.LQWWI WG.SLGFWM C..S.VMGNL WVTVYYGVPV
98BWM014_1 ....MRVMGT LRNC.QQWWI WG.ILGFWM MICS.VGGNL WVTVYYGVPV
98BWM018_d ....MRVMGI QKNC.QHWWI WG.ILGFWM MICN.GK.DL WVTVYYGVPV
98BWM036_a ....MRVRGI LRNC.PQWWI WG.ILGFWM MTCN.MEGNL WVTVYYGVPV
98BWM037_d ....MRVRGI LRNY.QQWWI WG.ILGFWM MICN.VVGNL WVTVYYGVPV
99BW3932_1 ....MRVRGI PRNW.QQWWI WS.ILG....FCS.VVGQL WVTVYYGVPV
99BW4642_4 ....MRVKGI LRNW.QQWWI WG.ILGFWM MICN.VVGNL WVTVYYGVPV
99BW4745_8 ....MRVRGI LRDY.QQWWI WS.ILGFWM .ICN.GMGNL WVTVYYGVPV
99BW4754_7 ....MRVMGI KRNC.QQWWI WG.ILGFWM MI...CNGNL WVTVYYGVPV
99BWM016_8 ....MRVMEI WRNC.PPWWI WG.ILGFWM MICN.GG.NR WVTVYYGVPV
A2_CD_97CD ....TRVMGT QRNC.QKWE WG.ILVFGMI MMCK.AAD.L WVTVYYGVPV
A2_CY_94CY ....MRVMGT QRNY.QHLWR GG.ILILGML IMCK.ATD.L WVTVYYGVPV
A2D_97KR ....MRVRGI QRNY.QHLWK WG.ILILGML MISK.ATEDL WVTVYYGVPV
A2G_CD_97C ....MRVKGM QRNW.QNLWK WG.ALILGLV IICS.ASNL WVTVYYGVPV
A_BY_97BL0 ....MKARGM XRNY.QHLWR XG.TMLFWM IMCK.AAEDL VX.VYXVPV
A_KE_Q23_A ....MRVMGI QRNC.QHLLT WG.IMILGTI IFCS.AVENL WVTVYYGVPV
A_SE_SE659 ....MRVMGI QRNC.QHLLR WG.TIILGLI IICS.VADKL WVTVYYGVPV
A_SE_SE725 ....MRVMGT QMNW.QHLLR WG.TIILGMI MICS.TADNL WVTVYYGVPV
A_SE_SE753 ....MRAMGI QRNC.QHLLR WG.TMILGLV IICS.VAGNL WVTVYYGVPV
A_SE_SE853 ....MRVKGI QRNS.QHLLR WG.TMILGMI IICS.TADKL WVTVYYGVPV
A_SE_SE889 ....MRVMGT QMNW.QNLWR WG.TMILGII IICS.AAENL WVTVYYGIPV
A_SE_UGSE8 ....MRVMGT QRNC.QHLLN WG.IMILGMI IICS.TAENL WVTVYYGVPV
A_UG_92UG0 ....MRVMGI ERNY.PCWWT WG.IMILGMI IICN.TAENL WVTVYYGVPI
A_UG_U455 ....MRVMGI QRNY.PCLWR WG.TMILGLI IICN.AQQL WVTVYYGVPV
AC_IN_2130 ....MRVRGI LRNY.QQWWI WG.SLGFWM MVCN.VVGNL WVTVYYGVPV
AC_RW_92RW ....MRVMGT LMNY.QNLWG WG.TMILGML TICS.AANNL WVTVYYGVPV

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AC_SE_SE94      ....MRVTGT QRSC.QPWWI WG.ILGFWML IICS.ATDKL WVTVYYGVPV
ACD_SE_SE8      ....MRVMGI QRNW.QHLLR WG.TMILGMI LICS.AVDKL WVTVYYGVPV
ACG_BE_VI1      ....MRVKGI QRNY.QQWWT WG.SLGLWML LICN.VMGNL WVTVYYGVPV
AD_SE_SE69      ....MRVRGI EMN.YQNLWR WG.TLLLGML MT.CSVTGRL WVTVYYGVPV
AD_SE_SE71      ....MRVMGI QRNC.QNLLT WG.TMILGMI IICS.VAENL WVTVYYGVPV
ADHK_NO_97      ....MKVMGT QRN.YPNWWR WG.VLILGML LICS.TTGNL WVTVYYGVPV
ADK_CD_MAL      ....MRVREI QRN.YQNWWR WG.MMLLGML MT.CSIAEDL WVTVYYGVPV
AG_BE_VI11      ....MRVRGT QMSWP.HLWN GG.ILILGLV IICS.ASNL WVTVYYGVPV
AG_NG_92NG      ....MRVKGT QRNWQ.HLWT WW.TLILGLV IICS.ASNL WVTVYYGVPV
AGHU_GA_VI      ....MRVMET QRN.YPRLWR WG.TIILGML MICN.AKENL WITVYYGVPV
AGU_CD_Z32      ....MKVKGI QRNC.QHLWK WG.TFILGLV IICS.AAENL WVTVYYGVPV
AJ_BW_BW21      ....MRVMET LMNCT.NLWR WG.LMIFGML MTCS.ATGNM WVTVYYGVPV
B_AU_VH_AF      ....MKVKET KRN.WQRLWR WG.IMLLGML MICS.ATEKL WVTVYYGVPV
B_CN_RL42       ....MRVTGI RKN.YQHLWR WG.TMLLGML MICN.AAENL WVTVYYGVPV
B_DE_D31_U      ....MKVKEI RKN.YQHLWR WG.TMLLGML MICS.ATEKL WVTVYYGVPV
B_DE_HAN_U      ....MKVKET RKN.YQRLWR GG.TLLLGML MISS.VAGNL WVTVYYGVPV
B_FR_HXB2       ....MRVKEK YQHLWRWGW WG.TMLLGML MICS.ATEKL WVTVYYGVPV
B_GA_OYI        ....MTARGET RKN.YQRLWR WG.TMLLGML MICS.AAENL WVTVYYGVPV
B_GB_CAM1       ....MRAKGI RKN.CQRLWR WG.TMLLGML MICS.AADKL WVTVYYGVPV
B_GB_GB8_C      ....MKAKGT RKN.YQHLWK WG.IMLLGML MICS.ATEKL WVTVYYGVPV
B_GB_MANC       ....MKVKEI RKN.YQNLWR WG.TLFLGML MICS.AEEKL WVTVYYGVPV
B_KR_WK_AF      ....MRVKGI RKN.YQHWWR WG.IMLLGMW MICS.AAEKL WVTVYYGVPV
B_NL_3202A      ....MKVKET RKN.YQHLWR WG.TMLLGML MICS.AAEQL WVTVYYGVPV
B_TW_TWCYS      ....MRVRGT RMN.CQHLWR WG.TMLLGML MISS.AAENL WVTVYYGVPV
B_US_BC_L0      ....MRVKEI RKN.YQHLWR WG.TMLFGIL MIYS.AAGNL WVTVYYGVPV
B_US_DH123      ....MRVMGI RKN.YQHLWK GG.TLLLGIL MICS.AAEQL WVTVYYGVPV
B_US_JRCSE      ....MRVKGI RKN.YQHLWK GG.ILLGLT MICS.AVEKL WVTVYYGVPV
B_US_MNCG       ....MRVKGI RRN.YQHWWR WG.TMLLGLL MICS.ATEKL WVTVYYGVPV
B_US_P896       ....MRVKEI RKN.WQHLR. GG.ILLGLM MICS.AAEKT WVTIYYGVPV
B_US_RF_M1      ....MRVMEM RKN.CQHLWK WG.TMLLGML MICS.AAEDL WVTVYYGVPV
B_US_SF2_K      ....MKVKGT RRN.YQHLWR WG.TLLLGML MICS.ATEKL WVTVYYGVPV
B_US_WEAU1      ....MRVKGI RKN.YQHLWK WG.IMLLGIL MICS.AAENL WVTVYYGVPV
B_US_WR27       ....MRVKGI RKN.CQHLWR WG.IMLLGML MICN.ATEQL WVTVYYGVPV
B_US_YU2_M      ....MRATEI RKN.YQHLWK GG.TLLLGML MICS.AAEQL WVTVYYGVPV
BF1_BR_93B      ....MRVRGM QRN.WQHLGK WG.LLFLGIL IICN..AENL WVTVYYGVPV
C_BR_92BR0      ....MRVEGI QRNW.QQWWI WG.ILGFWMV MIYN.VRGNL WVTVYYGVPV
C_BW_96BW0      ....MRVMGI QRNC.QQWWI WG.ILGFWMI INGM.GSW.. VT.VYYGVPV
C_BW_96BW1      ....MRVMGI MRNC.QPWWI WG.ILGFWML MICN.VMGKS WVTVYYGVPV
C_BW_96BW1      ....MRVRGI LRNY.LQWWI WG.ILGFWML MVCS.K.ENM WVTVYG.VPV
C_BW_96BW1      ....MRVRGI LRSW.QQWWI WG.TLGFW.. ICS.GLGNL WVTVDGVPV
C_ET_ETH22      ....MKVMGI QRNC.QQWWI WG.ILGFWML MICN.GMGNL WVTVYYGVPV
C_IN_93IN1      ....MRVRGT LRNY.QQWWI WG.VLGFWML MICN.GGGNL WVTVYYGVPV
C_IN_93IN9      ....MRVRGT LRNY.QQWWI WG.VLGFWML MICN.VGGNL WVTVYYGVPV
C_IN_93IN9      ....MRVRGI LRNY.QQWWI WG.ILGFWML MICN.VVGNL WVTVYYGVPV
C_IN_94IN1      ....MRVRGT LRNY.QQWWI WG.VLGFWML MICN.GGKDL WVTVYYGVPV
C_IN_95IN2      ....MRVRGI LRNY.QQWWI WG.VLGFWML MICN.VVGNL WVTVYYGVPV
CRF01_AE_C      ....MGVKGT QMNW.PHLWK WG.TLILGLV IICS.ASDTL WVTVYYGVPV
CRF01_AE_C      ....MRVKGT RRNW.PNLWK WG.TLILGLV IICS.ASDNL WVTVYYGVPV
CRF01_AE_C      ....MRVKGT QMNW.PNLWK WG.TLILGLV IMCS.ASDNL WVTVYG.VPV
CRF01_AE_T      ....MRVKET QMNW.PNLWK WG.TLILGLV IICS.ASDNL WVTVYYGVPV
CRF01_AE_T      ....MRVKET QMN..PNLWK WG.TLILGLV IICS.ASDDL WVTVYYGVPV
CRF01_AE_T      ....MRVKET QINW.PNLWK WG.TLILGLV IMCS.ASNL WVTVYYGVPV
CRF01_AE_T      ....MRVKET QMSW.PNLWK WR.TLILGLV IICS.ASDNL WVTVYYGVPV
CRF01_AE_T      ....MRVKET QMNW.PNLWK WG.TLILGLV IICS.ASDNL WVTVYYGVPV
CRF01_AE_T      ....MRVKET QMNW.PNLWK WG.TLILGLV IICS.ASENL WVTVYYGVPV
CRF02_AG_F      ....MRVMGM QRNY.PLLWK WG.TIIFWIM IICN..AEKL WVTVYYGVPV
CRF02_AG_F      ....MRVMGI QRNY.PLLWK WG.MIIFWIM IICN..AEKL WVTVYYGVPV
CRF02_AG_G      ....MRVRGM QRNC.QNLWR WA..HDFWIL IICN.AAENL WVTVYYGVPV
CRF02_AG_N      ....MRVMGI QKNY.PLLWR WG.TNIFWIM IICN..AEQL WVTVYYGVPV
CRF02_AG_S      ....MRVMGI QKNY.PLLWR WG.MIIFWIM TICS..AGNL WVTVYYGVPV

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CRF02_AG_SMRVMGI	LKSC.PPFWR	WGMIMLLWIL	IICN..AENL	WVTVYYGVPV
CRF03_AB_RMRVKEI	RKH....LWR	WG.TLFLGML	MICS.ATENL	WVTVYYGVPV
CRF03_AB_RMRVKEI	RKH....LWR	WG.TLFLGML	MICS.ATENL	WVTVYYGVPV
CRF04_cpx_MRVMGM	QRN.YPHLWE	WG.TLILGLV	IICS.ASNNL	WVTVYYGVPV
CRF04_cpx_MRVMGI	QRN.YPHLWE	WG.TLILGLV	IMCS.ASKDM	WVTVYYGVPV
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CRF11_cpx_MRVKET	QRNWH.NLWR	WG.LMIFGML	MICN.AEK.M	WVTVYYGVPV
D_CD_84ZR0MRVKEI	KRN.YQPLWK	WG.IMLLGML	MMTYSAADNL	WVTVYYGVPV
D_CD_ELI_KMRARGI	ERN.CQNWWK	WG.IMLLGIL	MT.CSAADNL	WVTVYYGVPV
D_CD_NDK_MMRAREK	ERN.CQNLWK	WG.IMLLGML	MT.CSAAEDL	WVTVYYGVPV
D_UG_94UG1MRVRET	KRN.YQHLWK	WG.TMLLGML	MI.CSVTGKS	WVTVYYGVPV
F1_BE_VI85MRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICN.AADNL	WVTVYYGVPV
F1_BR_93BRMRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICN.AAENL	WVTVYYGVPV
F1_FI_FIN9MRVRGM	QRN.WQHLGK	WG.LLFLGML	IICK.AADDL	WVTIYYGVPV
F1_FR_MP41MRVRGM	QRN.WQHLGK	WG.LLFLGIL	IICS.AADNL	WVTVYYGVPV
F2_CM_MP25MRVREM	QRN.WQHLGR	WG.LLFLGIL	IICS.AADKL	WVTVYYGVPV
F2KU_BE_VIMRVRER	RRN.WQPLGR	WG.ILFLGIF	IICN.AAEDL	WVTVYYGVPV
G_BE_DRCBLMRVKEI	QRNWQ.HLWN	WG.ILILGLV	IICS.AEK.L	WVTVYYGVPV
G_UG_92NG0MRVKEI	QRNWQ.HLWK	WG.TLILGLV	IICS.ASDNL	WVTVYYGVPV
G_SE_SE616MRVTGI	QRNW..HLWK	WG.TLILGLV	IICS.ASNNL	WVTVYYGVPV
H_BE_VI991TRVMET	QRN.YPSLWR	WG.TLILGML	LICS.VVGNL	WVTVYYGVPV
H_BE_VI997TRV	MRN.YPQWWR	GG.ILLLGML	LIYS.AAGNL	WVTVYYGVPV
H_CF_90CF0TRVMET	QRN.YPSLWR	WG.TLILGML	LICS.AAQNL	WVTVYYGVPV
J_SE_SE702TRVMET	QTSWL.SLWR	WG.LMIFGML	MICS.ARENL	WVTVYYGVPV
J_SE_SE788TRVMET	QKNWQ.TLWR	GG.LMIFGML	MICK.AKEDL	WVTVYYGVPV
K_CD_EQTB1MRAREI	QRN.WQHLGK	RG.ILFLGIL	IICS.AANNL	WVTVYYGVPV
K_CM_MP535MRVRGM	QRN.WQTLGN	WG.ILFLGIL	IICS.NADKL	WVTVYYGVPV
N_CM_YBF30MKVMGM	QSGWMGMKSG	WLLFYLLVSL	IKVIG.SEQH	WVTVYYGVPV
O_CM_ANT70MKAMEK	RNK...K..L	WTLYLAMALI	TPCLSLR.QL	YATVYAGVPV
O_CM_MVP51MKVMKK	NNR...K..S	WSLYIAMALL	IPCLSYSKQL	YATVYSGVPV
O_SN_99SE	MTVTMKVMEQ	RNR...K..L	GILCIVMALI	TPCLSYN.QH	YATVYAGVPV
O_SN_99SE	MTVTMKVMEK	RNR...K..L	GILCMVMALI	TPCLSHN.QH	YATVYAGVPV
U_CD__83CMRVKEI	QRN.YQHLWK	WS.LIILGMI	MICK.AIEKS	WVTVYYGVPV

00BW0762_1	WREAKTTLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
00BW0768_2	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
00BW0874_2	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPDPQEM	VLENVTFNFN
00BW1471_2	WREAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	YLVNVTENFN
00BW1616_2	WKEAKTTLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEI	GLENVTFNFN
00BW1686_8	WKEAKTTLFC	ASDAKAYEKE	VHNIWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1759_3	WRETKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEL	VLGNVTESFN
00BW1773_2	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	PLKNVTENFN
00BW1783_5	WKEAKTTLFC	ASDAKAYEKE	AHNIWATHAC	VPTDPNPQEI	FLENVTFNFN
00BW1795_6	WREAKAPLFC	ASDAKAYDRE	VHNVWATHAC	VPTDPNPQEM	VLKNVTENFN
00BW1811_3	WKEAKTTLFC	ASDAKGYDRE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
00BW1859_5	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1880_2	WKEAKATLFC	ASEAKAYESE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW1921_1	WKEAKTTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPNPQEM	ALENVTFNFN
00BW2036_1	WREAKTTLFC	ASDAKAYETE	VHNIWATHAC	VPTDPNPQEI	VLGNVTENFN
00BW2063_6	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
00BW2087_2	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	ELKNVTENFN
00BW2127_2	WKEAKAPLFC	ASDAKAYEKE	AHNVWATHAC	VPTDPNPQEI	ELKNVTENFN
00BW2128_3	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
00BW2276_7	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
00BW3819_3	WREAKATLFC	ASDAKAHERE	VHNVWATHAC	VPTDPNPQEM	VMENVTFNFN
00BW3842_8	WKEAKTTLFC	ASDAKGYETE	VHNVWATHAC	VPTDPDPQEM	VLGNVTENFN
00BW3871_3	WREAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	LLKNVTENFN
00BW3876_9	WKEAKTTLFC	ASDAKVYEKE	VHNVWATHAC	VPTDPNPQEM	VLDNVTFNFN
00BW3886_8	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLGGVTENFN
00BW3891_6	WREAKTTLFC	ASDAKGYEKE	VHNVWATHAC	VPTDPDPQEM	VLENVTFNFN
00BW3970_2	WKEAKTTLFC	ASDAKGYERE	VHNIWATHAC	VPTDPNPQEM	FLHNVTFNFN
00BW5031_1	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPSQEI	VLENVTFNFN
96BW01B21	WKEAKTTLFC	ASDAKAYEKG	VHNVWATHAC	VPTDPNPQEV	FLENVTFNFN
96BW0407	WKEAKATLFC	ASDARAYDRE	VHNVWATHAC	VPTDPNPQEV	ILENVTFNFN
96BW0502	WKEAKTTLFC	TSDAKAYETE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
96BW06_J4	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPSQEI	VLGNVTENFN
96BW11_06	WREAKATLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEV	VLENVTFNFN
96BW1210	WKEAKTTLFC	ASDAKAYEGE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
96BW15B03	WREASNTLFC	ASYAKAYEKE	VHNVWATHAC	VPTDPNPQEI	ELDNVTENFN
96BW16_26	WKEAKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	ILKNVTENFN
96BW17A09	WREAKTTLFC	ASDAKAFESE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
96BWM01_5	WREAKTTLFC	ASDAKAYEAE	VHNVWATHAC	VPTDPNPQEI	ELKNVTENFN
96BWM03_2	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWMC12_2	WREAKTTLFC	ASDAKAYERE	VHNIWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWMC13_4	WKEAKAPLFC	ASDAKVYEKE	VHNVWATHAC	VPTDPNPQEL	VLENVTFNFN
98BWMC14_a	WREATTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
98BWM014_1	WKEAKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPSQEM	FLANVTENFN
98BWM018_d	WREAKATLFC	ASNAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
98BWM036_a	WKEAKATLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPDPQEI	VLENVTFNFN
98BWM037_d	WKEAKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEM	VLENVTFNFN
99BW3932_1	WKEAKATLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQKL	VLGNVTENFN
99BW4642_4	WKEAKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
99BW4745_8	WREAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLKNVTENFN
99BW4754_7	WREAKTTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	VLENVTFNFN
99BWMC16_8	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPDPQEI	ALENVTFNFN
A2_CD_97CD	WRDADTTLFC	ASDAKAYATE	KHNVWATHAC	VPTDPNPQEV	NLANVTEDFN
A2_CY_94CY	WKDADTILFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	NLENVTFNFN
A2D_97KR	WRDAETTLFC	ASDAKAYDTE	AHNVWATHAC	VPTDPNPQEI	NLENVTFNFN
A2G_CD_97C	WEDANTPLFC	ASDAKSYSTE	RHNVWATHAC	VPTDPNPQEM	ILENVTFNFN
A_BY_97BLO	XXDAATTLFC	ASDAKAXDKE	VHNVWATHAC	VPTDPDPQEI	ILGNVTEKFD
A_KE_Q23_A	WRDADTTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLDNVTEKFN
A_SE_SE659	WKDAETTLFC	ASDAKAYDPE	VHNVWATHAC	VPTDPNPQEM	HLENVTEESN
A_SE_SE725	WKDAETTLFC	ASDAQAYKTE	MHNVWATHAC	VPTDPNPQEL	HLKNVTEEFN

A_SE_SE753	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
A_SE_SE853	WKDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEL	HLANVTEEFN
A_SE_SE889	WRDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	NLENVTEEFN
A_SE_UGSE8	WKDAETTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	YLENVTEDFN
A_UG_92UG0	WKDANTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPSPQEL	KMENVTSEFN
A_UG_U455_	WKDAVTTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	DLVNVTEEFN
AC_IN_2130	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLENVTEDFN
AC_RW_92RW	WKDAETTLFC	ASDAKAYDPE	KHNVWATHAC	VPIDPDPQEI	HLENVTEEFN
AC_SE_SE94	WKEAKTTLFC	ASDAKAYEAE	VHNVWATHAC	VPTDPNPHEI	NLENVTENFN
ACD_SE_SE8	WKDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	LLGNVTEDFN
ACG_BE_VI1	WKEAKTTLFC	ASDAKAYETE	AHNVWATHAC	VPTDPSPQEI	ELKNVTENFN
AD_SE_SE69	WRDAETTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	NLENVTEEFN
AD_SE_SE71	WKDAETTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEI	HLENVTENFN
ADHK_NO_97	WKEAKTTLFC	ASDAKAYDTE	MHNVWATHAC	VPTDPSPQEI	VLENVTENFN
ADK_CD_MAL	WKEATTLFC	ASDAKSYETE	VHNIWATHAC	VPTDPNPQEI	ELENVTEGFN
AG_BE_VI11	WEDADTTLFC	ASDAKAYSTE	SHNVWATHAC	VPTDSNPQEI	PLENVTENFN
AG_NG_92NG	WEDADTPLFC	ASDAKAYSTE	RHNVWATHAC	VPTDPNPQEI	TLENVTETFN
AGHU_GA_VI	WRDAKTSLFC	ASDAKSYSTE	SHNVWATHAC	VPTDPNPQEI	NLENVTENFN
AGU_CD_Z32	WKDAETTLFC	ASDAKAYDTE	KHNVWATHAC	VPTDPNPQEL	SLGNVTEKFN
AJ_BW_BW21	WKEAKTTLFC	ASNAKAYSTE	GHNIWATHAC	VPTDPNPQEI	ILENVTENFN
B_AU_VH_AF	WKEATTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPNPQEI	LLENVTEEFN
B_CN_RL42	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_DE_D31_U	WKEATTLFC	ASDAKAYDKE	VHNVWATHAC	VPTDPDPQEV	VLENVTEDFN
B_DE_HAN_U	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VMGNVTENFN
B_FR_HXB2	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLVNVTENFN
B_GA_OYI	WKEATTLFC	ASDARAYATE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFD
B_GB_CAM1	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
B_GB_GB8_C	WKEATTLFC	ASDAKAYDTE	KHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_GB_MANC	WKEATTLFC	ASDAKAHYTE	VHNVWATHAC	VPTDPNPQEI	VLENVTEYFD
B_KR_WK_AF	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPIDPNPQEV	FLENVTENFN
B_NL_3202A	WKEATTLFC	ASDAKASDTE	VHNVWATHAC	VPTDPNPQEV	ALENVTEDFD
B_TW_TWCYS	WKEATTLFC	ASDAKTYDTE	VHNVWATHAC	VPTDPNPQEV	TLGNVTENFN
B_US_BC_L0	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	IPTDPNPQEI	VLENVTEDFN
B_US_DH123	WKEANTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	LLENVTEDFN
B_US_JRCSF	WKETTTTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTEDFN
B_US_MNCG	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	ELVNVTENFN
B_US_P896	WREATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_US_RF_M1	WKEATTLFC	ASEAKAYKTE	VHNVWATHAC	VPTDPNPQEV	LLENVTENFN
B_US_SF2_K	WKEATTLFC	ASDARAYDTE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
B_US_WEAU1	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
B_US_WR27	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	RLENVTEDFN
B_US_YU2_M	WKEATTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEV	KLENVTENFN
BF1_BR_93B	WKEATTLFC	ASDAKAYEKE	AHNVWATHAC	VPTDPNPQEV	VLENVTENFD
C_BR_92BR0	WKEAKTTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEM	VLENVTENFN
C_BW_96BW0	WKEAKATLFC	ASDARAYDRE	VHNVWATHAC	VPTDPNPQEV	NLENVTENFN
C_BW_96BW1	WREAKATLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEV	VLENVTENFN
C_BW_96BW1	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEL	VLGNVTENFN
C_BW_96BW1	WREASNTLFC	ASYAKAYEKE	VHNVWATHAC	VPTDPNPQEI	ELDNVTENFN
C_ET_ETH22	WKDASPTLFC	ASDAKAYDTE	VHNVWGTFAC	VPTDPSPQEL	GLENVTENFN
C_IN_93IN1	WKEAKTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPNPQEI	VLGNVTENFN
C_IN_93IN9	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	PLGNVTENFN
C_IN_93IN9	WKEAKTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEM	VLENVTENFN
C_IN_94IN1	WKEAKTTLFC	ASDAKAYGKE	VHNVWATHAC	VPTDPNPQEI	SLENVTENFN
C_IN_95IN2	WKEANTTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEI	VMENVTENFN
CRF01_AE_C	WRDADTTLFC	ASDANAQETE	VHNVWATHVC	VPTDPNPQEI	HLENVTENFD
CRF01_AE_C	WRDADTILFC	ASDAKAHVTE	VHNVWATHAC	VPTDPNPQEI	YLENVTENFD
CRF01_AE_C	WRDADTTLFC	ASDAKAHETE	VHNIWATHAC	VPTDPNPQEI	DLENVTENFN
CRF01_AE_T	WKDADTTLFC	ASDAKAHETE	VHNVWTTTHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HLENVTENFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	IPTDPNPQEM	HLENVTENFN

CRF01_AE_T	WRDADTTLFC	ASDAKAHEAE	VHNVWATHAC	VPTDPNPQEI	HLENVTFNFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HLENVTFNFN
CRF01_AE_T	WRDADTTLFC	ASDAKAHETE	VHNVWATHAC	VPTDPNPQEI	HMENVTFNFN
CRF02_AG_F	WRNAETTLFC	ASDAKAYDAE	VHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
CRF02_AG_F	WRDAETTLFC	ASDAKAYDVE	VHNVWATHAC	VPTDPNPQEI	HLKNVTEKFN
CRF02_AG_G	WKTAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLENVTEEFN
CRF02_AG_N	WKTAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLENVTEKFN
CRF02_AG_S	WRDAETTLFC	ASDAKAYDTE	VHNVWATHAC	VPTDPNPQEI	HLGNVTEDFN
CRF02_AG_S	RRDAETTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPS PQEM	HLENVTFNFN
CRF03_AB_R	WKEATTTLFC	ASDAKAYSKE	VHNVWATHAC	VPTDPS PQEI	PLKNVTENFN
CRF03_AB_R	WKEATTTLFC	ASDAKAYSKE	VHNVWATHAC	VPTDPS PQEI	PLENVTFNFN
CRF04_cpx	WRDAETTLFC	ASEAKAYEKE	VHNIWATHAC	VPTDPNPQEV	ALINVTFNFN
CRF04_cpx	WRDAETKPCX	ASDAKAYDKE	IHNIWATHAC	VPTDPNPQEL	ALTNVTENFN
CRF04_cpx	WRDAETSPFC	ASDAKAYDKE	VHNIWATHAC	VPTDPNPQEI	FLKNVTEDFN
CRF05_DF_B	WREACTTLFC	ASDAKGYDKE	VHNVWATHAC	VPTDPNPQEV	VLGNVTENFN
CRF05_DF_B	WKEANTTLFC	ASDAKGYEKE	AHNVWATHAC	VPTDPNPQEL	ALENVTFNFN
CRF06_cpx	WEDADTILFC	ASDAKAYSPE	KHNVWATHAC	VPTDPNPQEI	SLKNVTENFN
CRF06_cpx	WEDADTILFC	ASDAKAYSPE	KHNVWATHAC	VPTDPNPQEI	PLKNVTENFN
CRF06_cpx	WEDADTILFC	ASDAKAYSPE	KHNVWATHAC	VPTDPNPQEI	PLENVTFNFN
CRF06_cpx	WEDADTILFC	ASDAKAYSPE	KHNVWATHAC	VPTDPNPQEI	KLENVTFNFN
CRF11_cpx	WKDANTTLFC	ASDAQAYSPE	KHNVWATHAC	VPTDPNPQEI	LLGNVTENFN
CRF11_cpx	WRDADTILFC	ASDARTYSKE	KHNVWATHAC	VPTDPNPREL	SLKNVTENFN
D_CD_84ZR0	WKEATTTLFC	ASDAKSYKTE	AHNIWATHAC	VPTDPNPQEI	ELKNVTENFN
D_CD_ELI_K	WKEATTTLFC	ASDAKSYETE	AHNIWATHAC	VPTDPNPQEI	ALENVTFNFN
D_CD_NDK_M	WKEATTTLFC	ASDAKAYKKE	AHNIWATHAC	VPTDPNPQEI	ELENVTFNFN
D_UG_94UG1	WKEATTTLFC	ASDAKAYKAE	AHNIWATHAC	VPTDPNPQEI	KLENVTFNFN
F1_BE_VI85	WKEATTTLFC	ASDAKAYERE	AHNVWATHAC	VPTDPNPQEV	FLKNVTENFD
F1_BR_93BR	WKEATTTLFC	ASDAKSYEKE	AHNVWATHAC	VPTDPNPQEV	VLENVTERFN
F1_FI_FIN9	WKEANTTLFC	ASDAKSYEKE	VHNVWATHAC	VPTDPNPQEV	ALN.VTENFN
F1_FR_MP41	WKEATTTLFC	ASDAKGYERE	VHNVWATHAC	VPTDPNPQEI	WLKNVTENFD
F2_CM_MP25	WKEATTTLFC	ASDAKAYERE	VHNVWATHAC	VPTDPS PQEL	VLGNVSEKFN
F2KU_BE_VI	WKEANTTLFC	ASDAKPYDTE	VHNVWATHAC	VPTDPNPQEV	FLQNVTFNFN
G_BE_DRCBL	WEDANAPLFC	ASDAKAHSTE	SHNIWATHAC	VPTDPS PQEI	NMRNVTFNFN
G_NG_92NG0	WEDADTPLFC	ASDAKSYSSE	KHNVWATHAC	VPTDPNPQEI	AIENVTFNFN
G_SE_SE616	WEDADTTLFC	ASDAKSYSAE	SHNVWATHAC	VPTDPNPQEI	IMENVTEYFN
H_BE_VI991	WKEAKTTLFC	ASDAKAYDTE	RHNVWATHAC	VPTDPNPQEM	VLENVTETFN
H_BE_VI997	WKEAKTTLFC	ASDAKAYEPE	KHNVWATHAC	VPTDPS PQEM	VLANVTENFN
H_CF_90CF0	WKEAKTTLFC	ASDAKAYETE	KHNVWATHAC	VPTDPNPQEM	VMENVTESFN
J_SE_SE702	WRDAKTTLFC	ASDAKAYSTE	KHNVWATHAC	VPTDPNPQEM	SLPNVTENFN
J_SE_SE788	WKDAKTTLFC	ASDAKAYSTE	KHNVWATHAC	VPTDPS PQEM	NLPNVTFNFN
K_CD_EQTB1	WKEATTTLFC	ASDAKAYETE	VHNVWATHAC	VPTDPNPQEV	VLENVTFNFN
K_CM_MP535	WKEATPTLFC	ASDAKAYEKE	VHNVWATHAC	VPTDPNPQEV	EMENVTFNFN
N_CM_YBF30	WREAEATLFC	ASDAKAHSTE	AHNIWATHAC	VPTDPNPQEV	LLPNVTEKFN
O_CM_ANT70	WEDATPVLFC	ASDANLTSTE	QHNIWATHAC	VPTDPTPYEY	PLHNVTDNFD
O_CM_MVP51	WEEAAPVLFC	ASDANLTSTE	QHNIWATHAC	VPTDPNPHEF	PLGNVTDNFD
O_SN_99SE	WEEATPVLFC	ASDANLTSTE	QHNIWATHAC	VPTDPS PYEY	PLTKVTDNFD
O_SN_99SE	WEEATPVLFC	ASDVNLTSTE	QHNIWATHAC	VPTDPS PYEY	PLKNVTDNFD
U_CD_83C	WKDAETTLFC	ASDAKAYEKE	SHNVWATHAC	VPTDPS PQEL	VLGNVTENFN

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00BW0762_1	MWKNYMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCINV	TN.....
00BW0768_2	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCITLNCTSI	NG.....
00BW0874_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNY	NN.....
00BW1471_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLYCTNV	TKR.....
00BW1616_2	MWKNDMVNQM	HEDIISLWDQ	SLKPCVRLTP	LCVTLNCNNV	TT.....
00BW1686_8	MWKNDVVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLQCSNV	S.....
00BW1759_3	MWKNDMVDQM	HEDIISLWDQ	SLNPCVKLTP	LCVTLKCSNV	N.....
00BW1773_2	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLECEDA	N.....
00BW1783_5	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCSNL	NI.....
00BW1795_6	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNA	TI.....
00BW1811_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCINA	TN.....
00BW1859_5	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCKDY	N.....
00BW1880_2	MWENGMDVQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSNA	KA.....
00BW1921_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSDA	K.....
00BW2036_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NV.....
00BW2063_6	MWENDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCRNA	NN.....
00BW2087_2	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCVTV	NCT.....
00BW2127_2	MWKNDMVEQM	HEDIIRLWDE	SLKPCVRLTP	LCVTLRCSNA	GSG.....
00BW2128_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLSCNAT	N.....
00BW2276_7	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSIV	N.....
00BW3819_3	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTQ	LCVTLECSNV	N.....
00BW3842_8	MWENDMVDQM	HEDVISLWDE	SLKPCVKLTP	LCVTLNCTNY	NG.....
00BW3871_3	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLMCSNV	T.....
00BW3876_9	MWENDMVDQM	HEDIISLWDQ	SPKPCVKLTP	LCVTLKCTDA	T.....
00BW3886_8	MWKNDMVDQM	HEDVISLWDE	SLKPCVKLTP	LCVTLKCGNV	NN.....
00BW3891_6	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCVSI	N.....
00BW3970_2	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLECKNV	TTN.....
00BW5031_1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSAA	NN.....
96BW01B21	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTSY	N.....
96BW0407	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTKV	NGT.....
96BW0502	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCRNV	N.....
96BW06_J4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTS	LCVTLHCSNV	N.....
96BW11_06	MWENDMVNQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCT..
96BW1210	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSNN	VTR.....
96BW15B03	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNY	ST.....
96BW16_26	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNV	T.....
96BW17A09	MWKNDMVDQM	HEDIISLRDQ	SLKPCVKLTP	LCVTLNCTNA	TN.....
96BWM01_5	MWENDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCKNV	TS.....
96BWM03_2	MWKNDMADQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEA	KV.....
98BWMC12_2	MWKNDMVDQM	HEDIIRLWDQ	SLKPCVKMTP	LCVTLNCFANF	NAS.....
98BWMC13_4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCSNV	TV.....
98BWMC14_a	MWRNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCTNV	T.....
98BWM014_1	MWENDMVDQM	HQDIISLWDE	SLKPCVKLTP	LCVTLNCRNA	NLN.....
98BWM018_d	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLTCTNA	TKNVTN....
98BWM036_a	MWKNDMVDQM	HEDVISIWDQ	SLKPCVKLTP	LCVTLNCSNV	N.....
98BWM037_d	MRDNDMVDQM	HEDIINLWDQ	SLKPCVRLTP	LCVTLNCKDA	SVN.....
99BW3932_1	MWKNDMVDQM	HEDMIRLWDQ	SLKPCVKLTP	LCVTLKCREV	N.....
99BW4642_4	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNV	N.....
99BW4745_8	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLICSNV	I.....
99BW4754_7	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCNKV	TV.....
99BWMC16_8	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCVNV	TKNVTK....
A2_CD_97CD	MWKNNMVEQM	HADIISLWDQ	SLKPCVKLTP	LCVTLNCSNA	NTTNT.....
A2_CY_94CY	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVILNCSNA	NTSTH.....
A2D_97KR	MWKNGMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCSRV	KNTIS.....
A2G_CD_97C	MWKNDMVEQM	HVDIISLWDQ	SLKPCVKLTP	FCVTLNCTNA	TFPNA.....
A_BY_97BL0	MXKNNXVEQM	QTDIISL,DQ	SLKPCVKLTP	LCVTLNCAEP	NSTRS.....
A_KE_Q23_A	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLHCTNV	TSV.....
A_SE_SE659	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV
A_SE_SE725	MWKNSMVEQM	HTDIISLWDE	SLKPCVKLTP	LCVTLNCTNA

A_SE_SE753	MWKNYMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLECHYN	ITV.....
A_SE_SE853	MWKNSMVEQM	HTDIISLWDQ	SLIPCVKLTP	LCVTLECN DY	NYN.....
A_SE_SE889	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCSSV	TN.....
A_SE_UGSE8	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLNCSSN	VTA.....
A_UG_92UG0	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLD CSYN	ITN.....
A_UG_U455	MWKNNMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNI	TIN.....
AC_IN_2130	MWKNSMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNC SNV	NG.....
AC_RW_92RW	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLECN NI	TNVNN.....
AC_SE_SE94	IWKNYMVEQM	HQDIISLWDQ	SLKPCVKLTP	LCVTLNC RDA	TV.....
ACD_SE_SE8	MWKNNMVEQM	HTDIISLWDQ	SLQPCVKLTP	LCVTLNCTNV	TIT.....
ACG_BE_VI1	MWKNDMVDQM	HQDIISLWDE	SLKPCVKLTP	LCVTLNC SNV	TAIN.....
AD_SE_SE69	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQLTP	LCVTLNCNNV	TNKIN.....
AD_SE_SE71	MWKNNMVKQM	HTDIISLWDQ	SLQPCVKLTP	LCVTLHCNDT	..N.....
ADHK_NO_97	MWENNMDVQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLNCTDP	AN.....
ADK_CD_MAL	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NGTAVNG.TN
AG_BE_VI11	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLTCTNV	NCTNN.....
AG_NG_92NG	MWKNNMVEQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNV	NCNSN...VT
AGHU_GA_VI	MWKNNMVEQM	HTDIISLWDQ	SLKPCVQITP	LCVTLECSKI	N.....
AGU_CD_Z32	MWKNNMVEQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLS CSDI	R.....
AJ_BW_BW21	IWKNDMVEQM	QEDIISVWDE	SLKPCVKLTP	LCVTLNCTNA	TVSNT.....
B_AU_VH_AF	MWKNNMVEQM	HEDIISLWDQ	SLKPCVQLTP	LCVTLNCTDE	LT.....
B_CN_RL42	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNL	K.....
B_DE_D31_U	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	K.....
B_DE_HAN_U	MWKNDMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLKCTDY	N.....
B_FR_HXB2	MWKNDMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVSLKCTDL	K.....
B_GA_OYI	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCTDV	NTTSSS....
B_GB_CAM1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLIC TNV	NN.....
B_GB_GB8_C	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	R.....
B_GB_MANC	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLDCTDY	VG.....
B_KR_WK_AF	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTDL	NDTNTN....
B_NL_3202A	MWKNNMVEQM	HEDIINLWDQ	SLKPCVKLTP	LCVTLNCTDF	G.....
B_TW_TWCYS	MWKNNMADQM	QEDIISLWDE	SLKPCVELTP	LCVTLKCN DT
B_US_BC_L0	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDE	LKNA.....
B_US_DH123	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLHCTDL	K.....
B_US_JRCSF	MWKNNMVEQM	QEDVINLWDQ	SLKPCVKLTP	LCVTLNCKDV
B_US_MNCG	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	R.....
B_US_P896	MWKNNMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCTNL
B_US_RF_M1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDA	NLN.....
B_US_SF2_K	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL	G.....
B_US_WEAU1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NVTN.....
B_US_WR27	MWKNNMXEQM	HEDIIXLWDQ	SLKPCVKLTP	LCVTLNCTDV
B_US_YU2_M	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTDL
BF1_BR_93B	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLRCSNA	TT.....
C_BR_92BR0	MWENDMVEQM	HQDIISLWDQ	SLKPCVKLTP	LCVTLHCSNR	T.....
C_BW_96BW0	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTEV	NGTSDSS...
C_BW_96BW1	MWENDMVNQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLNCTNV	TV.....
C_BW_96BW1	MWKNDMVDQM	HEDIISLWDE	SLKPCVKLTP	LCVTLNCSSN	VTR.....
C_BW_96BW1	MWKNDMVDQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLKCTNY	ST.....
C_ET_ETH22	MWKNDMVEQM	HQDIISLWDQ	GLKPCVKLTP	LCVTLNCNAI	KNNTKVT...
C_IN_93IN1	MWKNDMVDQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECRNV	S.....
C_IN_93IN9	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECKNV	K.....
C_IN_93IN9	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECSY	NGTSKAN...
C_IN_94IN1	MWKSDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECGNV	T.....
C_IN_95IN2	MWKNDMVNQM	HEDVISLWDQ	SLKPCVKLTP	LCVTLECRNV	NST.....
CRF01_AE_C	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLHCTKA	KLNDTYN...
CRF01_AE_C	MWKNNMVEQM	QEDVISLWDQ	SLQPCVKLTP	LCVTLHCTKA	SFTNATS...
CRF01_AE_C	MWKNNMVEQM	QEDVISL.DQ	SLKPCVKLTP	LCVTLDCTKA	DFYTTKF...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLQPCVKLTP	LCVTLHCTTA	KLNTVNTN...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NLTNVNN...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NWTNANV...

CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTTA	NFTNPNL...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNA	NLTNGSS...
CRF01_AE_T	MWKNNMVEQM	QEDVISLWDQ	SLKPCVKLTP	LCVTLNCTNV	NATNVS...
CRF02_AG_F	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NSS.....
CRF02_AG_F	MWKNNMVEQM	HEDIISLWDQ	SLKPCVELTP	LCVTLDCHNV	SS.....
CRF02_AG_G	MWKNNMVEQM	HVDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	KN.....
CRF02_AG_N	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NN.....
CRF02_AG_S	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	LT.....
CRF02_AG_S	MWKNNMVEQM	HVDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NYT.....
CRF03_AB_R	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	KK.....
CRF03_AB_R	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	KT.....
CRF04_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	T.....
CRF04_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	T.....
CRF04_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	T.....
CRF05_DF_B	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	KA.....
CRF05_DF_B	MWKNNMVEQM	HADIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TS.....
CRF06_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TLGNKTLGNN
CRF06_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NITSTNS...
CRF06_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TDHGIN....
CRF06_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NAT.....K
CRF11_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TS.....
CRF11_cpx	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	R.....
D_CD_84ZRO	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	SRN.....S
D_CD_ELI_K	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	LRNG....T
D_CD_NDK_M	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	LRN.....S
D_UG_94UG1	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	VTD.....
F1_BE_VI85	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TN.....
F1_BR_93BR	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	AT.....
F1_FI_FIN9	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TT.....
F1_FR_MP41	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NI.....
F2_CM_MP25	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	II.....
F2_KU_BE_VI	MWKNNMVEQM	HADIISLWDQ	GLQPCVKLTP	LCVTLDCHNV	IN.....
G_BE_DRCBL	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	N...N....
G_NG_92NG0	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	N.....
G_SE_SE616	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TKGNKR.NN
H_BE_VI991	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NA.....
H_BE_VI997	MWKNNMVEQM	QTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TR.....
H_CF_90CF0	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	RN.....
J_SE_SE702	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	NSNS....
J_SE_SE788	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TSNS....
K_CD_EQTB1	MWKNNMVEQM	HTDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	TN.....
K_CM_MP535	MWKNNMVEQM	HTDIISLWDQ	SLKPCVELTP	LCVTLDCHNV	KG.....
N_CM_YBF30	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	YGEER....
O_CM_ANT70	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV
O_CM_MVP51	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV
O_SN_99SE	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	VQ.....
O_SN_99SE	MWKNNMVEQM	QEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV
U_CD_83C	MWKNNMVEQM	HEDIISLWDQ	SLKPCVKLTP	LCVTLDCHNV	KN.....

00BW0762_1ATNVT N.....	A.....	DYKNCSFNIT	TELDRKRRKE
00BW0768_2THK V.....	TNDTLYG...	EIKNCSFNVT	TEIRDKKRKE
00BW0874_2T E.....	GNTTYGG...	EMRNCSFNIT	TELDRKKRQE
00BW1471_2VI T.....	YNNNMTE...	EMKNCSFNIT	TELDRKKRKE
00BW1616_2YNGTY S.....	D.....	GMKCSFNIT	TELDRKKRKE
00BW1686_8	..RDATSSSS E.....	GMREGMR...	EIKNCSFNVT	TELDRKKRKE
00BW1759_3KT.NFT D.....	TTNG.....	EIKNCSFNIT	TEVRDRKKNE
00BW1773_2NGS.....	...VTQG...	EIKNCSFNVT	TELDRKKRKE
00BW1783_5	.TNSTAFNTT I.....	K.....E...	EMKNCSFNMT	TEIRDKKRKE
00BW1795_6	.TDNTIDEGM G.....	N.....	EIKNCSFNIT	TELDRKKRKE
00BW1811_3SN T.....	YNNNIKE...	EMKNCSFNIT	TEIRDKKRKE
00BW1859_5KN I.....	TYD..NN...	EIKNCSFNIT	TELDRKKRKE
00BW1880_2NSNAS M.....	EG.....	EIKNCSFNIT	TELDRKKRKE
00BW1921_1	.GNGN.....	...RTG...	EIKNCSFNVT	TELDRKKRKE
00BW2036_1	.TYHNVTY.....	...NNTD...	EVKNCSFNMT	TELDRKKRKE
00BW2063_6	.NASNTYQVT T.....	PT..PPD...	IMKNCSFNIP	TELDRKKRKE
00BW2087_2NNVTSC L.....	CNNTICE...	QMRNCSFNAT	TEIRDKKRKE
00BW2127_2NATANR A.....	THNPMEG...	EIKNCSFNAT	TEIKDRKKQV
00BW2128_3KSNSTN V.....	TSENKEG...	EMKNCSFNIT	TELDRKKRKE
00BW2276_7GT.....	DMTNTCFNAT	TEIKDKKRKV	
00BW3819_3VTSSV N.....	ITKNMMD...	EIKNCSFNVT	TEVRDKKKQV
00BW3842_8	.TKVNDTK.. I.....	YNDTMYG...	EIKNCSFNMT	TELDRKKRKE
00BW3871_3	..RNQTKQN N.....	YTYEGIG...	EIKNCSFNMT	TELDRKKRKE
00BW3876_9VND T.....	VNHSMEKE...	ETKNCSFNAT	TEIRDKKRKE
00BW3886_8	.DTEN.....	...MKE...	EMRNCTFNIT	TEIRDKKRKE
00BW3891_6AT.SNG T.....	VTIN..G...	EIKNCSFNVT	TELDRKKRKE
00BW3970_2VTINN V.....	TANNNTS...	DMKNCSFNAT	TEVTDKIRKE
00BW5031_1	TVAEMKG...	EIKNCSFNIT	TEMRDKRKE
96BW01B21G..TYT D.....	N...YQE...	KIKNCSFNIT	TEIRDKKRKE
96BW0407NGTSN N.....	SSVPMEE...	EMKNCSFNIT	TELDRKKRKE
96BW0502ATNNIM I.....	D.NSNKG...	EMKNCSFNVT	TELDRKKRKE
96BW06_J4	..GSNN.ANS S.....	YSNDMKE...	EIKNCSFNMT	TELDRKKRKE
96BW11_06	.NDTLHQNL D.....	MKNCSFNVT	TELDRKKRKE
96BW1210N.....	YNNKNNG...	EIKNCSFNAT	TEIRDKKRKE
96BW15B03	.NYSNTMN.. S.....	YNNNTTE...	EIKNCTFNMT	TELDRKKRKE
96BW16_26SNATMG N.....	TLENGGG...	EMKNCSFNMT	TEIRDKKRKE
96BW17A09TN N.....	VTSSMIG...	GMKNCSFNIT	TELDRKKRKE
96BWM01_5	.KDINTSNAE M.....	K.....A...	EMKNCSFNIT	TELDRKKRKE
96BWM03_2	.NMKKDT.....	...MKE...	EIKNCSFNVT	TELDRKKRKE
98BWM012_2STS T.....	GTNSMNG...	QIKNCSFNIT	TELDRKKRKE
98BWM013_4	.NTTYNNAID G.....	ET..IDK...	EMKNCSFNIT	TELDRKKRKE
98BWM014_a	..VDANSTYV I.....	HVGNTT...	EMKNCSFNMT	TELDRKKRKE
98BWM014_1STRKS.....	.NPSMQG...	EIKNCSFNIT	TEIRDKKRKE
98BWM018_dN N.....	DTTYNIE...	EMRNCSFNIT	TEIRDKKRKE
98BWM036_aN. T.....	IDGAMKE...	GMKNCSFNIT	TEVRDKKKQV
98BWM037_dYTNAT G.....	WPTED...	KLQNCFSNVT	TVIRDKKHKE
99BW3932_1ATK N.....	GNITMKG...	EIKNCSFNAT	TEIKHKKKEM
99BW4642_4AT N.....	VNRTMTE...	EIKNCSFNIT	MELDRKKQV
99BW4745_8TI.TNT T.....	IYKYTTS...	DIRNCPFNV	TELDRKKRKE
99BW4754_7NTTVT V.....	TNNTMDT...	VMKNCSFNVT	TELDRKKRKE
99BWM016_8N.....	LNNNMKE...	EIKNCSFNIT	TELDRKKRKE
A2_CD_97CDNS.....TE	EIKNCSYNMP	TELDRKKRKE
A2_CY_94CYSNSSSTQ S.....PINE	EIKNCSYNTT	TELDRKKRKE
A2D_97KRSTQS.....PDSN	NTMNCSEFTT	TELDRKKRKE
A2G_CD_97CTGNN... S.....IFTE	EMKNCSYNIT	TELDRKKRKE
A_BY_97BL0NNSSVNS N.....	SSDSLFX...	XMKNCSFNMT	TELDRKKRKE
A_KE_Q23_ANTTGDR.....E	GLKNCSFNMT	TELDRKKRKE
A_SE_SE659NS..TRV V.....	NITDKE...	EIKNCSFNMT	TELDRKKRKE
A_SE_SE725NG..TQN V.....	NITN.V....	GMRNCSFNMT	TELDRKKRKE

A_SE_SE753	...KNITVSS	N.....	NNISISNSTE	DMRNCSFNMT	TELDRKQQKV
A_SE_SE853	...VTNSSHS	Y.....	NVTNMQ....	EMKNCSFNVT	TELDRKQKQV
A_SE_SE889SSVT	N.....	ITSDMAG...	EIKNCSFNMT	TEIRDKRQKV
A_SE_UGSE8	...NTNSTSA	N.....	LTDSVKG...	EMRNCSFNIT	TELDRKQKQV
A_UG_92UG0	...NITNSIT	N.....	SSVNMRE...	EIKNCSFNMT	TELDRKNRKV
A_UG_U455	...NTN.NNT	N.....	ITDGVR...E	EMKNCSFNMT	TELDRKQKQV
AC_IN_2130	...NSTGWGKE	EIKNCSFNIT	TELDRKQKQV
AC_RW_92RW	...TVN....	ITDDMKG...	EIKNCSFNMT	TELDRKQKQV
AC_SE_SE94	...TPNNATH	N.....	DSM..V...G	DMKNCPFNMT	TELDRKRRKE
ACD_SE_SE8	...TNATDSN	N.....	..ASLQDMAK	EMTNCSFNMT	TELDRKQKQV
ACG_BE_VI1	...SNGTAI	N.....	ITESIKG...	EMKNCSFKAT	TEIKDKKKKE
AD_SE_SE69	...ETSMN	G.....	EIKNCSFNMT	TELDRKEQQV
AD_SE_SE71	...VTNATNI	T.....	NANTITG...	EMKNCSFNMT	TELMDKKRV
ADHK_NO_97	...HTDTTNNTSIQPSQ	PSANCSFNVT	TAIRDKQKQV
ADK_CD_MAL	AGSNRTNAEL	KM.....EIG	EVKNCSFNIT	PVGSDKR.QE
AG_BE_VI11	..STREIRGKN	CSLD.....TEVG	ELKNCSFNIT	TELDRKQKQV
AG_NG_92NG	STGNSAGTNA	TCNI.....EEAN	NLKNCSFNIT	TEIRDKKKTE
AGHU_GA_VI	...ITNNSTD	KANV.....	...TNN..DA	EMRNCSFNIT	TEIRDKQKQV
AGU_CD_Z32NSTES	N.....	ITAEMQG...	EIKNCSYNMT	TELDRKQKQV
AJ_BW_BW21GCTNN	NCT.....VS	EMKECHFNIT	GGGR..RKKE
B_AU_VH_AF	...NVTFNNS	RHVTNS...	..SYVGSMEKG	EMKNCSFNIT	TSIRDKRHKE
B_CN_RL42	...NATNTSS	T.....MEGG	EIKNCSFNIT	TSIKTKVK.D
B_DE_D31_U	...NATNTNN	SSWT.....	...MTGEMKG	EIKNCSFNIT	TSIRDQVQKE
B_DE_HAN_U	...NATNSS.WGRMEKG	EIQNCSFKVT	TNIRDQVQKE
B_FR_HXB2	...NDTNTNS	SS.G.....	...RMIMEKG	EIKNCSFNIS	TSIRGKVQKE
B_GA_OYI	..LRNATNTTS	SS.....	...WETMEKG	ELKNCSFNIT	TSIRDKMQEQ
B_GB_CAM1	...TRTNSSD	WDRR.....	...EGEKMKG	EIKNCSFNVT	TSIRNKVRKE
B_GB_GB8_C	...NDTNTNN	SIME.....GG	EMKNCSFNIT	TSIRDQKQKE
B_GB_MANC	...NATNTTS	TNNTAS...	..GSWGAMR.G	EIKNCSFNIT	TNIRDQVHKE
B_KR_WK_AF	..N.SSTSENN	TNPTIS...	..GGEGMGEG	EMKNCSFNVT	TNIRDQVQKE
B_NL_3202A	...NATNTTS	S..S.....	...GVIIIEKG	EIKNCSFKIN	TNMKDKAQIE
B_TW_TWCYS	...TMSKND	N.....	...TLTMEKG	EIKNCSFNVT	TSLRNKVQKE
B_US_BC_L0	..TNTTSTNTP	SGS.....	...WKKMERG	EIKNCSFNVL	G...DKKQKA
B_US_DH123	...NGTNLKN	GTK.....	..IIGKSMRG	EIKNCSFNVT	KNIIDKVQKE
B_US_JRCSF	...NATNTTSSSEGMMERG	EIKNCSFNIT	KSIRDQVQKE
B_US_MNCG	...NTTNTNN	STANN.NS..	..NSEGTIKGG	EMKNCSFNIT	TSIRDQKQKE
B_US_P896	...NITKNTT	N...PTS..	..SSWGMMERG	EIKNCSFYIT	TSIRNKVQKE
B_US_RF_M1	...GTNVTS	SSG.....	...GTMMENG	EIKNCSFQVT	TSRRDKTQKK
B_US_SF2_K	...KATNTNS	SN.....	...WKEEIKG	EIKNCSFNIT	TSIRDQKQKE
B_US_WEAU1	..LKNETNTNS	SSG.....	...GEKMEEG	EMKNCSFNVT	TLIRNKRKTE
B_US_WR27	...WNATSTS	KNTTITNS..	..SNERPMEKG	EMKNCSFSIT	TSIRDQVQKE
B_US_YU2_M	..R.NATNTTS	SS.....	...WETMEKG	EIKNCSFNIT	TSIRDQVQKE
BF1_BR_93B	...NST....	.QND.....	...TLKEEPG	AIQNCSFNMT	TEVRDKQLKV
C_BR_92BR0	...IDYN..	N.....	RTDNMGG...	EIKNCSFNMT	TEVRDKREKV
C_BW_96BW0	V..PANGTSN	SSVSMKE...	EMRNCSFNIT	TELDRKQKQV
C_BW_96BW1	..NDTLHQNFT	D.....MKNCSFNVT	TELDRKQKQV
C_BW_96BW1	...NS..NA	T.....	YNNKNG...	EIKNCSFNAT	TEIRDQKQKV
C_BW_96BW1	..NYSNTMNAT	S.....	YNNNTTE...	EIKNCTFNMT	TELDRKQKQV
C_ET_ETH22N	N.....	SIN\$AND...	EMKNCSFNIT	TELDRKQKQV
C_IN_93IN1	...RVVSSY	N.....	TYNGSVE...	EIKNCSFNAT	PEVRDRKQRM
C_IN_93IN9	...NDSTHN	E.....	TYTESVK...	EIKNCSFNAT	TEIRDQKQTV
C_IN_93IN9	ATNNVNATS	N.....	NATSNGE...	EIQQCFNVT	TEMRDKQKQV
C_IN_94IN1	...QNGTYN	D.....	...ESNK...	EITNCTFNIT	TEIRGRKQKV
C_IN_95IN2	...GNGTHS	K.....	TYNESMK...	EIKNCSFNAT	TVIKDKQKQV
CRF01_AE_C	GTAKL....	N.....	...DTICD	EVRNCSFNVT	TELDRKQKQV
CRF01_AE_C	DRIK.....MED	AVRNCSFNMT	TELQDKQKQV
CRF01_AE_C	NTTEK....	P.....	..IEISEMQK	EVSNCNPFNIT	TELDRKEQEV
CRF01_AE_T	I.....TNVP	N.....	..IG..NITD	EVRNCSFNMT	TEIRDQKQKV
CRF01_AE_TNVS	N.....	..IIG.NITD	EVRNCSFNMT	TELDRKQKQV
CRF01_AE_T	TNVN..NNVT	N.....	..IVG.NITE	EVRNCSFNMT	TELDKQKQV

CRF01_AE_T	TKADNMTNVS	N.....	..ITIGNITD	EVRNCTFNMT	TDLIDKKQKV
CRF01_AE_T	K.....TNVS	N.....	..IIG.NITD	EVRNCTFNMT	TELTDKKQKV
CRF01_AE_T	T.....TEAP	N.....	..IV...GTD	EVKNCFSNVT	TELRDKTQQV
CRF02_AG_F	...NSSTSNS	SNSSTPINRT	IDSDMQE...	EIKNCFSNMT	TELRDKKQKV
CRF02_AG_F	...NSSISVK	S.....	ISRDMQG...	EIKNCFSNMT	TELRDKKQKV
CRF02_AG_G	ISDGSNS...	EIKNCFSNMT	TELRDKKQKV
CRF02_AG_N	...SYSNSS	N.....	LTSDMNG...	EIKNCFSNIT	TEVRDKKKKM
CRF02_AG_S	...SS.GN.	ISENMQG...	EIKNCFSNMT	TELRDKKQKV
CRF02_AG_S	...RNN....	SKINEVQ...	EMKNCFSNMT	TVLKDKKKKM
CRF03_AB_R	...EVTSTNT	S.....SIKMM	EMKNCFSNIT	TDLRDKVKKE
CRF03_AB_R	...NDTSTNA	S.....GIEMM	KN..CSFNIT	TDLRDKVKKE
CRF04_cpx_	...TTNSTN	GTVI.....	...K.....E	GIKNCSDIT	TEIRDKKKKE
CRF04_cpx_	TNNSTTNSTG	NSTV.....	...KS...TA	EIKNCFSNIT	TEVRDKQKKE
CRF04_cpx_	...STNSTP	NVTT.....	...T.....N	EMKNCFSNIT	TEIRDKKKKA
CRF05_DF_B	...NSTANST	TNST.....	...TLKEETG	AVQNCSFNMT	TEVNDKKLKV
CRF05_DF_B	...ATTTSKN	ISATPTSN..	PNDTLKEEQG	AIQNCTFNIT	TEVKDKNKR
CRF06_cpx_	STNSTLGNN	TIVD.....DISK	EIKNCFSNIT	TEIRDKTKE
CRF06_cpx_T.KNI	TVES.....GE	EIKNCFSNVT	TEIRDQKKEE
CRF06_cpx_NNN	TVEG.....KE	EIKNCFSNVT	TEIKDKKKKE
CRF06_cpx_	YSNETVGKSL	TVKD.....RE	EIKNCFSNIT	TEVRDQKKTE
CRF11_cpx_YNTT	EMKNCFSNVT	TELIDRRKQE
CRF11_cpx_DNAT	DIKNCFTNIT	TELEDKKKNE
D_CD_84ZR0	TDNNSTLPTV	KP.....GE.	.MKNCSFNIT	TVVTDKRRQV
D_CD_ELI_K	MGNNVVTEEK	G.....MKNCSFNVT	TVLKDKKKQV
D_CD_NDK_M	KGNKGVEEEE	K.....RKNCSFNVRDKREQV
D_UG_94UG1TTNTT	G.....MANCSFNIT	TEIRDKKKQV
F1_BE_VI85	...NSQ....EK...PG	AMQNCSFNMT	TEVRDKKLKL
F1_BR_93BR	...NGNTDTI	AIND.....	...TLKEDPE	AIQNCSFNIT	TEIRDKQLKV
F1_FI_FIN9	...TNDTLS.	DQSS.....	...TLKEEPG	AIQNCSFNMT	TEVEDKKQKV
F1_FR_MP41	...TSNATTT	NDTS.....	...TP.EESG	AIQNCSFNMT	TEVKDKKLRV
F2_CM_MP25	...NVTSSNN	TTLA.....	...PNVTISE	EMKNCFSNIT	TEIRDQKKE
F2KU_BE_VI	...INSTDLT	NWANKTNNWA	NETTLLNITT	GMRNCSFNIT	TMLKDKKKKQ
G_BE_DRCBLNS	TRNI.....TEEY	RMTNCSFNMT	TELRDKKKAE
G_NG_92NG0	.SANHTEANN	..TV.....ENKE	EIKNCSEFKIT	TERGGKKKEE
G_SE_SE616	STDNSTETNN	S.TV.....DNPG	EIKNCFSNVT	TEIRDKKKKE
H_BE_VI991	...TNVTKSN	NSTD.....	...INIGEIQ	EQRNCSFNVT	TAIRDKNQKV
H_BE_VI997	...NDTNSSS	TVNA.....	...TSSPSAN	ELTNCSFNVT	TVIRDKQQRV
H_CF_90CF0	...NTSNSTS	SMEA.....	...GG.....	ELTNCSFNVT	TVLRDKQQKV
J_SE_SE702	...TDSNS	SASN.....NSPE	IMKNCFSNVT	TEIRNKRKQE
J_SE_SE788	...TTSNS	SVS.....SPD	IMTNCSFNIT	TEIRNKRKQE
K_CD_EQTB1	...NRTNANK	NDT.....	NINATVTSTD	EIKNCFSNIT	TELKDKKKRV
K_CM_MP535	...TNSTN..	NATSTVVS	EIKNCFSNIT	TEIKDKKKKE
N_CM_YBF30	...NNTNMTT	R.....	...EPDIGYK	QMKNCSFNAT	TELTDKKKQV
O_CM_ANT70	...IAG....TTNEN	LMKKCEFNVT	TVIKDKKEKK
O_CM_MVP51	...LQTNKTG	LLN...ETIN	EMRNCSFNVT	TVLTDKKEQK
O_SN_99SE_	..GNYTNSS	INNDTSSPEN	LVKQCEFNVT	TVVKDKKEKK
O_SN_99SE_	..VNDETNSS	VKNDTSSSEN	LMKKCEFNVT	TVLKDKKEKQ
U_CD_83CSTNN	N.....TEEA	TITNCSFKVP	TELKDKTETV

201				250
00BW0762_1	YALFYRLDIV	QLGE.....	NNAN SE.....	YRLI
00BW0768_2	HALFYRLDIV	PLDEKDK...	SSN SN.....	YRLI
00BW0874_2	SALFYRLDIV	PLNGS.....	ERNK SE.....	YRLI
00BW1471_2	RALFYRLDIV	PLNESDN...	NSY RE.....	YRLI
00BW1616_2	YALFYSLDIV	PLEN.....	SEN SE.....	YRLI
00BW1686_8	YALFYKLDIV	PLEE.....	NDI ST.....	YRLI
00BW1759_3	HALFYRLDIV	PLEGE.....	NNTN NE.....	YRLI
00BW1773_2	HALFYRLDIV	QLD.....	N SS.....	YRLI
00BW1783_5	YALFYKLDIV	PLEGNNS...	E.....	YRLI
00BW1795_6	YALFYRLDIV	SLDNENN...	KT. AE.....	YRLI
00BW1811_3	YALFYKPDIV	PLDGS.....	NS SE.....	YRLI
00BW1859_5	YALFYKIDIV	PLND....N.	NSN.N SM.....	YRLI
00BW1880_2	YALFYRLDVV	PLDSPS....	NATN SR.....	YRLI
00BW1921_1	YALFYRLDVV	QLN.....	SE.....	YRLI
00BW2036_1	YALFYKLDIV	PLNGNSG...	SE.....	YRLI
00BW2063_6	YALFYKLDIV	PLGNTNG...	T.. E.....	YRLI
00BW2087_2	YALFYKLDIV	SLDD.....	NN S.....	YRLI
00BW2127_2	YALFYRLDVV	PLDND.....	SA TN.....	YRLI
00BW2128_3	YALFYKLDIV	PLNNS.....	SDNSS GE.....	YRLI
00BW2276_7	QALFYKLDIV	PLNSTGE...	NNN TE.....	YRLI
00BW3819_3	YALFYRLDVV	PLNGK.....	NS SS.....	YRLI
00BW3842_8	HALFYRLDIV	PLEDNNG...	NSS SN.....	YRLI
00BW3871_3	YALFYKLDIV	PLND.....	N.. NE.....	YRLI
00BW3876_9	NALFYKLDVV	PLHE.....	GN S.....	YRLI
00BW3886_8	YALFYRLDIV	PLHDSSS...	DG. SE.....	YVLI
00BW3891_6	HALFYRLDIV	PLNG.....	KNQS NE.....	YRLI
00BW3970_2	NALFYTLDIV	PLDENQ....	N.....	YRLI
00BW5031_1	FALFNILDIV	PLNNEN.....	NTKN SD.....	YRLI
96BW01B21	YALFYKFDVV	PLN.....	GNNT SE.....	YILI
96BW0407	RALFYSLDIV	QPNN.....	S TE.....	YRLI
96BW0502	HALFYRLDVV	PLQG.....	NN NE.....	YRLI
96BW06_J4	YALFYRLDVV	PLGD.....	N.. SS.....	YRLI
96BW11_06	YALFYRLDIV	PLNNKNE...	S.. SE.....	YRLI
96BW1210	YALFYRLDIV	PLDN.....	NS SE.....	YRLI
96BW15B03	YALFYKLDIV	PLNSNS.....	SE.....	YRLI
96BW16_26	YALFYRLDVV	PLNGE.....	NSNSS GE.....	YRLI
96BW17A09	SALFYRLDIV	PLNENNS...	SSN SE.....	YRLI
96BWM01_5	YALFYKLDIV	PLTNDAS...	EN. SE.....	YRLI
96BWM03_2	YALFYKLDIV	PLDGNNE...	DGN KQ.....	YRWI
98BWM012_2	SALFYRLDIV	PLK.....	ENS SE.....	YRLI
98BWM013_4	QALFYRLDIV	PLDNANG...	T.. SE.....	YRLI
98BWM014_a	YALFYRLDIV	PLGE.....	D.. SS.....	YRLI
98BWM014_1	YALFYKLDIV	ELDG.....	NS SN.....	YVLI
98BWM018_d	SALFYKLDIV	PLD.....	NSS SK.....	YILI
98BWM036_a	YVLFYKLDIV	PLNGNG....	SN SE.....	YRLI
98BWM037_d	YALFYRPDIV	PLNEG.....	N.....	YRLI
99BW3932_1	YALFYRLDIV	PLKN.....	S SE.....	YRLI
99BW4642_4	NALFYKLDIV	PLNE....K.	ANNSY SY.....	YRLI
99BW4745_8	YALFYRIDIV	PLDE.....	NNNS SE.....	YRLI
99BW4754_7	HALFYRLDIV	PLETK.....	NSNE SA.....	YRLI
99BWM016_8	YALFYKVIV	PLSE.....	NST SE.....	YRLI
A2_CD_97CD	YSLFYELDVV	LLNRSKN...	SSY ST.....	YRLI
A2_CY_94CY	YSLFYRLDVV	QLDESENKNT	SGSN TL.....	YRLI
A2D_97KR	QALFYELDIV	QLNSSDSND..	TLN RQ.....	YRLI
A2G_CD_97C	RSLFYTLDIV	QINKDNN...	T.....	YRLI
A_BY_97BL0	HSLFYKLDIV	STSNNDX...	Q.....	YRLI
A_KE_Q23_A	YSLFYRLDIV	PINEN.....	QG..... SE.....	YRLI
A_SE_SE659	HSLFYRLDIV	QMNNEN.....	RGNSSNSSY NE.....	YRLI
A_SE_SE725	YSLFYKLDIV	QINDN.....	GNNSNNS.. SE.....	YRLI

A_SE_SE753	YSLFYRLDLV	KIDEN.....	.KSN...SSN	SK.....YRLI
A_SE_SE853	TSLFYKLDVV	PIGNN.....DTNS	TQ.....YRLI
A_SE_SE889	HALFYRLDVV	PMDN.....NNS.	.L.....YRLI
A_SE_UGSE8	YSLFYKLDIV	KINKNKSFRG	.KNSSGNSSS	DR.....YRLI
A_UG_92UG0	YSLFYKLDVV	QINNG.....NNS	NL.....YRLI
A_UG_U455	YSLFYRLDIV	QINKTD....N	NS.....YRLI
AC_IN_2130	YSLFYRLDVV	PIEEGQGNS.SNSGY	KE.....YRLI
AC_RW_92RW	YSLFYRLDIV	QINSNSN...NSSH	NQ.....YRLI
AC_SE_SE94	HALFYRLDIV	PLDEGNSNSNESNNNY	SD.....YRLI
ACD_SE_SE8	YSLFYKLDVV	QINSN.....QNNS	SQ.....YRLI
ACG_BE_VI1	YALFYRLDIL	PLNKENK...GSS	GK.....YRLI
AD_SE_SE69	HSLFYKLDVV	QMGNSNS...	SQ.....YRLI
AD_SE_SE71	YSLFYKLDVV	QINENQ....	..YNSSNNSN	KE.....YRLI
ADHK_NO_97	HALFYRVDLV	SIDN.....NDNN	TQ.....YRLI
ADK_CD_MAL	YATFYNLDLV	QIDDSDN...S	S.....YRLI
AG_BE_VI11	HALFYRPDVV	PINNDN....	SSYMLI
AG_NG_92NG	YALFYRLDVV	PIDGNNV...S	NNYRLI
AGHU_GA_VI	YALFYKHDIV	PITN.....ET	KT.....	FILI
AGU_CD_Z32	YSLFYRLDIV	PIEENSSNG.N..S	SE.....YRLI
AJ_BW_BW21	YALFYKEDIA	LIKDRPN...NS	NY.....	SEYILV
B_AU_VH_AF	FALFYKLDVV	QIDGS.....N	TS.....YRLI
B_CN_RL42	YALFYKVDVV	PIGND.....S	TS.....YRLI
B_DE_D31_U	YAHFYKLDVV	PIDND.....N	TS.....YRLI
B_DE_HAN_U	SALFYKTDVV	PIDNNKTS..NRDNT	TS.....	YMLI
B_FR_HXB2	YAFFYKLDII	PIDND.....T	TS.....	YKLT
B_GA_OYI	YALFYKLDVL	PIDKN.....D	TK.....	FRLI
B_CB_CAM1	YALFYKLDVV	PIDKAN....	TS.....	YTLI
B_GB_GB8_C	YALLYKLDIV	SIGSD.....N	TS.....	YILT
B_GB_MANC	YALFYKLDVV	PIBKK.....N	TS.....	FRLI
B_KR_WK_AF	YALFYKLDII	PIDN.....	TS.....	YALR
B_NL_3202A	YALFYKLDVV	PIDNN..N..TNTSY	TS.....	YRLI
B_TW_TWCYS	YASFYRLDLV	QTDEN.....S	TS.....	YRLI
B_US_BC_L0	YALFYKLDVV	PIDNDKNS..	TK.....	YRLI
B_US_DH123	YALFYRHVV	PIDRN.....I	TS.....	YRLI
B_US_JRCFS	YALFYKLDVV	PID.....NKNN	TK.....	YRLI
B_US_MNCG	YALLYKLDIV	SIDND.....S	TS.....	YRLI
B_US_P896	YALFNRLDVV	PIE.....NTNN	TK.....	YRLI
B_US_RF_M1	YALFYKLDVV	PIEKGNISPK	N.NTSNNTSY	GN.....	YTLI
B_US_SF2_K	NALFRNLVV	PIDN..AS..TTNY	TN.....	YRLI
B_US_WEAU1	YALFYKLDVM	PIDHDNTS..	YTLI
B_US_WR27	HALFYRLDVV	PIDK.....NNTN	TS.....	YRLI
B_US_YU2_M	YALFYNLVV	PIDN.....AS	YRLI
BF1_BR_93B	HALFYRLDIV	PISNDNSSNDNSS	RE.....	YRLI
C_BR_92BR0	HALFYRLDIV	PLKNE.....SSNTS	GD.....	YRLI
C_BW_96BW0	RARFYRLDIV	QLNNN.....SNS	NE.....	YRLI
C_BW_96BW1	YALFYRLDIV	PLNNKNE...SN.	SE.....	YRLI
C_BW_96BW1	YALFYRLDIV	PLDN.....NS	SE.....	YRLI
C_BW_96BW1	YALFYKLDIV	PLNSNS...	SE.....	YRLI
C_ET_ETH22	YALFYKLDIV	PLN.....NGS	TD.....	YRLI
C_IN_93IN1	YALFYGLDIV	PLN...KKN.SSENS	SE.....	YRLI
C_IN_93IN9	YALFYRLDIV	QLN...SDD.KKNSS	EY.....	YRLI
C_IN_93IN9	HALFYRLDLV	PLDNENKSS.FSNSS	KT.....	YRLI
C_IN_94IN1	YALFYKLDIV	PIS...ETS.NQS..	RLI
C_IN_95IN2	YALFYKLDIV	PLDNEEQEN.DSNSS	GY.....	YRLI
CRF01_AE_C	HALFYVPDIV	RIG...EK.	..NKNSSGNS	SE.....	YILI
CRF01_AE_C	HALFYTSVV	QISSVQNNN	NSNTSGQNN	HK.....	FRLI
CRF01_AE_C	YALFYKLDIV	PIE.....	..RNSGENNG	SS.....	YRLI
CRF01_AE_T	HALFYKLDIV	QIEDK.....NDS	SK.....	YGLI
CRF01_AE_T	HALFYKLDIV	QMN.....KNS	SE.....	YRLI
CRF01_AE_T	YALFYKLDIV	QMN.....SNS	SE.....	YRLI

CRF01_AE_T	YALFYKLDTI	PIG.....	NNN	NM.....	YRLI
CRF01_AE_T	HALFYKLDIV	QIEDK.....	KTS	SE.....	YRLI
CRF01_AE_T	QALFYKLDIV	QMGG.....	NDS	GE.....	YRLI
CRF02_AG_F	SALFYRLDVV	QINES.....	GN	SQ.....	YRLI
CRF02_AG_F	SALFYRLDVV	QINES.....	SN	SQ.....	YRLI
CRF02_AG_G	NALFYRVDVV	QMNS.....	.Q.....	YRLI	
CRF02_AG_N	HALFYRLDVV	QINEN.....	NG	SQ.....	YRLI
CRF02_AG_S	YALFYRYDVV	QINETG.....	DN	IQ.....	YRLI
CRF02_AG_S	AALFYKIDIV	PIDKN.....	A	TY.....	YRLI
CRF03_AB_R	YALFYKLDVV	QIDND.....	.S.....	YRLI	
CRF03_AB_R	HALFYKLDVV	QIDND.....	.S.....	YRLI	
CRF04_cpx	YALFYRIDIV	PINARVPING	SNRNNST	EE.....	YMLI
CRF04_cpx	HALFYRLDVV	PINNVPINN	TSNTSEY	RE.....	YRLM
CRF04_cpx	YALFYRLDIV	PINDNNSTN.	SRRSSNT	SD.....	YMLI
CRF05_DF_B	HALFYRLDIV	PISSD....D	SSN	SS.....	YRLI
CRF05_DF_B	HALFYRLDIV	SINS.....	SRK	E.....	YRLI
CRF06_cpx	YALFYRPDIV	PIGDD.....	S	NN.....	SDYRLI
CRF06_cpx	YALFYRLDVV	PINDG.....	S	NN.....	NSYRLI
CRF06_cpx	RALFYTLDVV	PINDN.....	G	NN.....	STYRLI
CRF06_cpx	YALFYRPDVM	QVDG.....	K	NS.....	STYRLI
CRF11_cpx	YALFYKLDIV	PINDNNN...	SS	NV.....	SDYRLI
CRF11_cpx	RALFYRLDVV	PINDS.....	SS	NI.....	GQYRLI
D_CD_84ZR0	HALFYRLDVV	QIDNEGKNE.	INDTY	GT.....	YRLI
D_CD_ELI_K	YALFYRLDIV	PIDNDSS...	TNS	TN.....	YRLI
D_CD_NDK_M	YALFYKLDIV	PIDNNNR...	TNS	TN.....	YRLI
D_UG_94UG1	QALFYKLDVV	KINDNDS...	DN	TS.....	YRLI
F1_BE_VI85	SALFYRLDIV	PIGNN...N.	S	SE.....	YRLI
F1_BR_93BR	HALFYKLDIV	QINKD..DN.	RT.....	YRLI	
F1_FI_FIN9	HALFYRLDIE	PISNN...N.	SR	EE.....	YRLI
F1_FR_MP41	NALFYKLDII	PINNS.....	SS	SD.....	YRLI
F2_CM_MP25	YALFYKLDVV	QINNS.....	NTS.....	YRLI	
F2KU_BE_VI	YALFYREDIV	PINIKKNNKT	NSN	SKNNNTSNN	SIENSKYRLI
G_BE_DRCBL	YALFYRTDVV	PINEMNNENN	GT	NS.....	TWYRLT
G_NG_92NG0	YALFYKLDVV	PISNGN....	.K.....	TSYRLI	
G_SE_SE616	YAFFYRLDVV	PINN.....	.A.....	TNYRLT	
H_BE_VI991	HALFYRADIV	QIDEGER...	NKSD	NH.....	YRLI
H_BE_VI997	HALFYRLDVV	PIDETSNNN.	NSNS	TK.....	YRLI
H_CF_90CF0	HALFYRLDVV	PIDNNS....	TQ.....	YRLI	
J_SE_SE702	YALFYRQDVV	PIN.....	S	DN.....	KSYILI
J_SE_SE788	YALFYRQDVV	PID.....	S	NN.....	KNYILI
K_CD_EQTB1	SALFYKLDIV	QIKQSEINQS	ESE	DRLI
K_CM_MP535	SALFYRLDVL	PLN.GEGNNS	STE	YRLI
N_CM_YBF30	YSLFYVEDVV	PINAYN....	KTYRLI	
O_CM_ANT70	QALFYVSDLM	ELNETSSTNK	T	NS.....	KMYTLT
O_CM_MVP51	QALFYVSDLS	KVNDNAVN.	.G.....	TTYMLT	
O_SN_99SE	QALFYVSDLM	KINEANDT..	.K.....	DMYTLT	
O_SN_99SE	QALFYVSDLM	KVNENND...	TMYTLI	
U_CD_83C	HTLFYKLDVV	PLNVTN....	N	SS.....	ISSTYRLI

	251				300
00BW0762_1	NCNTSTITQA	CPKVNFDPIP	IHYCAPAGYA	ILKCNTKTFD	GTGPCTNVST
00BW0768_2	NCNTSAVTQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNVST
00BW0874_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1471_2	NCNTSTITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1616_2	KCNTSTITQA	CPKVNFDPIP	IHYCAPAGYA	ILKCRNKTFN	GTGPCNNVST
00BW1686_8	NCNTSSISQA	CPKVSFGPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW1759_3	NCNTSAVTQA	CPKVTFDPIP	VHYCAPAGYA	ILKCNNKTFN	GAGPCNNVST
00BW1773_2	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNQTFN	GTGPCNDVSS
00BW1783_5	NCNTSAITQA	CPKVSFEPIP	IHFCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1795_6	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1811_3	NCNTSALTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNVST
00BW1859_5	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKTFN	GTGPCQNVST
00BW1880_2	NCNTSAITQA	CPKINFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW1921_1	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2036_1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2063_6	NCNTSTITQS	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW2087_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2127_2	NCNTSAITQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2128_3	NGNTSALTQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW2276_7	NCNTSAITQA	CPKITFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVSP
00BW3819_3	NCNTSAVTQS	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3842_8	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3871_3	NCNTSAISQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GIGPCQNISI
00BW3876_9	HCNTSTITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCNDKTFN	GTGPCQNVST
00BW3886_8	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
00BW3891_6	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW3970_2	NCNTSKVTQA	CPKVSFDPIP	LHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
00BW5031_1	SCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW01B21	NCNTSAISQA	CPKVSFDPIP	IHYCTPAGFA	ILKCNNKTFN	GTGPCNNVST
96BW0407	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW0502	NCNTSAITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNQTFN	GTGPCNNVSS
96BW06_J4	NCNTSTISQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
96BW11_06	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW1210	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNVST
96BW15B03	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
96BW16_26	NCNTSALTQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BW17A09	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILECNNKTFN	GTGPCTNVST
96BWM01_5	NCNTSTITQS	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
96BWM03_2	NCNTSSITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCQNVST
98BWMC12_2	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWMC13_4	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWMC14_a	NCNTSAISQA	CPKISFDPIP	IHYCAPAGYA	ILKCNNKTFN	GIGPCNNVST
98BWM014_1	NCNTSTVKQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM018_d	NCNTSVITQA	CPKVTFEPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM036_a	NCNTSTLTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
98BWM037_d	NCNTSTVTQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNNKTFN	GKGPCNNVST
99BW3932_1	NCYTSIAAQT	CPKISFDPIP	IHYCAPAGYA	ILKCYNKTFN	GTGPCKNVST
99BW4642_4	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCQNVST
99BW4745_8	NCNTSAVTQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
99BW4754_7	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTRPCNNVST
99BWMC16_8	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNDVST
A2_CD_97CD	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGYA	ILKCKDKEFN	GKGSNSNVSS
A2_CY_94CY	NCNTSTITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDPRFN	GTGSCKNVSS
A2D_97KR	HCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPRFN	GTGPCKNVSS
A2G_CD_97C	KCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPKFN	GTGPCNVSS
A_BY_97BL0	NCNTSAMTQA	CPXVTFEPIP	IYYCAPAGFA	ILKCDTNTFT	RTXPCKNVST
A_KE_Q23_A	NCNTSAITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCKDEGFN	GTGLCKNVST
A_SE_SE659	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDDAFN	GTGRCKNVST
A_SE_SE725	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKEFN	GTGPCNNVST

A_SE_SE753	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNDKEFN	GTGLCNNVST
A_SE_SE853	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDENFN	GTGPCKNVST
A_SE_SE889	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKEFN	GTGPCKNVSS
A_SE_UGSE8	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEDEFN	GTGTCRNVST
A_UG_92UG0	NCNTSALTQA	RPKVTFEPIP	IHYCAPAGYA	ILKCNDKEFN	GTGLCKNVST
A_UG_U455	NCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDPEFN	GKGPCRNVST
AC_IN_2130	NCNTSAITQA	CPKVTFNPIP	IHYCTPAGYA	ILKCNEETFN	GTGPCKNVST
AC_RW_92RW	NCNTSAITQA	CPKVSFEPIP	INYCAPAGFA	ILKCKDKKFN	GTGPCKNVST
AC_SE_SE94	NCNTSAITQA	CPKVSFDPIP	IHYCAPPGFA	ILKCKDAKFN	GIGPCNNVST
ACD_SE_SE8	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKEFN	GTGPCKNVST
ACG_BE_VI1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCKNVST
AD_SE_SE69	NCNTSAIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDTEFN	GTGPCKNVST
AD_SE_SE71	NCNTSAITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCKDEKFN	GTGPCKNVST
ADHK_NO_97	NCNTSVITQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCKNVST
ADK_CD_MAL	NCNTSVITQA	CPKVTFDPIP	IHYCAPAGFA	ILKCNDKKFN	GTEICKNVST
AG_BE_VI11	NCNSSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILCRDKKFN	GTEPCKNVST
AG_NG_92NG	NCNVSTIKQA	CPKVSFDPLP	IHYCAPAGFA	ILKCRGKNFT	GTGQCKNVSS
AGHU_GA_VI	HCNTSTITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCKDKAFN	GTGPCKNVST
AGU_CD_232	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDEEFE	GKGPCRNVST
AJ_BW_BW21	KCNTTVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILQCNDKKFN	GTGPCKNVST
B_AU_VH_AF	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GKGPANIST
B_CN_RL42	NCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKKFN	GTGPCTNVST
B_DE_D31_U	SCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	MLKCKDKRFN	GKGQCKNVST
B_DE_HAN_U	HCNRSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GKGPCKNVST
B_FR_HXB2	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCTNVST
B_GA_OYI	HCNTSTITQA	CPKISFEPIP	MHYCTPAGFA	ILKCNDKKFN	GTGPCTNVST
B_GB_CAM1	HCNTSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDKKFN	GKGPCTNVST
B_GB_GB8_C	ECNASVITQA	CPKISFEPIP	IHFCAAGFA	ILKCNNKTFD	GKGPCTNVST
B_GB_MANC	SCNTSTITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKKFD	GKGQCTNVST
B_KR_WK_AF	HCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILQCNDKKFN	GTGPCKNVST
B_NL_3202A	SCNTSVITQA	CPKVSFEPIP	IHFCTPAGFA	LLKCNDKKFN	GTGPCKNVST
B_TW_TWCYS	SCNASVIKQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKTFN	GTGTCTNVST
B_US_BC_LO	SCNTSVTTQA	CPKISFEPIP	IHYCAPAGFA	ILKCKDKKFN	GTGSCKNVST
B_US_DH123	SCNTSTLTQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDKKFN	GTGPCTNVST
B_US_JRCSF	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GKGQCKNVST
B_US_MNCG	SCNTSVITQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFS	GKGSCKNVST
B_US_P896	SCNTSVITQA	CPKVSFQPIP	IHYCVPAGFA	MLKCNNKTFN	GSGPCTNVST
B_US_RF_M1	HCNRSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDKKFN	GTGPCKNVST
B_US_SF2_K	HCNRSVITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNNKTFN	GKGPCTNVST
B_US_WBAU1	NCKSSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GKGPCKNVST
B_US_WR27	HCNTSTITQA	CPKVSFEPIP	IHYCTPAGFA	ILKCNDKKFN	GTGQCKNVST
B_US_YU2_M	SCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
BF1_BR_93B	NCNTSTLTQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNDKKFN	GTGPCRNVST
C_BR_92BR0	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
C_BW_96BW0	NCNTSTITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GSGPCNNVST
C_BW_96BW1	NCNTSTITQS	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
C_BW_96BW1	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCTNVST
C_BW_96BW1	NCNTSAITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCKNNTFN	GTGPCQNVST
C_ET_ETH22	NCNTSTITQA	CPKVSFDPIP	IHYCAPAGYA	ILKCRDKTFT	GTGPCHNVST
C_IN_93IN1	NCNTSAITQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCNNVST
C_IN_93IN9	NCNTSAITQA	CPKVTFDPIP	IHYCTPAGYA	ILKCKDKTFN	GTGPCHNVST
C_IN_93IN9	NCNTSAITQA	CPKVTFDPIP	IHYCTPAGYA	ILKCNEKTFN	GTGLCQNVST
C_IN_94IN1	SCNTSVITQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKTFN	GTGPCRNVST
C_IN_95IN2	NCNTSALTQA	CPKVTFDPIP	IHYCAPAGYA	ILKCNNKTFN	GTGPCHNVST
CRF01_AE_C	HCNTSVIKQA	CPKVTFDPIP	IHYCTPAGYA	ILKCNEKTFN	GTGPCKNVSS
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_C	HCNTSVIKQA	CPKVSFDPIP	IHYCAPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCSTSVIKQA	CPKISFDPIP	IHYCTPAGYV	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS

CRF01_AE_T	NCNDSVIKQA	CPKISFDPIP	IHYCTPAGYA	MLKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKISFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF01_AE_T	NCNTSVIKQA	CPKVSFDPIP	IHYCTPAGYA	ILKCNDKNFN	GTGPCKNVSS
CRF02_AG_F	NCHTSAITKA	CPRVTLEPIP	IHYCAPAGLA	ILKCNDKKFN	GTGLCKNVST
CRF02_AG_F	NCNTSAIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCKNVST
CRF02_AG_G	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDRNFN	GTGPCQNVST
CRF02_AG_N	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCKDKGFN	GTGPCKNVST
CRF02_AG_S	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKFN	GTGPCKNVST
CRF02_AG_S	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKDFS	GTGSCKNVST
CRF03_AB_R	SCNTSVVTQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
CRF03_AB_R	SCNTSVVTQA	CPKISFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCTNVST
CRF04_cpx_	NCNASTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKNFT	GLGPCTNVSS
CRF04_cpx_	SCNTSNHKQA	CPKVTFEPNS	HTLLCPGWFC	DLKCNDKNSP	GLGSCTNVSP
CRF04_cpx_	NCNVSSITQA	CPKIKFEPIP	IHYCAPAGFA	ILQCNKERN	GSGPCKNVSS
CRF05_DF_B	NCNTSTIKQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNEKKFS	GTGPCKNVST
CRF05_DF_B	NCNTSTIKQA	CPKVCWDPIP	IHYCAPAGYA	ILKCKEKRFN	GTGPCKNVST
CRF06_cpx_	NCNVSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKDFN	GTGPCKNVST
CRF06_cpx_	NCNASTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF06_cpx_	NCNTSTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF06_cpx_	NCNASTIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGACKNVST
CRF11_cpx_	NCNVSTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
CRF11_cpx_	NCNVSAVKQA	CSKVTFEPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
D_CD_84ZR0	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKRFN	GTGPCKNVSS
D_CD_ELI_K	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCRDKKFN	GTGPCTNVST
D_CD_NDK_M	NCNTSTITQA	CPKISFEPIP	IHYCAPAGFA	ILKCRDKKFN	GTGPCKNVST
D_UG_94UG1	NCNTSAITQA	CPKMTFEPIP	IHYCAPAGFA	ILKCNEKKFN	GTGPCKNVST
F1_BE_VI85	NCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNDKRFN	GTGPCKNVST
F1_BR_93BR	NCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCNEKNFT	GTGSCKNVST
F1_FI_FIN9	NCNTSTITQA	CPKVSWDPIP	IHYCAPAGYA	ILKCKDKRFN	GTGPCKNVST
F1_FR_MP41	NCNTSTIKQA	CPKVSWDPIP	IHYCAPAGYA	ILKCRDPRFN	GTGPCKNVST
F2_CM_MP25	NCNTSTLTQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGLCRNVST
F2KU_BE_VI	NCNTSAITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNEKEFN	GTGPCKNVST
G_BE_DRCBL	NCNVSTIKQA	CPKVTFEPIP	IHYCAPAGFA	ILKCVDKKFN	GTGTCNNVST
G_NG_92NG0	HCNVSTIKQA	CPKVNFDPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
G_SE_SE616	HCNVSTIKQA	CPKVTFDPIP	IHYCAPAGFA	ILKCRDKNFN	GTGPCKNVST
H_BE_VI991	NCNTSVIKQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNGKKFN	GTGPCTNVST
H_BE_VI997	NCNTSVITQA	CPKVSFDPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCTNVST
H_CF_90CP0	NCNTSVITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNKTFN	GTGLCTNVST
J_SE_SE702	NCNTSVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILKCNNKTFN	GTGPCKNVST
J_SE_SE788	NCNTSVIKQA	CPKVSFQPIP	IHYCAPAGFA	ILKCNDKNFN	GTGSCKNVST
K_CD_EQTB1	NCNTSTVTQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNNNTCN	GTGPCTNVST
K_CM_MP535	NCNTSTITQT	CPKVTFEPIP	IHYCAPAGFA	ILKCKDKRFN	GTGPCKNVST
N_CM_YBF30	NCNTTAVTQA	CPKTSFEPIP	IHYCAPAGFA	IMKCNEGNFS	GNGSCTNVST
O_CM_ANT70	NCNSTTITQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNSTEFN	GTGTCRNVST
O_CM_MVP51	NCNSTIIKQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNDTDFN	GTGLCHNVST
O_SN_99SE_	NCNSTTIKQA	CPKVSFEPIP	IHYCAPAGYA	IFKCNSTEFN	GTGPCKNVST
O_SN_99SE_	NCNSTTIKQT	CPKVSFEPIP	IHYCAPAGYA	IFKCNTTGFN	GTGPCTNVST
U_CD_83C	NCNTSTITQA	CPKVSFEPIP	IHYCAPAGFA	ILKCNDKKFN	GTGPCKNVST

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00BW0762_1	VQCTHGIKP	VSTQLLN	LSEE.GIVIR	SENITNNAKT	IIVHLNESVE
00BW0768_2	VQCTHGIKP	VPTQLLN	LAEE.EIIIR	SEALTNNAKT	IIARLNKSVE
00BW0874_2	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLAQNDKT	IIVHLNESVE
00BW1471_2	VLCTHGIKP	VSTQLLN	LSEG.EIMIR	SENLTDNAKT	IIVQLNKPVE
00BW1616_2	VQCTHGIKP	VSTQLLN	LAEE.EIVIR	SENITNNAKI	IIVHLNETVD
00BW1686_8	VQCTHGIKP	VSTQLLN	LAEG.EIIIR	SENMTDNVKT	IIVHLNESVE
00BW1759_3	VQCTHEIKPV	VSTQLLN	LAEE.QIIIR	SENMTNNAKT	IIVHLKKPVQ
00BW1773_2	VQCTHGIKP	VSTQLLN	LAEK.EIIIR	SENLTNNAKI	IIVHLKDPVN
00BW1783_5	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTNNVKT	IIVHLNESIQ
00BW1795_6	VQCTHGIKP	VSTQLLN	LAEG.EIIIR	SKNLTDNART	IIVHLNESVQ
00BW1811_3	VQCTHGIKP	VSTQLLN	LAEE.DIIIR	SENLTNDVKT	IIVHLNESVE
00BW1859_5	VQCPHGIKP	VSTQLLN	LAEE.EIIIR	SENIEDNVKT	IIVHLNESIE
00BW1880_2	VQCTHGIKP	VATQLLN	LAEE.EIVIR	FKNITNNAKI	IIVQLNTSVG
00BW1921_1	VQCTHGIKP	VSTQLLN	LAEE.GIIIR	SENLTDNAKT	ITVQLDQAVE
00BW2036_1	VQCTHGIKP	VSTQLLN	LAEG.EIIIR	SENLAADNAKT	IIVHFNESVE
00BW2063_6	VQCTHGIKP	VSTQLLN	LAEK.EIIIR	SKNITDNVKT	IIVHLNEAVE
00BW2087_2	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTNNAKT	IIVHLNDSVE
00BW2127_2	VQCTHGIKPL	VSTQLLN	LAQQ.QIMIT	SENLTNNAKI	IIVHLKEAIN
00BW2128_3	VQCTHGIKP	VSTQLLN	LAEE.IIIR.	SENLTNNAKT	IIVQLKEPVK
00BW2276_7	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTNNVKT	IIVHLNKSVE
00BW3819_3	VQCTHGIKP	VSTQLLNG	LAEK.EIIIR	SENLTNNVKT	IIVHLNESVE
00BW3842_8	VQCTHGIKP	VSTQLLN	LAEG.EIIIR	SKNLSDNAKI	IIVHLNESVG
00BW3871_3	VQCTHGIKP	VSTQLLN	IAEG.EIIIR	SENLTNNAKT	IIVHLNESVK
00BW3876_9	IQCTHGIKP	VSTQLLN	LAEK.DIIIR	SENLTNNIKT	IIVHLNDSVQ
00BW3886_8	VQCTHGIKP	VSTQLLN	LAEG.EIIIR	SENLTNNAKT	IIVHLNESIE
00BW3891_6	VQCTHGIKP	VSTQLLSNG	LSEK.EIIIR	SENLTNNVKT	IIVHLNESVE
00BW3970_2	IQCTHGIKP	VSTQLLN	RAEK.EIIIR	SENMTNNAKT	IIVHLNESIE
00BW5031_1	VQCTHGIKP	VSTQLLN	LA.E.EIVIR	SENISDNAKT	IIVHLNESVE
96BW01B21	VQCTHGIKP	VSTQLLN	LAEE.DIIIR	SENLTNDVKT	IIVHLNESIE
96BW0407	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTDNAKI	IIVHLNESVR
96BW0502	VQCAHGIKP	VSTQLLN	VAKG.EIIIR	SENLTNNAKI	IIVQLNKPVK
96BW06_J4	VQCTHGIKP	VSTQLLN	LAEE.KIIIR	SGNVTNNAKT	IIVHLNESVE
96BW11_06	VQCTHGIKP	VSTQLLN	LAEK.EIIIR	FKNITNNAKT	IIVHLNESVE
96BW1210	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENITDNVKT	IIVHLNKSVE
96BW15B03	VQCTHGIKP	VSTQLLN	LAEG.EIIIR	SKNLSNNAYT	IIVHLNDSVE
96BW16_26	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTNNAKT	IIVHLNESVE
96BW17A09	VQCTHGIKP	VSTRLLN	LAEE.EIIIR	SENLTNNAKI	IMVQLNESIE
96BWM01_5	VQCTHGIKP	VSTQLLN	LAEK.EIIIR	SKNITDNVKT	IIVHLNESVE
96BWM03_2	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTDNAKT	IIVHFNESVQ
98BWMC12_2	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SENLTNNVKT	IIVHLNESVE
98BWMC13_4	VQCTHGIKP	VSTQLLN	LAEK.EIVIR	SENLTNDVKT	IIVHLNQSVQ
98BWMC14_a	VQCTHGIKP	VSTQLLN	LAEE.EVVIR	SENLTNNAKT	IIVQLKEPVK
98BWM014_1	VQCTHGIKP	VSTQLLN	LAEK.EIIIR	SENITNNIKT	IIVHLNEPVE
98BWM018_d	VQCTHGIKP	VSTQLLN	LAEE.EIIIR	SKNITNNANT	IIVQLKDPVD
98BWM036_a	IQCTHGIKP	VSTQLLN	IAEE.EIIIR	SENLTNDVKT	IIVHLKDPID
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99BW3932_1	VQCTHGIKP	VSTQLLN	LAEE.EIVIR	SENLTNNVKT	IIVHLNESIE
99BW4642_4	VQCTHGIKP	VSTQLLN	LAEG.EIIVR	SENLTNDVKT	IIVHLDKPVG
99BW4745_8	VQCTHGIKP	VSTQLLN	LAEK.EIIVR	SENLTNNAKI	IIVQLKQSVG
99BW4754_7	VQCTHGIKP	VSTQLLN	RAEK.EVVIR	AESLTDNAKV	IIVHLKDSVQ
99BWMC16_8	VQCTHGIKP	VSTQLLN	LAEE.DIIIR	SKNLTDNAKT	IIVHLNESVN
A2_CD_97CD	VQCAHGIRPV	ASTQLLN	LAEG.KVMIR	SENITDNAKN	IIVQFNKPPV
A2_CY_94CY	VQCTHGIKP	ASTQLLN	LAEGGKIMIR	SENITNNAKN	IIVQFTKPV
A2D_97KR	VQCTHGIRPV	ASTQLLN	LAEGNKTIIR	SANITDNNTKN	IIVQFTKPVQ
A2G_CD_97C	VQCTHGIRPV	VSTQLLN	LAEE.EVMIR	SENITDNAKN	IIVQFDKPVE
A_BY_97BL0	VQCTHXIKPV	VSTQLLN	LAEX.VMIR	SENITDNVKT	IIVQLTEPVN
A_KE_Q23_A	VQCTHGIKP	VSTQLLN	LAEKN.ITIR	SENITNNAKI	IIVQLVQPV
A_SE_SE659	VQCTHGIKP	VSTQLLN	LAKGG.IRIR	SENITNNVKT	ILVQLDKPVN
A_SE_SE725	VQCTHGIKP	VSTQLLN	LAEEK.IMIR	SENISDNAKT	IIVQLTEPVT

SECRET

A_SE_SE753	VQCTHGIKPV	VSTQLLLNGS	LATK..IMIR	SENITNNAKT	IIVQLVEPVE
A_SE_SE853	VQCTHGIKPV	VSTQLLLNGS	LAREK.VMIR	SENITNNVKN	IIVQLKEPVE
A_SE_SE889	VQCTHGIRPV	VSTQLLLNGS	LAETE.VMIR	AENITNNIKN	IIVQFNKSVE
A_SE_UGSE8	VQCTHGIRPV	VSTQLLLNGS	LAKEE.VRIR	SENISDNAKT	IIVQFTKPVE
A_UG_92UG0	VQCTHGIRPV	VSTQLLLNGS	LAEGK.VMIR	SENITNNVKN	IIVQLNESVT
A_UG_U455_	VQCTHGIKPV	VSTQLLLNGS	LAERE.IRIR	SENFNTNAKT	IIVQLVNPVK
AC_IN_2130	VQCTHGIKPV	VSTQLLLNGS	LAEEK.VIIR	SENITNNVKN	IIVQLAEPVR
AC_RW_92RW	VQCTHGIKPV	VSTQLLLNGS	LAEEE.IIIR	SENITNNAKT	IIVQLNETVQ
AC_SE_SE94	VQCTHGIKPV	ISTQLLLNGS	LSETG.VKIR	SENITNNAKT	IIVQLDEAVE
ACD_SE_SE8	VQCTHGIKPV	VSTQLLLNGS	LAEEE.IIVR	SENLTNNAKI	IIIQLNETVI
ACG_BE_VI1	VQCTHGIKPV	VSTQLLLNGS	LAEK..VVIR	SENITNNAKT	IIVQFDSPIK
AD_SE_SE69	VQCTHGIKPV	VSTQLLLNGS	LA.BGKVIR	SENITDNTKN	IIVQFTEPVT
AD_SE_SE71	VQCTHGIKPV	VSTQLLLNGS	LAKEE.VIIR	SENITNNAKN	IIVQFVKPVT
ADHK_NO_97	VQCTHGIKPV	VSTQLLLNGS	LA..EKVIIR	SKNITDNTKN	IIVHFNESVQ
ADK_CD_MAL	VQCTHGIKPV	VSTQLLLNGS	LA.BEEIMIR	SENLTDNTKN	IIVQLNETVT
AC_BE_VI11	VQCTHGIKPV	VSTQLLLNGS	LA.BEEIIVR	SENFNTNAKV	IIVQLKEPIE
AG_NG_92NG	VQCTHGIKPV	VSTQLLLNGS	LA.EGEIVIR	SENLTDNAKV	IIVQLNKTTIG
AGHU_GA_VI	VQCTHGIRPV	VTTQLLLNGS	LA.EGEIIR	SENITENTKN	IIVQLNETVE
AGU_CD_Z32	VQCTHGIKPV	VSTQLLLNGS	LAEEK.VRIR	SENFSDNAKI	IIVQLAKPVN
AJ_BW_BW21	VQCTHGIKPV	VSTQLLLNGS	IA.BEEIIR	SENITNNAKT	IIVQLNNTVE
B_AU_VH_AF	VQCTHGIRPV	VSTQLLLNGS	LA.EKEIVIR	SDNFTDNAKS	IIVQLNESVE
B_CN_RL42_	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIK	PSNFTDNARV	IIVQLNESVE
B_DE_D31_U	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SDNFTDNAKT	IIVQLKESVE
B_DE_HAN_U	VQCTHGIRPV	VSTQLLLNGS	LA.EKEVVIR	SDNFTDNTKT	IIVHLNESVE
B_FR_HXB2_	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SVNFTDNAKT	IIVQLNTSVE
B_GA_OYI_	VQCTHGIKPV	VSTQLLLNGS	LA.BEEVIIR	SSNFTNNAKI	IIVQLNKSVE
B_GB_CAM1_	VQCTHGIRPV	VSTQLLLNGS	LA.EKEVVIR	SENFNTNNAKT	IIVQLKEPVE
B_GB_GB8_C	VQCTHGIRPV	VSTQLLLNGS	LA.EEKVVIR	SDNFTDNVKT	IIVQLKEAVE
B_GB_MANC_	IQCTHGIRPV	VSTQLLLNGS	LA.BEEVLR	SDNFTDNAKT	IIVHLNESVE
B_KR_WK_AF	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVIR	SENFNTNNAKT	IIVQLNASVE
B_NL_3202A	VQCTHGIRPV	VSTQLLLNGS	IA.BEEILIK	SANFSNNAKT	IIVQLNESVA
B_TW_TWCYS	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVIR	SENITNNAKT	IIIQLNKSVM
B_US_BC_L0	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SANFSDNAKT	IIVQLKEAVE
B_US_DH123	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SSNFTDNAKI	IIVQLNETVE
B_US_JRCSF	VQCTHGIRPV	VSTQLLLNGS	LA.EEKVVIR	SDNFTDNAKT	IIVQLNESVM
B_US_MNCG_	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SENFNTDNAKT	IIVHLNESVQ
B_US_P896_	VQCTHGIRPV	VSTQLLLNGS	LA.EBDIVIR	SENFNTDNAKT	IIVQLNESVV
B_US_RF_M1	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SENFNTDNVKT	IIVQLNASVQ
B_US_SF2_K	VQCTHGIRPI	VSTQLLLNGS	LA.BEEVVIR	SDNFTNNAKT	IIVQLNESVA
B_US_WEAU1	VQCTHGIRPV	VSTQLLLNGS	LA.EEDIVIR	SENFNTDNAKN	IIVQLNVSIE
B_US_WR27_	VQCTHGIRPV	VSTQLLLNGS	LA.BEEVVIR	SANFTNNAKT	IIVQLKESVE
B_US_YU2_M	VQCTHGIRPV	VSTQLLLNGS	LA.BEEIVIR	SENFNTNNAKT	IIVQLNESVV
BF1_BR_93B	VQCTHGIKPV	VSTQLLLNGS	LA.EKDIIIR	SQNISDNAKT	IIVQLNVSPV
C_BR_92BR0	IQCTHGTKPV	VSTQLLLNGS	LAEE.EIIR	SKNLTDNVKT	IIVHLNESVE
C_BW_96BW0	VQCTHGIKPV	VSTQLLLSGS	LAEE.EIVIR	SENLTNNAKI	IIVHLNKTVR
C_BW_96BW1	VQCTHGIKPV	VSTPLLLNGS	LAEK.EIIR	FKIITNNAKT	IIVHLNESVE
C_BW_96BW1	VQCTHGIKPV	VSTQLLLNGS	LAEE.EIIR	SENITDNVKT	IIVHLNKSVE
C_BW_96BW1	VQCTHGIKPV	VSTQLLLNGS	LAEGGEIIR	SKNLSNNAYT	IIVHLNDSVE
C_ET_ETH22	VQCTHGIKPV	VSTQLLLNGS	IAEG.ETIIR	FENLTNNAKI	IIVQLNESVE
C_IN_93IN1	VQCTHGIKPV	VSTQLLLNGS	LAEG.EIIR	SENLTNNVKT	IIVHLNQSVE
C_IN_93IN9	VQCTHGIKPV	VSTQLLLNGS	LAEG.EIIR	SENLTNNAKT	IIVHLNQSVM
C_IN_93IN9	VQCTHGIKPV	VSTQLLLNGS	LAEG.EIIR	SENLTNDNVKT	IIVHLNQSVE
C_IN_94IN1	VQCTHGIKPV	VSTQLLLNGS	LSEG.EIIR	SENLTNNVKT	IIVHLNKSVE
C_IN_95IN2	VQCTHGIKPV	VSTQLLLNGS	LAEG.GIIR	SENLTNNVKT	IIVHLNQPVE
CRF01_AE_C	VQCTHGIKPV	VSTQLLLNGS	LAEE.DIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_C	VQCTHGIKPV	VSTQLLLNGS	LAEE.EIIR	SEDLTDNAKT	IIVHLNKSIE
CRF01_AE_C	VQCTHGIKPV	VSTQLLLNGS	LAEE.EIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLNGS	LAEE.EIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLNGS	LAEE.EIIR	FENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKPV	VSTQLLLNGS	LAEE.KIIR	SENLTNNAKT	IIVHLHESVE

CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAEE.BIIIR	SENLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAEE.BIIIR	SEDLTNNAKT	IIVHLNKSVE
CRF01_AE_T	VQCTHGIKP	VSTQLLLNGS	LAKE.BIIIR	SENLTNNAKT	IIVHLNKSVE
CRF02_AG_F	VQCTHGIKP	VSTQLLLNGS	LAEEE.VVIR	SENITNNAKN	IIVQLVAPVR
CRF02_AG_F	VQCTHGIKP	VSTQLLLNGS	LAEEE.VVIR	SENITNNAKN	IIVQLVTPVR
CRF02_AG_G	VQCTHGIKP	VSTQLLLNGS	LAEEE.IVIR	SENITNNVKN	IIVQLAKPVR
CRF02_AG_N	VQCTHGIKP	VSTQLLLNGS	LAEGE.VVIR	SENITNNAKT	IIVQLANPVK
CRF02_AG_S	VQCTHGIKP	VSTQLLLNGS	LAEEE.IVIR	SENFTNNAKI	IIVQLHESVK
CRF02_AG_S	VQCTHGIKP	VSTQLLLNGS	LAEGD.IVIR	SENISNNAKT	IIVQLNKPVW
CRF03_AB_R	VQCTHGIKP	VSTQLLLNGS	LA.EEBVVIR	SVNFTDNTKT	IIVQLKEPVE
CRF03_AB_R	VQCTHGIKP	VSTQLLLNGS	LA.EEBVVIR	SVNFTDNTKT	IIVQLKEPVE
CRF04_cpx_	VRCTHGIKP	VSTQLLLNGS	LA.TBEVVIR	SKNITDNTKN	IIVQLAKAVK
CRF04_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.TGGVVIR	SKNFTDNPKN	IIVQLDKAVK
CRF04_cpx_	VQCTHGIKP	VSTQLLLNGS	LS.TEGVVIR	SKNFTDNTKN	IIVQLAEAVK
CRF05_DF_B	VQCTHGIKP	VSTQLLLNGS	LA.KEGIIIR	SONISDNAKN	IIVHLNESVH
CRF05_DF_B	VQCTHGIKP	VSTQLLLNGS	LA.EBSIIIR	SONILDNTKT	IIVHLNESVQ
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EGNITIK	TENITDNTKN	IIVQLNQPVE
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEBIIIK	SKNLTNTKI	IIVQLNKSVE
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EDBIIIK	SENHTNNAKI	IIVQLNKTVQ
CRF06_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEBIIIK	TENLTDNSKN	IIVQLNKSIE
CRF11_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EEKVKIR	SENFTNNAKT	IIVQFNNTVR
CRF11_cpx_	VQCTHGIKP	VSTQLLLNGS	LA.EGEVRIR	SENLTNNAKT	IIVQLNSTVR
D_CD_84ZR0	VQCTHGIRPV	VSTQLLLNGS	LA.EEBIVIR	SENLTNNAKI	IIVHLNQSV
D_CD_ELI_K	VQCTHGIRPV	VSTQLLLNGS	LA.EEBVIIR	SENLTNNAKN	IIVHLNESVK
D_CD_NDK_M	VQCTHGIRPV	VSTQLLLNGS	LA.EEBIIIR	SENLTNNVKT	IIVQLNASIV
D_UG_94UG1	VQCTHGIKP	VSTQLLLNGS	LA.EEBIIIR	SENLTNNAKI	IIVQLNESVP
F1_BE_VI85	VQCTHGIKP	VSTQLLLNGS	LA.EEGIVIR	SONISNNAKT	IIVHLNESVQ
F1_BR_93BR	VQCTHGIKP	VSTQLLLNGS	LA.EEGIVIR	SONISDNAKT	IIVHLNESVQ
F1_FI_FIN9	VQCTHGIRPV	VSTQLLLNGS	LS.EGGIIIR	SONLSDNAKT	IIVHLNESVQ
F1_FR_MP41	VQCTHGIRPV	VSTQLLLNGS	LA.EEDIIIR	SONISDNAKT	IIVHLNESVQ
F2_CM_MP25	VQCTHGIKP	VSTQLLLNGS	LA.EEKMIIR	SENISDNTKT	IIVQFKNPVK
F2KU_BE_VI	VQCTHGIRPV	ISTQLLLNGS	LA.EKEIIIR	SGNISDNTKN	IIVQLNETVE
G_BE_DRCBL	VQCTHGIKP	VSTQLLLNGS	LA.EKDIIIS	SENISDNAKV	IIVHLNRSVE
G_NG_92NG0	VQCTHGIKP	VSTQLLLNGS	LA.EEDIRIR	SENFTDNTKV	IIVQLNNSIE
G_SE_SE616	VQCTHGIKP	VSTQLLLNGS	LA.EGKIKVR	SENFTDNTKV	IIVQLNKTVE
H_BE_VI991	VQCTHGIRPV	VSTQLLLNGS	LA.EVEEVIIR	SKNITDNTKN	IIVQLNEPVQ
H_BE_VI997	VQCTHGIKP	VSTQLLLNGS	LA.EGQVIIR	SKNISDNTKN	IIVQLDSPIE
H_CF_90CF0	VQCTHGIRPV	VSTQLLLNGS	LA.BEQIIIR	TKNISDNTKN	IIVQLKTPVN
J_SE_SE702	VQCTHGIKP	VSTQLLLNGS	VA.EGDIIIR	SENISDNAKN	IIVQLNDTVE
J_SE_SE788	VQCTHGIKP	VSTQLLLNGS	IA.EGDIIIR	SENISDNAKN	IIVQLNKTVE
K_CD_EQTB1	VQCTHGIKP	VSTQLLLNGS	LA.EEBIIIR	SEDITKNTKN	IIVQLNEAVE
K_CM_MP535	VQCTHGIKP	VSTQLLLNGS	LA.EEBIIIR	SENITDNTKN	IIVQLNETVQ
N_CM_YBF30	VQCTHGIKP	ISTQILNGS	LNTDGIVIR.NDSHSN	LLVQWNETVP
O_CM_ANT70	VTCTHGIRPT	VSTQILNGT	LS.KGKIRMM	AKDILEGGKN	IIVTLNSTLN
O_CM_MVP51	VTCTHGIRPT	VSTQILNGT	LS.REKIRIM	GKNITESAKN	IIVTLNTPIN
O_SN_99SE_	VTCTHGIRPT	VSTQILNGT	LS.EGNIRIM	GKNISDNMKN	IIVTLNSTIN
O_SN_99SE_	VTCTHGIRPT	VSTQILNGT	IS.EGKIRIM	GKNISDTGKN	IIVTINSTIN
U_CD_83C	VQCTHGIRPV	VSTQLLLNGS	LSEB.EVIIR	SENITNNAKT	IIVQLNETVK

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00BW0762_1	IVCTRPNNN.	.TRRSVRIG.	.PGQTFYATGDIIGN	IRQAHCNISK
00BW0768_2	IECTRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IREAHCNINK
00BW0874_2	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATGDVIGD	IRQAHCNTSE
00BW1471_2	IVCTRPNNN.	.TRKSVRIG.	.PGQTFYATGDIIGN	IRQAHCNISN
00BW1616_2	IVCTRPNNN.	.TRKSMRIG.	.PGQTFYATGDIIGN	IREAHCNISK
00BW1686_8	INCTRPNNN.	.TRKSIRIG.	.PGQTFYATGAIIGD	IRQAYCTVNA
00BW1759_3	IVCTRPNNN.	.TRRSVRIG.	.PGQTFYARGDIIGN	IRQAHCNISR
00BW1773_2	ITCTRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISA
00BW1783_5	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
00BW1795_6	IVCTRPNNN.	.TRKSVRLG.	.PGQAFYATGDIIGD	IRKAYCTINE
00BW1811_3	IVCTRPNNN.	.TRKSIRIG.	.PGQAFFATGEIIGD	IRQAHCNISA
00BW1859_5	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGN	IREAHCNITR
00BW1880_2	IVCTRPNNN.	.TKKSMRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
00BW1921_1	IECTRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGN	TRQAHCNVSA
00BW2036_1	IECIRPNNN.	.TRKSIRIG.	.PGQVIFYATGDIIGD	IREAHCNITE
00BW2063_6	IVCTRPNNN.	.TRKSVRIG.	.PGQTFYATGEVIGD	IREAHCNISE
00BW2087_2	IVCTRPNNN.	.TRKSIRIG.	.PGQAFYATDAIIGD	IRQAHCNISR
00BW2127_2	IVCTRPNNN.	.TRTSIRIG.	.PGHSFFATNGIIGD	IRQAHCSISK
00BW2128_3	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATGDIIGD	IRQAHCNISK
00BW2276_7	IVCVRPNNN.	.TRKSVRIG.	.PGQTFYATGNIIGD	IREAHCNISE
00BW3819_3	IKCTRPNNN.	.TRRSVRIG.	.PGQAFYTN.DIIGD	IRLAHCNISK
00BW3842_8	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYAGDIIGN	IRQAHCNISE
00BW3871_3	ITCTRPNNN.	.TRTSIRIG.	.PGQTFYATGDIIGD	IRKAYCNISI
00BW3876_9	IVCTRPNNN.	.IRKSVRIG.	.PGQAFYATGDIIGD	IREAYCNING
00BW3886_8	IVCVRPNNN.	.TRKSIRIG.	.PGQTFYATGEIIGN	IRQAYCSISG
00BW3891_6	IECTRPNNN.	.TRRSIRIG.	.PGQTFYATGEIIGD	IRQAYCTINE
00BW3970_2	IECIRPNNN.	.TRKSIRIG.	.PGQTFYATNGMIGD	IRQAHCNISG
00BW5031_1	IECRRPNNN.	.TGKSVRIG.	.PGQTFYATGGIIGE	IRRAHCDING
96BW01B21	INCTRPNNN.	.TRKSIRIG.	.PGQTFYAGEIIGK	IRLAYCNISE
96BW0407	IECTGPNNN.	.TRKSMRIG.	.PGQTFYATGEIVGD	IRQAHCNISE
96BW0502	IVCVRPNNN.	.TRKSVRIG.	.PGQTFYATGEIIGD	IRQAYCIINK
96BW06_J4	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYAT.DIIGD	IRQAYCNVSK
96BW11_06	IVCIRPNNN.	.TRKSVRIG.	.PGQTFYATEAIIGN	IREAHCNISE
96BW1210	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISK
96BW15B03	IVCTRPNNN.	.TRKGIRIG.	.PGQTFYATENIIGD	IRQAHCNISA
96BW16_26	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCIING
96BW17A09	IVCTRPNNN.	.TRKSTRIG.	.RGQTFYAMGRIIGD	IRQAHCNISG
96BWM01_5	IECTRPNNN.	.TRRSVRIG.	.PGQAFYATGDIIGD	IRAAHCNISE
96BWM03_2	INCTRPNNN.	.TRKSVRIG.	.PGQAFYATGDIIGD	IRKAYCNISK
98BWMC12_2	IVCTRPNNN.	.TRKSMRIG.	.PGQIFYATGDIIGD	IREAHCNISK
98BWMC13_4	IECTRPNNN.	.TRKSMRIG.	.PGQAFYATGEIIGN	IRQAYCNINE
98BWMC14_a	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
98BWM014_1	IVCTRPNNN.	.TRTSIRIG.	.PGQTFYATGDIIGD	IRQAHCNISE
98BWM018_d	ILCVRPSNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISA
98BWM036_a	IVCTRPNNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNISK
98BWM037_d	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATNDIIGD	IRQAHCNISE
99BW3932_1	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATGAIIGN	IREAYCNISG
99BW4642_4	IVCIRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGN	IKEAYCNIKE
99BW4745_8	IECIRPNNN.	.TRKSIRIG.	.PGQTFYATGEIIGD	IRKAHCTINK
99BW4754_7	INCTRPNNN.	.TRKSMRIG.	.PGQTFYATGEIIGD	IRQAHCNISR
99BWMC16_8	ITCTRPNNN.	.TRKSIRIG.	.PGQTFYATGDIIGD	IRQAHCSINK
A2_CD_97CD	INCTRPNNN.	.TRKSIRIFG.	.PGQAFYTNNIIGD	IRQAHCNISI
A2_CY_94CY	ITCIRPNNN.	.TRKSIRIFG.	.PGQAFYTN.EIIGD	IRQAHCNINK
A2D_97KR	INCTRPDVG.	.QRRSVRIG.	.PGRIFYTRQ	TYTR.QAKGD	IRQAQCNISS
A2G_CD_97C	ITCIRPNNN.	.TRKSIRIFG.	.PGQAFYTN.SIIGD	IRQAYCNISK
A_BY_97BLO	ITCIRPNNN.	.TRTSIRIG.	.PGQTFYATGDVIXD	IRKAYCNVSR
A_KE_Q23_A	IKCIRPNNN.	.TRKSIRIG.	.PGQAFYATGDIIGD	IRQAHCNVTR
A_SE_SE659	ITCIRPYHN.	.TRTRIHIH.	.PG.RSFYTGDIKGS	IRQAHCTVNR
A_SE_SE725	INCTRPNNN.	.TRTSIRIG.	.PGQAFYATGDITGD	IRQAHCNVSR

A_SE_SE753	INCTRPNNN.	.TRTSVPIG.	.PGKVFYATG	EIIGD	IRQAHCNVSK
A_SE_SE853	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATG	EVIGD	IRQAHCNVSR
A_SE_SE889	IICIRPNNN.	.TRKSIRIG.	.PGQAFYATG	DIIGD	IRQAYCDVNR
A_SE_UGSE8	IICTRPNNN.	.TRKSIRIG.	.PGQAFYGMG	DIIGD	IRKAHCNVSR
A_UG_92UG0	INCTRPNNN.	.TRRSVRIG.	.PGQTFYATG	DIIGD	IRQAHCNVSG
A_UG_U455	INCSRPNYNT	KNIRRSYIG.	.SGQAFYVTG	KIIGD	IRQAHCNVSR
AC_IN_2130	INCTRPNNN.	.TRTSIRIG.	.PGQTFYTS.	NIIGD	IRQAHCNVSR
AC_RW_92RW	INCSRPNNN.	.TRKSVHIG.	.PGQAFYATG	DVIGD	IRQAYCTVNG
AC_SE_SE94	INCTRPNNN.	.TRRSVHIG.	.PGQAFYATG	DITGD	IRKAHCIVNG
ACD_SE_SE8	INCTRPNNN.	.TRNSIRIG.	.PGQAFYATG	AITGD	IRQAHCNVSR
ACG_BE_VI1	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATG	DIIGD	IRQAHCNISG
AD_SE_SE69	INCTRPNNNT	.RK.SVRIG.	.PGQALYVTG	GII..G...D		IRQAFCEVNR
AD_SE_SE71	INCTRPNNN.	.TRKSVHMG.	.PGKVFYATG	DIIGD	IRQAHCNVSK
ADHK_NO_97	INCTRIANNT	RKS..IHIG.	.PGQAFYAAE	PVI..G...D		IRQAHCNISE
ADK_CD_MAL	INCTRPNNNT	.RR.GIHFG.	.PGQALYTTG	IVG.....D		IRRAYCTINE
AG_BE_VI11	INCTRPNNNT	RKSIIGLPG.	...QAFYATG	DII..GD...D		IRQAHCNVSG
AG_NG_92NG	INCTRPNNNT	RKSIRIGPG.	...QAFYATG	EII..G....		
AGHU_GA_VI	INCTRPNNNT	RKG..IRIG.	.PGRVIYATS	AIT..G...D		IRQAHCNISK
AGU_CD_Z32	ITCMRPNNY.	.TRKSIHIG.	.PGRALYPEG	DIIGD	IRQAHCNVSR
AJ_BW_BW21	IKCVRPANNT	RKGIHTGPG.	...QVLYATG	AVV..GD...D		IRQAHCNVSR
B_AU_VH_AF	IHCMRPNNNT	.RK.GIYVG.	.PGRHIYATE	KIV..G...D		IRQAHCNISR
B_CN_RL42	IKCIRPNNNT	.RK.SIHLG.	.PGKAWYTTG	QII..G...D		IRQAHCNLSS
B_DE_D31_U	INCTRPNNYT	.SK.RIRIG.	.ARRAFYTKG	KII..G...D		IRQAHCNISG
B_DE_HAN_U	INCTRPNNNT	.RK.GIHIG.	.PGRAVYTTG	RIV..G...D		IRLAHCNISR
B_FR_HXB2	INCTRPNNNT	.RK.RIRIQR	GPGRAFTIG	KIG.....N		MRQAHCNISR
B_GA_OYI	INCTRPNNNT	.RN.RISIG.	.PGRFHTTK	QII..G...D		IRQAHCNLSS
B_GB_CAM1	INCTRLNNNT	.RK.SIAIG.	.PGRTVYATD	RII..G...D		IRQAHCNLSS
B_GB_GB8_C	INCTRPNNNT	.RK.GIYMG.	.PGRRFYTTG	RII..G...D		IRQAHCNISK
B_GB_MANC	INCTRPNNNS	.RK.SIYIG.	.PGRRFHVTR	AVT..G...D		IRQAHCNISK
B_KR_WK_AF	INCTRLNNNT	.RK.SIRIG.	.PGSTFYATG	AII..G...D		IRQAHCNISR
B_NL_3202A	INCTRPNNNT	.RK.GIHIG.	.PGKAFYATG	QII..G...D		IRQAHCNLSS
B_TW_TWCYS	INCTRPNNIS	KRR.SMHIG.	.TGRVFYQT	..I..G...N		IRQAHCNLSS
B_US_BC_L0	INCTRPNNKT	.RK.RITTG.	.PGRVYTTG	EIV..G...D		IRQAHCNLSS
B_US_DH123	INCTRPNNNT	.RK.GITLG.	.PGRVFYTTG	EIV..G...D		IRKAHCNISK
B_US_JRCSF	INCTRPNNNT	.RK.SIHIG.	.PGRAFYTTG	EII..G...D		IRQAHCNISR
B_US_MNCG	INCTRPNNYK	.RK.RIHIG.	.PGRAFYTTK	NII..G...T		IRQAHCNISR
B_US_P896	INCTRPNNNT	.RR.RLSIG.	.PGRAFYARR	NII..G...D		IRQAHCNISR
B_US_RF_M1	INCTRPNNNT	.RK.SITKG.	.PGRVIYATG	QII..G...D		IRKAHCNLSS
B_US_SF2_K	INCTRPNNNT	.RK.SIYIG.	.PGRAFHTTG	RII..G...D		IRKAHCNISR
B_US_WEAU1	INCTRPNNNT	.RK.KITLG.	.PGRVLYTTG	EII..G...D		IRRAHCNLSS
B_US_WR27	INCTRPNNKI	.RR.RIHIG.	.PGRAFYTDR	..V..G...D		IRQAYCNISG
B_US_YU2_M	INCTRPNNNT	.RK.SINIG.	.PGRALYTTG	EII..G...D		IRQAHCNLSS
BF1_BR_93B	INCTRPNNNT	RKS..IPIG.	.PGRAFYTTG	EII..G...D		IRKAHCNVSG
C_BR_92BR0	INCTRPNNN.	.TRKSIRIG.	.PGQAFYATG	EIIGD	IRQAHCNISR
C_BW_96BW0	IVCTRPNNN.	.TRRSVRIG.	.PGQTFYATG	EIIGD	IR.AHCNISE
C_BW_96BW1	IVCIRPNNN.	.TRKSVRIG.	.PGQTFYATE	AIIGN	ISEAHCNISE
C_BW_96BW1	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISK
C_BW_96BW1	IVCTRPNNN.	.TRKGIRIG.	.PGQTFYATE	NIIGD	IRQAHCNISA
C_ET_ETH22	ITCTRPNNN.	.TRESIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISE
C_IN_93IN1	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISR
C_IN_93IN9	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	EIIGD	IRQAHCNISK
C_IN_93IN9	IECVRPNNN.	.TRESIRIG.	.PGQTFYATG	EIIGD	IRQAHCNISR
C_IN_94IN1	IVCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	EIVGN	IRQAHCNISK
C_IN_95IN2	IMCTRPNNN.	.TRKSIRIG.	.PGQTFYATG	DIIGD	IRQAHCNISE
CRF01_AE_C	INCTRPNNK.	.MRTSARIG.	.PGQVFYKTG	SITGD	IRKAYCEING
CRF01_AE_C	INCTRPNNK.	.VRISARIG.	.PGRVFHTTG	NINGD	IRKAYCEINK
CRF01_AE_C	INCTRPNNK.	.MRTSVRIG.	.PGRVFYKTG	SITGD	IRKAYCEING
CRF01_AE_T	INCTRPNNN.	.MRTSMRIG.	.PGQVFYRTG	SITGD	IRKAYCEING
CRF01_AE_T	INCTRPNNN.	.TRTSITMG.	.PGQVFYRTG	DIIGD	IRKAYCEING
CRF01_AE_T	INCTRPNNN.	.KRTRTSIG.	.QGRVLYRTG	DITGN	IGKPYCEING

CRF01_AE_T	INCTRPSGK.	.EEKRMTIG.	.PGKVFYSTGKITGD	IRKAYCVING
CRF01_AE_T	INCTRPSNN.	.TRTSITIG.	.PGRVIFYRTGDIIGN	IRKAYCBING
CRF01_AE_T	INCTRP.TI.	.YKKKTTMG.	.PARVYHRTGDVIGD	IRKAYCQING
CRF02_AG_F	INCPRPNNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNVSR
CRF02_AG_F	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNVSR
CRF02_AG_G	INCTRPNNN.	.TRKSVRIG.	.PGQTFYATGGIIGD	IRQAHCNVSR
CRF02_AG_N	INCTRPNNN.	.TRKGVHIG.	.PGQAFYATGDIIGD	IRQAHCNVSK
CRF02_AG_S	INCTRPGNN.	.TRKSVRIG.	.PGQTFYATGDIIGD	IRQAHCNVSW
CRF02_AG_S	INCTRPSNN.	.TRKSVRIG.	.PGQTFYTTGAVIGD	IRQAHCNVSR
CRF03_AB_R	INCTRPNNNT	.RK.GIHIG.	.PGRAFYATG	DIT..G...D	IRQAHCNISI
CRF03_AB_R	INCTRPNNNT	.RK.GIHIG.	.PGRAFYATG	DII..G...D	IRQAYCNISR
CRF04_cpx	INCTRPGNNT	RKS..VHIG.	.PGLTWYATG	EII..G...D	IRQAHCNISG
CRF04_cpx	INCTGLNNNT	GGSERIGIG.	.PGHTWYATG	NIV..G...D	IRQAHCNISG
CRF04_cpx	INCTRPNNNT	RKG..VHIG.	.PGKTWFATG	EVI..G...D	IRKAHCNISE
CRF05_DF_B	INCTRPNNNT	RKS..IHLG.	.PGQAFYATG	DII..G...D	IRKAHCNVSR
CRF05_DF_B	INCTRPNNNT	RKS..IPLG.	.PGQAFYTTG	DII..G...D	IRKAHCNVSG
CRF06_cpx	IRCTRPGNNT	RKSISFGPG.	...QAFIATG	DII..GD...	IRQAHCNVSR
CRF06_cpx	ISCSRPNNT	RKSIHIGPG.	...QAFYATG	EII..GN...	IRKAHCNVSR
CRF06_cpx	IRCTRPSNNT	RKSIPLGPG.	...QAFYATG	DII..GD...	IRQAHCNVSR
CRF06_cpx	IKCTRPNNT	RKSISFAPG.	...QAFYATG	DII..GD...	IRQAHCNVSR
CRF11_cpx	INCTRPGNNT	RKSIHLGPG.	...HAFYATG	AII..GD...	IRQAHCNVSK
CRF11_cpx	INCTRPNNNT	RKGIHIGPG.	...QAFYATG	DII..GD...	IRQAHCNVSR
D_CD_84ZRO	INCTRPYKKE	.RQ.RTPIG.	.OGOALYTTR	YT....TRI	IGQAYCNISG
D_CD_ELI_K	ITCARPYQNT	.RQ.RTPIG.	.LGQSLYTTR	SR.....SI	IGQAHCNISR
D_CD_NDK_M	INCTRPYKYT	.RQ.RTSIG.	.LRQSLYTIT	GKK..KKTGY	IGQAHCNISR
D_UG_94UG1	INCIRPYNNT	.RQ.STRIG.	.PGQALFTTK	VIG.....D	IRQAHCNISG
F1_BE_VI85	INCTRPNNNT	RKG..IHLG.	.PGQTFYATG	AII..G...D	IRKAHCNISG
F1_BR_93BR	INCTRPNNNT	RKR..ISLG.	.PGRVIFYTTG	EII..G...D	IRKAHCNVSG
F1_FI_FIN9	INCTRPNNNT	RKS..IRIG.	.PGQSFYATG	EII..G...D	IRKAHCNISG
F1_FR_MP41	INCTRPNNNT	RKS..IHLG.	.PGQAFYATG	DII..G...D	IRKAHCNISE
F2_CM_MP25	INCTRPNNNT	RRS..IHIG.	.PGRAFYATG	EII..G...D	IRKAHCNISE
F2KU_BE_VI	IVCIRPGNNT	RKS..IRIG.	.PGQTFYATG	DII..G...D	IRQAHCNITG
G_BE_DRCBL	INCTRPNNNT	RRSVAIGPG.	...QAFYTTG	EVI..GD...	IRKAHCNVSW
G_NG_92NG0	INCIRPNNNT	RKSIPIGPG.	...QAFYATG	DII..GD...	IRQAHCNVSR
G_SE_SE616	INCTRPNNNT	MKRIRMGIGP	...GQTFYATG	AII..GD...	IRQAHCNVTK
H_BE_VI991	INCTRTGNNT	RKS..IRIG.	.PGQAFYATG	DII..G...D	IRRAYCNISG
H_BE_VI997	ITCTRPNNNT	RKG..IHFG.	.PGQAFYATG	DII..G...N	IRQAHCNVSE
H_CF_90CF0	ITCTRPNNNT	RTS..IHLG.	.PGRAFYATG	DII..G...D	IRQAHCNISR
J_SE_SE702	IVCTRPNNNT	RKGIHMGPG.	...QVLYATG	EII..GD...	IRKAYCNISR
J_SE_SE788	IVCYRPNNNT	RKGIHMGPG.	...QVLYATG	EII..GN...	IRETHCNISE
K_CD_EQTB1	INCTRPSNNT	RKS..IHIG.	.PGRAFYATG	DII..G...D	IRQAHCNISG
K_CM_MP535	INCTRPNNNT	RKS..IHMG.	.PGKAFYTTG	DII..G...D	IRQAHCNISG
N_CM_YBF30	INCTRPGNN.	.TGGQVQIG.	.PAMTFYNIE	K....IVGD	IRQAYCNVSK
O_CM_ANT70	MTCERP.QI.	.DIQEMRIG.	..PMAWYSMG	IGG..TAGNS	SRAAYCKYNA
O_CM_MVP51	MTCIREGIA.	.EVQDIYTG.	..PMRWRSMT	LKRSNNTSPR	SRVAYCTYNK
O_SN_99SE	MTCVRQGNQ.	.SVQEIQIG.	..PMAWYSMS	LAQE.GKPNN	SRIAYCKYNI
O_SN_99SE	MTCERPGNQ.	.TVQKILTG.	..PVAWYSMG	LKN...NLTN	SRAASCKYNS
U_CD_83C	INCTRPGSDK	KIRQSIRIG.	.PGKVFYAKGGI	TGQAHCNITD

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00BW0762_1	TKWNKTLRSRI	GEKLKEHFPN	...KTIRFN.	.SSAGGDLEI	TTHSFNCRGE
00BW0768_2	EKWNSTLQGV	REKLEKHFPN	...KNITFE.	.PSSGGDLEI	TTHSFNCRGE
00BW0874_2	QKWNKTLEQV	GKKLAEHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCRGE
00BW1471_2	SNWNSTLQOV	ARKLEKYFPN	...KTIKFO.	.PSSGGDLEI	TTHSFNCRGE
00BW1616_2	TKWENTLHMV	SEKLKENFPN	...KTIVFN.	.SSAGGDLEI	TTHSFNCRGE
00BW1686_8	SKWNETLQKV	KKKLGEHFPD	...KNITFE.	.SPSGGDLEI	TTHSFNCRGE
00BW1759_3	GEWNETLMEV	SKELRKYFPN	...KNITFA.	.PSSGGDLEI	TTHSFNCRGE
00BW1773_2	AQWNKTLQEV	GAKLEEHPN	...KTIKFN.	.QSSGGDLEI	TTHSFICRGE
00BW1783_5	KAWNKTLLHRV	SEXLKEHFPN	...KTIKFT.	.SPSGGDLEI	IQHTFNCRGE
00BW1795_6	SKWITTLHRV	SEKLKEHFPN	...KAINFT.	.QPKGGDLEI	TTHSFNCRGE
00BW1811_3	TNWNKTLQMV	SEKLQOHFPN	...KTIKFD.	.KHSGGDLEI	TTHSFNCRGE
00BW1859_5	EEWNKTLQGV	EEKLKEHFPN	...KKITFK.	.PSSGGDLEI	TTHSFNCRGE
00BW1880_2	DVWRKTLFNV	SNKLKEYFPK	...RNITFN.	.SSTGGDLEI	TTHSFNCRGE
00BW1921_1	GAWNKTLLQV	GEELRKHFPN	...KTIQFN.	.SSSGGDLEI	TTHSFNCRGE
00BW2036_1	SAWNRTLHRV	SKKLREHFPN	...TTIKFO.	.PASGGDLEI	TTHSFNCRGE
00BW2063_6	EKWNKTLYRV	SEKLKEYFPN	...KTIKFD.	.QPTGGDLEI	TKHSFNCRGE
00BW2087_2	DKWNKTLQOV	GEKLAEHFPN	...KTIKFA.	.PSSGGDLGI	TTHSFNCRGE
00BW2127_2	DAWNKTLQOV	GKKLEEYFPN	...KTIKFA.	.NSSGGDLBI	TTHSFNCRGE
00BW2128_3	EEWNKTLREV	KGKLGKHFN.	...KTIKFA.	.PSSGGDLEI	TAHSFNCRGE
00BW2276_7	NQWNKTLQV	GKKLKEHFN.	...KTIKFE.	.QSSGGDLEI	TMHSFNCRGE
00BW3819_3	KAWNKTLLQV	VKKLKEHFPN	...RTIKFT.	.PPPGGNLEI	TTHSFNCRGE
00BW3842_8	GNWTKTLQV	SRKLRQIFNK	...SNIEFK.	.PHSGGDPEI	TTHSFNCRGE
00BW3871_3	HEWNKTLQV	KKKLGEHFPN	...KTIKFO.	.PSSGGDLEI	ATHTFNCRGE
00BW3876_9	SDWNRTLQV	KKKLGEHFPN	...TVIKFE.	.PSSGGDLEI	TTHSFNCRGE
00BW3886_8	GNWTETLRRV	KKKLGEHFPN	...KTITFG.	.PSSGGDLEI	TTHSFNCRGE
00BW3891_6	STWNRTLQEV	SRKLVERFPN	...KTIRFO.	.PPSGGDLEI	TTHSFNCRGE
00BW3970_2	ADWNRTLQOV	GRKLAGEYFPN	...KTISFO.	.PSSGGDLEI	TTHSFNCRGE
00BW5031_1	TKWTETLQKI	SEKLGRGYFK.	...KTIIFA.	.PSSGGDPEI	TTHSFNCRGE
96BW01B21	EVWKKTLQV	GRKLKEHFPN	...KTIQFO.	.PPSGGDLEI	TTHSFNCRGE
96BW0407	KDWNKTLHRV	RKKLAEHFS.	...KNITFK.	.PSSGGDLEI	TTHSFNCRGE
96BW0502	TEWNSTLQGV	SKKLEEHPN	...KAICKE.	.PSSGGDLEI	TTHSFNCRGE
96BW06_J4	TNWNKTLQV	KGELRKHFH.	...KNITFO.	.PASGGDLEI	TTHSFNCRGE
96BW11_06	SQWNKTLHRV	IEKLKEHFPN	...KTIGFS.	.QAAGGDLEI	TTHSFNCRGE
96BW1210	GAWNKTLQV	GKKLKEHFPN	...KTIRFK.	.ESSGGDLEI	TTHSFNCRGE
96BW15B03	GEWNKAVQV	SAKLREHFPN	...KTIEFO.	.PSSGGDLEI	TTHSFNCRGE
96BW16_26	SEWKRTLQV	SEKLGRKHFN	...KTIKFA.	.PHSGGDLEI	TTHVLNCRGE
96BW17A09	..WNNTLQV	VKKLRKHFPN	...KTITFA.	.PPSGGDLEI	TTHSFNCRGE
96BWM01_5	SKWNKILYRV	SEKLKEHFPN	...KTIQFG.	.QPIGGDLEI	TTHSFNCRGE
96BWM03_2	GEWAKVMQV	TGKLKEHFP.	...KNITFO.	.PPSGGDLEI	TTHSFNCRGE
98BWMC12_2	QKWNKTLQV	GKKLAHYFPN	...RTIAFN.	.SSAGDLEI	ATHSFNCRGE
98BWMC13_4	SLWNKTLQV	SEKLKEYFN.	...TTIEFO.	.QPAGGDLEI	TTHSFNCRGE
98BWMC14_a	EEWNNSLQV	AKKLREHFPN	...KTIAFN.	.SSSGGDLEI	TTHSFNCRGE
98BWM014_1	GNWTKTLHRV	GEKLKEHFPN	...KTIKFA.	.PPSGGDLEI	IMHSFNCRGE
98BWM018_d	DDWKSTLQV	SEKLRRHFPN	...KTIVFN.	.SPSGGDLEI	ITHSFNCRGE
98BWM036_a	ERWNKTLQEV	GEKLREHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCRGE
98BWM037_d	KKWYKALHGV	REKLKVLFPN	...KNISFO.	.PAAGGDLEI	TTHSFNCRGE
99BW3932_1	DAWNKTLQV	GRKLKEYFPG	...STIRFA.	.PHSGGDLEI	TTHSFNCRGE
99BW4642_4	SEWNRTLQV	GEKLGRYFPN	...KTIKFN.	.SSSGGDLEI	TTHSFNCRGE
99BW4745_8	KAWNNTLQEV	GRKLAEHFPN	...KTIKFO.	.PHSGGDPEI	TMHSFTCRGE
99BW4754_7	SQWNKTLQEV	SEKLREKFPN	...KTIQFN.	.SSTGGDLEI	TTHSFNCRGE
99BWMC16_8	EAWNKTLLRV	SKKLREHFPN	...KTIIFD.	.KSSGGDLEI	TTHSFNCRGE
A2_CD_97CD	TEWNATLKKV	VEQLREHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCRGE
A2_CY_94CY	TLWNKTLQV	AEQLREKFPK	...KTIIFT.	.NSSGGDPEI	TTHSFNCRGE
A2D_97KR	RQWNKTLQV	AEQLRKYFSN	...KTIIFT.	.NSSGGDPEI	TTHSFNCRGE
A2G_CD_97C	AGWNKTLQV	AEQLGRKHFSG	...KNITFA.	.NSSGGDLEI	TTHSFNCRGE
A_BY_97BL0	AAXNSTLQKI	STQLRKYFNN	...KTIIFK.	.SSTGXDLEI	TTHSFNCRGE
A_KE_Q23_A	SRWNKTLQEV	AEKLRTYFGN	...KTIIFA.	.NSSGGDLEI	TTHSFNCRGE
A_SE_SE659	SEWNNTLQV	AKQLRTYFGN	...KTIIFT.	.NSSGGDLEI	TTHSFNCRGE
A_SE_SE725	SSWNKTLQDI	VTQLRVYWN.	...RTIIFN.	.SSSGGDLEI	TTHSFNCRGE

A_SE_SE753	SKWNATLQKV	AIKLREYFDD	...KTIIFT.	.KPSGGDLEI	TTHSFNCGGE
A_SE_SE853	AKWNKTLHEV	AKQLRITYFNN	...KTIIFT.	.NSSGGDLEI	TTHTVNCGGGE
A_SE_SE889	TEWNEALQKV	VNQLKTHFKN	...KTIIFN.	.SSSGGDLEI	TTHSFNCGGE
A_SE_UGSE8	SKWNETLKKV	AIQLRKYWN.	...TTIIFT.	.NSSGGDLEI	TTHSFNCGGE
A_UG_92UG0	SQWNKTLHQV	VEQLRKYWNN	...NTIIFN.	.SSSGGDLEI	TTHSFNCAGE
A_UG_U455_	RDWNRTIQVQ	AEQLKKKFNN	...KTIIFA.	.SSSGGDIEI	TTHSFNCGGE
AC_IN_2130	AEWNKALNKI	GKQLRKYFVN	...KTIKFA.	.NSSGGDLEI	TTHSFNCGGE
AC_RW_92RW	TKWNRTLQKV	AEKLSHYFEN	...ITTIIFK.	.NSSGGDLEI	TTHSFNCGGE
AC_SE_SE94	TKWNKTLHKV	VTQLRKYFVN	...KPIIFT.	.PSSGGDVEV	TTHSFNCRGE
ACD_SE_SE8	SEWNKTLQQV	AKKLGDPLNK	...TEIIFK.	.PPSGGDLEI	TTHSFNCGGE
ACG_BE_VI1	KEWNKTLQAV	GKKLAEYYPN	...KTINFT.	.QASGGDLEI	VTHSFNCGGE
AD_SE_SE69	TKWDKTLREV	AIQLKHYYG.	...NKTIVIFAN	.SS.GGDIEI	TTHSFNCRGE
AD_SE_SE71	SAWNNTLQQV	VIQLRRYFNN	...KTIIFT.	.NSSGGDLEI	TTHSFNCGGE
ADHK_NO_97	GSWMKTLHKV	ATQLXQHFS.	...NKTIIIFNA	.SA.GGDIEI	TTHSFNCAGE
ADK_CD_MAL	TEWDKTLQQV	AVKLGSLLN.	...KTKIIFNS	.SS.GGDPEI	TTHSFNCRGE
AG_BE_VI11	KDWGKMLQEV	SRQLKKFFNN	...KTIFFNS	.SA.GGDLEI	TTHSFNCRGE
AG_NG_92NG	QEWQEMLOKV	QAQLEQVFN.	...KSITFNS	.SA.GGDLEI	TTHSFNCRGE
AGHU_GA_VI	EQWNRTLERV	KEKLGRHFK.	...NKTITFKP	.AS.GGDPEV	TMHIFNCRGE
AGU_CD_Z32	KEWSETLSKV	AAQLRKHFVN	T.RTDIIFA.	.NSSGGDVEI	TTHSFNCGGE
AJ_BW_BW21	KNWTDTLHKV	TAKLKEYFN.	...TTIEFQP	.AS.AGDLEI	MTHTFNCGGE
B_AU_VH_AF	TNWTSLVRQI	AVKLRRERFK.	...NKTIVFNH	.SS.GGDPEI	VRHSFNCGGE
B_CN_RL42_	TKWNNTLKQI	TKKLREQFG.	...NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_DE_D31_U	AKWDSTLRQI	VKKLRERFG.	...NKTIVFNQ	.SS.GGDPEI	VTHSFNCGGE
B_DE_HAN_U	ARWNKTLNQI	FRKLREIRQF	...ENKTIVFNR	.SS.GGDPEI	VMHSFNCGGE
B_FR_HXB2_	AKWNNTLKQI	ASKLREQFG.	...NNKTIIFKQ	.SS.GGDPEI	VTHSFNCGGE
B_GA_OY1_	ATWEKTLEQI	ATKLKRQFR.	...N.KTIAFDR	.SS.GGDPEI	VMHSFNCGGE
B_GB_CAM1_	TKWNNTLKQI	VTKLKEQFG.	...NKTIIIFNQ	.SS.GGDPEI	VMHSFNCGGE
B_GB_GB8_C	EKWNNTLHQI	VIELRKQFR.	...NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_GB_MANC_	AKWEKTLKQI	VEKLREKFG.	...NKTIIIFNQ	.SS.GGDPEI	VTHSFNCGGE
B_KR_WK_AF	EKWNNTLKQI	VIKLGEQFG.	...NSNIIVFKQ	.SS.GGDPEI	VMHSFNCGGE
B_NL_3202A	AKWNNTLKQI	VSKLRKQFG.	...NKTIVFSQ	.PL.GGDPEI	VMHSFNCGGE
B_TW_TWCYS	AEWNNTLPQI	VKKFREQFG.	...NKTIVFNQ	.SS.GGDLEI	VMHSFNCGGE
B_US_BC_L0	AKWNNTLRQI	VIKLREKFG.	...ENKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_DH123	VKWHNTLKRQ	VEKLREKFE.	...NKTIVFNK	.SS.GGDPEI	VMHSFNCGGE
B_US_JRCFS	AQWNNTLKQI	VEKLREKFE.	...NNKTIVFTH	.SS.GGDPEI	VMHSFNCGGE
B_US_MNCG_	AKWNNTLRQI	VSKLKEQFK.	...NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_P896_	AKWNNTLQOI	VIKLREKFE.	...RNKTIAFNQ	.SS.GGDPEI	VMHSFNCGGE
B_US_RF_M1	AQWNNTLKQV	VTKLREKFE.	...DNKTIVFTH	.SS.GGDPEI	VLHSFNCGGE
B_US_SF2_K	AQWNNTLEQI	VKKLREQFG.	...NNKTIVFNQ	.SS.GGDPEI	VMHSFNCRGE
B_US_WEAU1	TSWNNTLKQI	VEKLREIKQF	...KNKTIVFKQ	.SS.GGDPEI	VMHSFNCGGE
B_US_WR27_	TKWKNTLEKI	VAKIREIKQF	...KNKTIVFNH	.SS.GGDPEI	VMHSFNCGGE
B_US_YU2_M	TQWENTLEQI	AIKLKEQFG.	...NNKTIIFNP	.SS.GGDPEI	VTHSFNCGGE
BF1_BR_93B	TKWNETLEKV	RAKLKPHFPN	...ATIKFNS	.SS.GGDLEI	TMHSFNCRGE
C_BR_92BR0	TAWNKTLOEV	GKKLAEHFPN	...KAIFKA.	.KHSGGDLEI	TTHSFNCRGE
C_BW_96BW0	RDWNNTLNRV	SKKLAEHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCRGE
C_BW_96BW1	SQWNNTLQV	SEKLKEHFPN	...KTIFKN.	.QPAGGDLEI	TTHSFNCGGE
C_BW_96BW1	GAWNNTLQV	GKKLKEHFPN	...KTIRFK.	.ESSGGDLEI	TTHSFNCGGE
C_BW_96BW1	GEWNKAVQV	SAKLREHFPN	...KTIEFQ.	.PSSGGDLEI	TTHSFNCRGE
C_ET_ETH22	EKWNKTLQKV	KEKLQKHFPN	...KTIEFK.	.PSSGGDLEI	TTHSFNCGGE
C_IN_93IN1	DKWNNTLQV	GKKLAEHFPN	...KTIKFA.	.SSSGGDLEI	TTHSFNCRGE
C_IN_93IN9	ENWTDTLQV	SKKLAEHFPN	...KTIKFD.	.SPSGGDLEI	TTHSFNCRGE
C_IN_93IN9	DRWNNTLQV	GEKLAEHFPN	...KTIKFA.	.PSSGGDLEI	TTHSFNCRGE
C_IN_94IN1	RDWNNTLQV	SEKLAKHFPN	...KTIKFA.	.PSSGGDLEI	TTHSFNCRGE
C_IN_95IN2	DKWNNTLQV	SKKLAEHFPN	...KTIIFN.	.SSSGGDLEI	TTHSFNCRGE
CRF01_AE_C	TKWNNTLKQV	TKKLREHFPN	...KTIIFQ.	.PSSGGDPEI	TMHFNCRGE
CRF01_AE_C	TKWKETLKQV	TRKLREHFPN	...TMTISFR	.PSSGGDPEI	TMHFNCRGE
CRF01_AE_C	TKWNNTLQV	IRKLEEHFPN	...KTIQFKP	.PSSGGDLEI	TMHFNCRGE
CRF01_AE_T	TKWNKVLQV	TEKLKEHFPN	...KTIIFQ.	.PPSGGDLEI	TMHFNCRGE
CRF01_AE_T	TKWNEVLQV	AGKLKEHFPN	...KTIIFK.	.PPSGGDLEI	TMHFNCRGE
CRF01_AE_T	TKWNKVLQV	TEKLKEHFPN	...RNISFQ.	.PPSGGDLEI	TMHFNCRGE

CRF01_AE_T	TKWNETLKQV	AGKLREHFNN	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLKQV	TEKLKEHFN.	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGE
CRF01_AE_T	TKWNKVLKQV	TEKLKEHFN.	...KTIIFQ.	.PPSGGDLEI	TMHHFNCRGG
CRF02_AG_F	SEWNRTLQOV	ATQLRKHFN.	...KTIIFA.	.NSSGGDIEI	TTHSFNCGGE
CRF02_AG_F	SKWNNTLQOV	AIQLRKHFN.	...TTIIFA.	.NPSGGDIEI	TTHSFNCGGE
CRF02_AG_G	TDWNTTLQOV	ATQLGKYFRD	T..TRIKFD.	.NPSGGDLEI	MTHSFNCGGE
CRF02_AG_N	TEWNKTLHQV	VTQLKTYFKN	...TTIIFA.	.NPLGGDVEI	TTHSFNCGGE
CRF02_AG_S	QQWNKTLHDV	ATKLREYFNN	...TTIIFD.	.EPSGGDLEI	TTHSFNCGGE
CRF02_AG_S	EKWNSTLQKV	VTKLKGHFNS	...SKIIFT.	.NSSGGDLEI	TTHSFNCGGE
CRF03_AB_R	TKWNNTLKQI	VIKLKQFG.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
CRF03_AB_R	TKWNNTLEQI	VSKLRKQFR.	..NKTIVFNQ	.SS.GGDPEI	VMHSFNCGGE
CRF04_cpx_	NDWNTDLKVI	SEELKRLFP.	..NKTIKFAP	.PV.GGDLEI	TTHSFNCKGE
CRF04_cpx_	SDWNEALQKV	VVKLREHFP.	..NKTIIFNQ	.SS.GGDLEI	TTHSFNCGGE
CRF04_cpx_	KDWNNTLQKI	VDELKHFHP.	..NKNITFAP	.SA.GGDVEI	TTHSFRLGGE
CRF05_DF_B	EQWNKTLIQV	AKELQSHFP.	..NKTIKFNS	.SS.GGDLEI	TMHSFNCRGE
CRF05_DF_B	AQWNKTLEQV	KEELRAHIK	IGNKTIVFNS	.SA.GGDLEI	TSHIFNCRGE
CRF06_cpx_	ANWTDILGEV	KVKLEEVFNN	...THITFKS	.SA.GGDLEI	TTHSFNCGGE
CRF06_cpx_	KAWNSMLQNV	TAKLKELFNN	...KNITFNS	.SA.GGDLEV	TTHSFNCGGE
CRF06_cpx_	TAWKETLQNV	TEKLKQLLN.	...TNITFNP	.SA.GGDLEI	TTHSFNCRGE
CRF06_cpx_	TDWNNMLKNV	TTKLIEVFK.	...KNITFNS	.SA.GGDLEI	TTHSFNCGGE
CRF11_cpx_	AEWLNTLQOV	ATQLRGKFN.	...KTIIFDN	.PSPGGDIEI	TSHSFNCRGE
CRF11_cpx_	ADWNTTLQOV	AEQLHNNFN.	...KTIVFNE	.HS.GGDLEV	TTHSFNCGGE
D_CD_84ZR0	VKWNNTLRQV	ARKLGNLLN.	...QTKIIFKP	.SS.GGDPEI	TTHSFNCGGE
D_CD_BLI_K	AQWSKTLQOV	ARKLGTLLN.	..KTIIKFKP	.SS.GGDPEI	TTHSFNCGGE
D_CD_NDK_M	AEWNKALQOV	ATKLGNLLN.	..KTTITFKP	.SS.GGDPEI	TSHMLNCGGD
D_UG_94UG1	AGWNKTLQOV	AEKLGNLLN.	..QTTIIFKP	.SS.GGDPEI	TTHSFNCGGE
F1_BE_VI85	TQWNNTLEYV	KAEKSHFNP	N..TAIKFNQ	.SS.GGDLEI	TMHSFNCRGE
F1_BR_93BR	TQWRNTLAKV	KAKLGSYFPN	...ATIKFNS	.SS.GGDLEI	TRHNFNCMGE
F1_FI_FIN9	EQWNKTLDRV	KAEKLHFNK	...TIQFNS	.SS.GGDLEI	TMHSFNCRGE
F1_FR_MP41	TQWSKTKTQV	QEKLRALFNKTIKFNQ	.SS.GGDLEI	TMHSFNCRGE
F2_CM_MP25	KQWYDTLIKI	ATEFKDQYN.	...KTVGFQP	.SA.CCDLEI	TTHSFNCRGE
F2KU_BE_VI	ENWNKTLQOV	KAKLHGFFTN	...KTIIIFKP	.HS.GGDPEV	VMHTFNCGGE
G_BE_DRCBL	TKWNETLRDV	QAKLQEYFIN	...KSIEFNS	.SS.GGDLEI	TTHSFNCGGE
G_NG_92NG0	IKWREMLKNV	TAQLRKIYN.	..NKNITFNS	.SA.GGDLEI	TTHSFNCRGE
G_SE_SE616	RKWKEALQNV	AAELGKIFNK	S.SENITFNS	.SA.GGDLEI	TTHSFICRGE
H_BE_VI991	KQWNETLHKV	ITKLGSYFD.	..NKTIILOP	.PA.GGDIEI	ITHSFNCGGE
H_BE_VI997	EKWNKTLQOI	ATQLSKYFV.	..NRTLIFKP	.HS.GGDLEV	TTHSFNCRGE
H_CF_90CF0	TDWNKTLHQV	VTQLGIHLN.	..NRTISFKP	.NS.GGDMEV	RTHSFNCRGE
J_SE_SE702	KDWNNTLRRV	AKKLREHFN.	...KTIDFTS	.PS.GGDIEI	TTHSFNCGGE
J_SE_SE788	RDWSNTLRRV	ATKLREHFN.	...KTINFTS	.PS.GGDIEI	VTHSFNCGGE
K_CD_EQTB1	GQWNKTVNQV	KKELGKHFN.	...KTIIFQP	.SS.GGDPOV	TRHIFNCRGE
K_CM_MP535	EKWNMTLSRV	KEKLKEHFNK	...GTITFKP	.PNPGGDPEI	LTHMFNCAGE
N_CM_YBF30	ELWEPMMWRT	REEIKILGK	..NNITFRA	RERNEGDLEV	THLMFNCRGE
O_CM_ANT70	TDWGKILKQT	AERYLELVNN	TGSINMTFN.	.HSSGGDLEV	THLHFNCHGE
O_CM_MVP51	TVWENALQQT	AIRYLNVLVNO	TENVTIIFS.	.RTSGGDAEV	SHLHFNCHGE
O_SN_99SE	SDWEKALKQT	AERYLDLRNN	TNTVNITFE.	.RSIGGDSEV	THLHFNCHGE
O_SN_99SE	SVWEEALKQT	AERYLELMNN	TNTVNITFN.	.HSTGGDPEV	THLHFNCHGE
U_CD_83C	GEWRNTLQOV	AIALRRQFNN	...KSIIFN.	.SSSGGDIEI	THTFNCGGE

451		500
00BW0762_1	FFYCNTTRLF NGTYN.....	STGD TNS.....TN STITLQCRK
00BW0768_2	FFYCDTSNLF NKTRR.....	DN.....AN ETITLPCRIK
00BW0874_2	FFYCNTSRLF NSTYN.....	PNST YIEGR...SN ATITLQCRK
00BW1471_2	FFYCYTTKLF NSTYN.....	STYT GSESN.....ITIPCRK
00BW1616_2	FFYCNTSKLF NGTYN.....	SNNN TA.....DITLQCRK
00BW1686_8	FFYCNTSNLS NETYL.....	ANLT SNVTK...N ATITLPCRIK
00BW1759_3	FFYCNTSNLF NNTYR.....	ADNN ITNDNSN...ITLQCRK
00BW1773_2	FFYCNTSALF NSTYN.....	STNT SGHN...DT RIITLPCRIK
00BW1783_5	FFYCNTSKLF NGTYN.....	GTS...ISS...N SSITLQCRK
00BW1795_6	FFYCNTSELF NGTYN.....	STG...DSN...S NLITLQCRK
00BW1811_3	FFYCNTSQLF NGTYM.....	PNTY MS...SSDN RNITIPCRK
00BW1859_5	FFYCNTTHLF NGNG.....ESD INITLPCRIK
00BW1880_2	FFYCDTTKLF NGTYN.....	STEQ TN.....STITLQCRK
00BW1921_1	FFYCNTSQLF NGTYN.....	DT.Y ESNSG...N STITLPCRIK
00BW2036_1	FFYCDTSKLF NSSYN.....	DTL YSYNS...T ANITLPCRLK
00BW2063_6	FFYCNTSQLF NSSYS.....	RHN...NTS...N STITLPCNIK
00BW2087_2	FFYCNTSGLF N.....	GTF NGT...HSTN TNITLPCRIK
00BW2127_2	FFYCNTTILF NSTYY.....	P...NTK...SDTT ETITLPCRIK
00BW2128_3	FFYCNTSLLF DETQL.....	SKE.....N NTINIQCRIK
00BW2276_7	FFYCNTSKLF NGTYM.....	PNYN TSN...SSNN SNITLPCRIK
00BW3819_3	FFYCNTSGLF NGTYN.....	G...TND...NDTD SDITLPCRIK
00BW3842_8	FFYCNTSLLF NSSYN.....	GNSS YNDTGS...N STITLQCRK
00BW3871_3	FFYCNTSILF NDTYW.....	FNGT ANDTG...S NNITIPCRK
00BW3876_9	FFYCNTSGLF NNNLI.....	NNG.....AE DTIRLPCRIK
00BW3886_8	FFYCNTSKLF NSTNN.....	NTE...SES...N ATITLPCRIK
00BW3891_6	FFYCNISRLF NRPNM.....	TKNM TSDIKNN...STITLPCRIK
00BW3970_2	FFYCNTSSLF NNTYR.....	PTYW PGTE...SN STITLQCRK
00BW5031_1	FFYCNTSQLF NSTYR.....	ANTS NS.....NITLPCRIK
96BW01B21	FFYCDTSELF NSTYM.....	SNGG NISS.....S TIIMLPCRIE
96BW0407	FFYCNTSRLF NESYN.....	FDES YWN.N...TN KTIMLPCRIK
96BW0502	FFYCDTSOLF NSTYS.....	PSNG TENK...LN GTITITCRK
96BW06_J4	FFYCNTSRLF DETYL.....	S...GTDED...N GTITLPCRIK
96BW11_06	FFYCNTSKLF NSTYI.....	QLN...STETP...N STITLPCRIK
96BW1210	FFYCNTSQLF NSTYN.....Y MPS...NNTG TNITLQCRK
96BW15B03	FFYCNSKLL NSSYN.....	GTSY RGTESN...S SIITLPCRIK
96BW16_26	FFYCNTSKLF NSTYN.....	STDR SNN.....T DNITIQCRK
96BW17A09	FFYCNTSILF NSTYN.....	STYT GSDSNS....TITIPCRK
96BWMO1_5	FIYCNTSKLF NGTYN.....	STG...TS...N STITLSCRIK
96BWMO3_2	FFYCNTSELF NGTYN.....	GTD...NNS...N KTITLLCRIK
98BWMC12_2	FFYCNTSGLF NSTYN.....	PNST YTESK...AN SNITLHCRIK
98BWMC13_4	FFYCNTTKLF NGTYS.....	QPN...STGTP...H SNITLPCRIK
98BWMC14_a	FFYCNTSQLF NSTYN.....	G...RNSTT...N ATITLPCRIK
98BWMO14_1	FFYCNTSKLF NSTYN.....	ATY NST...DTSN STITIPCRK
98BWMO18_d	FFYCNTSGLF NS.....	AFNDN...SG GTITLQCRIE
98BWMO36_a	FFYCNTSGLF NSTYY.....	SNKT SSN...MTN EIITIPCKIK
98BWMO37_d	FFYCNTSKLF NTSWL.....	DSYI SNTG...NN SIITLPCRIK
99BW3932_1	FFYCNTSRLF NSTYN.....	P...NTK...SNTG SWIILPCRIK
99BW4642_4	FFYCNTSKLF TYQSN.....	TY...VAN STITLPCRIK
99BW4745_8	FFYCNTSELF NSTYN.....	ANTY NTATGNNS..TTIILPCRIK
99BW4754_7	FFYCNTSKLF NSTFN.....	SNGH DST....GN DPLTIPCRK
99BWMC16_8	FFYCNTSNLF NNTYY.....	PNMT NTDTK...SN LTITLPCRIK
A2_CD_97CD	FFYCNTTGLF NSTWEN.....	GTNK QNYTE...SN DTITLQCRK
A2_CY_94CY	FFYCNTTGLF NGTWNN.....	GTWN GPYTPNN.TN GSIIILPCRIK
A2D_97KR	FFYCDTSGLF NSTWPAN...	ASRE NEEKD...R.NVTLPCRIK
A2G_CD_97C	FFYCNTTNLF NSTFNTT...	SLFN STGRNGTNDN TTITIPCRK
A_BY_97BL0	FFYCNTTDLF NSTX.....	DGTVT NSTKAN....GTITLPCRIK
A_KE_Q23_A	FFYCNTSGLF NSTWY.....	VNSTW NDTSDTQESN DTITLPCRIK
A_SE_SE659	FFYCNTSSLF NSTWS.....	NDNNT QGSNSTET.K GTITLPCRIK
A_SE_SE725	FFYCNTSGLF NSTWS.....	Q.NDT GVSNSTES.N DTIILPCRIK

A_SE_SE753	FFYCNTSGLF	NSTIL.....NSTKM	NDNASRESYD	DTITLQCRIC
A_SE_SE853	FFYCNTSGLF	NSTWS.....SNASE	PMSNSTES.N	DTITLQCRIR
A_SE_SE889	FFYCNTSGLF	NSTWN.....GTDSM	QKLNST....	GNITLPCRIK
A_SE_UGSE8	FFYCNTSGLF	NSSWN.....END.T	KVNYNTES.N	DTITLQCRIC
A_UG_92UG0	FFYCNTSGLF	NSTWV.....NGTTS	STSN.....	GTITLPCRIK
A_UG_U455_	FFYCNTSGLF	NSIWN.....GSMNS	DMGP.....N	GTITLQCRIC
AC_IN_2130	FFYCNTSGLF	NGTWNASMQ.ES	NSTESN....	ETIILPCRIK
AC_RW_92RW	FFYCNTSGLF	NSTWS.....KR	NGTWQSNSTE	LNITLPCRIK
AC_SE_SE94	FFYCDTSGLF	NSTWPFNS..T	NSTGPN....	GTITLQCRIC
ACD_SE_SB8	FFYCNTSGLF	NSTWV.....NGSRE	SNSTDN....	DTITLPCRIK
ACG_BE_VI1	FFYCNTSGLF	NSTYN.....PSYN	STESVN...E	TTIILPCKIK
AD_SE_SE69	FFYCNTTGLF	NSTWNDTAT.EQKPN..	DTIRLQCRIC
AD_SE_SE71	FFYCNTSGLF	NSTWN.....NTDSM	QESHSTET.N	DTITLPCRIK
ADHK_NO_97	FFYCNTSQLF	NSTWNHTST.YNST	EN.....	GTITLPCRIK
ADK_CD_MAL	FFYCNTSKLF	NSTWQNGA.RLSN	S..TE.ST..	GSITLPCRIK
AG_BE_VI11	FFYCNTSALF	NFSSETNST.FP.N.....	TTTLTPCRIK
AG_NG_92NG	FFYCNTSGLF	NESGGNDT..TITLPCRIK
AGHU_GA_VI	FFYCNTTKLF	NDTENKN...NDAEN...	KTITLPCRIK
AGU_CD_Z32	FFYCNTSGLF	NSTWK.....NSTSI	NDTVSN....	GTITLPCRIK
AJ_BW_BW21	FFYCNTSGLF	NKSLNETS.NETT	DGAN.....	NTITLTCRIK
B_AU_VH_AF	FFYCNTSQLF	NSTWFNSTG.NDTE	RATNN..T..	ENITLPCRIK
B_CN_RL42_	FFYCNTSQLF	NSTWNDTG..T	WNDTTGNS..	.TITLPCRIK
B_DE_D31_U	FFYCNSAQLF	NSTWNDTK..ES	NNTNG.....	.TITLPCRIK
B_DE_HAN_U	FFYCNTSKLF	NSTWNNTST.WN..	DNGND.....	.TITLPCRIK
B_FR_HXB2_	FFYCNTSQLF	NSTWFNSTW.STEG	SNNTGSD..	.TITLPCRIK
B_GA_OYI_	FFYCNTSQLF	NSTWNDTTR.AN..	.STEV.....	.TITLPCRIK
B_GB_CAM1_	FFYCNTTQLF	NTTWLFNGT.WNDT	EGLNNTER..	.NITLPCRIK
B_GB_GB8_C	FFYCKTAQLF	NSTWNSTGN.GTIK	SNTTE.....	.IITLPCRIK
B_GB_MANC_	FFYCNTSQLF	NSTWNTGND.TRES	NDTNN..T..	GNITLPCRIK
B_KR_WK_AF	FFYCNTTQLS	NSTWQRS DG.TWRN	TGGLNETK..	ENITLPCRIK
B_NL_3202A	FFYCNTSQLF	NSTWNDTGN.VTER	SNNNE.....	.NITLPCRIK
B_TW_TWCYS	FFYCNTATPLF	NSTWNATST.LNAT	NEENE.....	.NITLLCRIK
B_US_BC_L0	FFYCKSTQLF	NSTWAGNNT.WNSS	AERSDDTG..	GNITLPCRIK
B_US_DH123	FFYCNTKKLF	NSTWNGTEG.SYNI	EGND.....	.TITLPCRIK
B_US_JRCSF	FFYCNTSQLF	NSTWNDTEK.SSG.	TEGND.....	.TITLPCRIK
B_US_MNCG_	FFYCNTSPLF	NSTWNGNNT.WNNT	TGSNN.....	.NITLQCKIK
B_US_P896_	FFYCNTAQLF	NSTWNVITGG.TNG.	TEGND.....	.IITLQCRIC
B_US_RF_M1	FFYCNTTQLF	NSTWNSTEG.SNNT	GGND.....	.TITLPCRIK
B_US_SF2_K	FFYCNTTQLF	NNTWRLNHT.EG..	TKGND.....	.TITLPCRIK
B_US_WEAU1	FFYCNTSQLF	NSTWHANGT.WKNT	EGADN.....	.NITLPCRIK
B_US_WR27_	FFYCNTSQLF	NSTWNSTEG.NS..	TWSDK.....	.IIRLPCRIK
B_US_YU2_M	FFYCNTSQLF	..TWNDTRK.LN..	.NTGR.....	.NITLPCRIK
BF1_BR_93B	FFYCNTSGLF	NDTVDN....	GTITLPCRIK
C_BR_92BR0	FFYCNTSSLF	NSTYT.....PNST	ENITGT..EN	SIITIPCRIK
C_BW_96BW0	FFYCNTSRLF	NESYS.....FNES	HWSND...TN	ATITLPCRIK
C_BW_96BW1	FFYCNTSKLF	NGTYI.....QPNS	.TEDTP...N	STITLPCRIK
C_BW_96BW1	FFYCNTSQLF	NSTYN.....S.TY	MPS...NNTG	TNITLQCRIC
C_BW_96BW1	FFYCNSKLL	NSSYN.....GTSY	RGTESN...S	SIITLPCRIK
C_ET_ETH22	FFYCNTSNLF	NSTKL.....E...	LFNSS...TN	LNITLQCRIC
C_IN_93IN1	FFYCNTSGLF	NGTYM.....PTYM	PNGTESN.SN	STITIPCRIK
C_IN_93IN9	FFYCNTSGLF	NGTYN.....TSSD	GNS.....S	STITIPCRIK
C_IN_93IN9	FFYCNTSSLF	DSLFN.....PNGT	RNDT....N	LTITIPCRIK
C_IN_94IN1	FFYCNTSGLF	NSTYM.....SGTY	MNSSADM.NS	SYITIPCRIK
C_IN_95IN2	FFYCNTSGLF	NRTYM.....PNDT	KSNSSSN.PN	ANITIPCRIK
CRF01_AE_C	FFYCNTTKLF	NSTWT.....TNE	IMEEFKGTNS	STITLPCRIK
CRF01_AE_C	FFYCNTTALF	NSTWI.....N.G	TMQEVNGTNS	GNITLPCRIK
CRF01_AE_C	FFYCNTTRLF	N.....ISTNGTTN	GTITLPCRIK
CRF01_AE_T	FFYCNTTQLF	NNTCI.....GNE	TMK...GCNG	.TITLPCRIK
CRF01_AE_T	FFYCNTTQLF	NSTWT.....GNE	TME...GSNG	.TITLPCRIK
CRF01_AE_T	FFYCNTTRLF	NNTCI.....GNK	TMK...ECND	.TITLPCRIK

CRF01_AE_T	FFYCNTTKLF	NSTWI.....GNE	TIG....SSG	.NIILPCRIK
CRF01_AE_T	FFYCNTTKLF	NNTCL.....GNE	TMA...GCND	.TITLPCRIK
CRF01_AE_T	FFYCNTTKLF	NSTWR.....GNE	TIESREGYNK	.TIILPCRIK
CRF02_AG_F	FFYCNTSELF	NSTW.....	..NSTWDNSS	NHIESNHT.E	GNITLQCRIC
CRF02_AG_F	FFYCNTSELF	N.....	..STWDNSL	NHTESNHT.E	DNITLQCRIC
CRF02_AG_G	FFYCNTSGLF	NSTWYKN...	..STWYSNST	ASSNHTEL.N	STITLQCRIC
CRF02_AG_N	FFYCNTSKLF	N.....	..STWDNSN	STANHTGS.N	DTITLQCRIC
CRF02_AG_S	FFYCNTSNLF	NRTWNHNGTW	NAPGPFNDTE	DKTINGTE.D	KTITLQCRIC
CRF02_AG_S	FFYCNTABLF	NSTWASN...	.TNGIWASNI	NASNKDA.N	DTITLKCKIK
CRF03_AB_R	FFYCNTTKLF	NSTWNGTEE.LN..	.NTEG.....	DIVTLPCRIK
CRF03_AB_R	FFYCNTTKLF	NSTWNNTTEE.SN..	.NTKG.....	DIVTLPCRIK
CRF04_cpx	FFYCNTTPLF	NSTHMONGT.NIT.	S.TDSTN...	STITLQCRIC
CRF04_cpx	FFYCNTSGLF	NSTYMFNST.NRTN	T.TNGTN...	STITLPCRIK
CRF04_cpx	FFYCNTSDLF	NRTYMVNKN.ETNS	T.NTTDE...	KIIRLPCRIK
CRF05_DF_B	FFYCDTSKLF	NATVFNDTV.FNAT	MFNND...SD	KNIIILPCRIK
CRF05_DF_B	FFYCNTSGLF	NVTVP.....NNE.....TITLPCRIK
CRF06_cpx	FFYCNTSNLF	NTSDLFNTS.R..G	NDTN.....	TTITLPCRIK
CRF06_cpx	FFYCNTSQLF	NNNITDSNE.T.....	TNFTLPCRIK
CRF06_cpx	FFYCNTSQLF	NSSIPESE.T.....	DIITLPCRIK
CRF06_cpx	FFYCNTSQLF	NSSNLNNS.	SDNN.....	GTITLPCRIN
CRF11_cpx	FFYCNTSGLF	NNTWLFNST.WNSS	QELNGT...E	PNITLPCRIK
CRF11_cpx	FFYCNTSGLF	NSTWYANDN.TSTQ	NDMQSN...D	.TITLPCRIK
D_CD_84ZR0	FFYCNTSGLF	NSAWNISGH.STGL	N.....D..	TIITIPCRIC
D_CD_BLI_K	FFYCNTSGLF	NSTWNISAW.NNIT	ESNNS.TN..	TNITLQCRIC
D_CD_NDK_M	FFYCNTSRLF	NSTWNQTN.TGFNN..	GTVTLPCRIK
D_UG_94UG1	FFYCNTTRLF	NSTWKRNS.EWSR	D..NT.PD..	ETITLQCRIC
F1_BE_VI85	FFYCDTSGLF	NDTGSN....N	GTITLPCRIK
F1_BR_93BR	FFYCNTDELF	NDTKFND...TG...FN	GTITLPCRIK
F1_FI_PIN9	FFYCNTSLLF	NNTVFN....N	GTITLPCRIK
F1_FR_MP41	FFYCDTSGLF	NESEKY....N	GTIILPCRIK
F2_CM_MP25	FFYCNTTILF	NHTRVNDIL.SNNH	TR.....EN	DTITLPCRIK
F2KU_BE_VI	FFYCNTTRLF	NDTLNHT...ID	QNITLPCRIK
G_BE_DRCBL	FFYCNTSGLF	NNSILKSNI.SENN	DTITLNCKIK
G_NG_92NG0	FFYCNTSGLF	NNNISNIN.N.....	ETITLPCRIK
G_SE_SE616	FFYCNTSGLF	NSSLLRSNS.	SE.N.....	GTITLPCRIK
H_BE_VI991	FFYCNTTKLF	NSTWTNSSY.TNDT	YNSNSTEDIT	GNITLQCRIC
H_BE_VI997	FFYCNTSGLF	NSSWTGDNI.NMPN	DTG.....	KNITLPCRIK
H_CF_90CF0	FFYCNTSGLF	NSSWEMHTN.YTSN	DTKG...N..	BNITLPCRIK
J_SE_SE702	FFYCNTSTLF	NSSWDENNI.KDTN	STNDN....	TTITIPCKIK
J_SE_SE788	FLYCNTSKLF	NSSWDKNSI.EATN	DTSX.....	ATITIPCKIK
K_CD_EQTB1	FSYCDTDTV	DDTEEE....ED	TTITIPCRIC
K_CM_MP535	FFYCNTTKLF	NETGE.....N	GTITLPCRIK
N_CM_YBF30	FFYCNTSKLF	NEELN....ETG.	EPITLPCRIR
O_CM_ANT70	FFYCNTAKMF	NYTFS.....CNGTTC	SVSNVSQ.G.	NNGTLPCRLR
O_CM_MVP51	FFYCNTSGMF	NYTFIN....CTKSGC	QEIKGSNETN	KNGTIPCKLR
O_SN_99SE	FFYCNTSKMF	NYTFS.....CIGTNC	TSNQNSSNS.	NDTRIYCRIC
O_SN_99SE	FFYCNTSQMF	NYTFS.....CTRNC	IRQSNSS...	INGTISCRIC
U_CD_83C	FFYCNTSELF	TGIWNG....TWDK	NCTSTESNCT	GNITLPCRIK

00BW0762_1	501	QIINMWQGVG	KAMYAPPIAG	NIICKSNITG	LLLTRDGGEB	N.....TTE	550
00BW0768_2		QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGKT	ED....NKSE	
00BW0874_2		QIINLWQEVG	RAIYAPPIAG	NITCKSNITG	LLLTRD.GG.	NNS....TTE	
00BW1471_2		QIINMWQGVG	QAMYAPPIAG	NITCRSNITG	LLLTRDGGIN	...EDDNTE	
00BW1616_2		QIINLWQGVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGGE	N.....NSTE	
00BW1686_8		QIINMWQEVG	RAIYAPPIAG	KITCISNITG	TLLTRDGGVS	NTTE...GNE	
00BW1759_3		QIINMWQEVG	RAMYAPPIEG	NITCNSSITG	LLLTRDGGKN	S...TNNGTE	
00BW1773_2		QIINMWQKVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGNT	S.....STEE	
00BW1783_5		QIINMWQGVG	QAIYAPPIAG	NITCKSNITG	LLLTRDGG..	NN...TENTE	
00BW1795_6		QIINMWQKVG	RAMYAPPIEG	NITCISNITG	LLLTRDGG..	YE...ANHTE	
00BW1811_3		QIINLWQEVG	RAMYAPPIAG	NITCKSNITG	LLLTRDGGGS	NTTN...ATE	
00BW1859_5		QIINMWQEVG	RAMYAPPIAG	NITCKSKITG	LLLTRDGGKQNESK	
00BW1880_2		QIINMWQGVG	RAMYAPPIEG	NITCNSNITG	LLLTRNRGRE	NGD...NTTE	
00BW1921_1		QIINMWQGVG	RAIYAPPIEG	NITCKSNITG	LLLTRDGGKG	NDT....AE	
00BW2036_1		QIINMWQKVG	RGIYAPPIEG	SITCNSNITG	LLLVRDGG..	IN...TSTVE	
00BW2063_6		QIINMWQGVG	RAMYAPPIAG	NITCTSNTG	LILTRDGGG.	NE...TNETE	
00BW2087_2		QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	ILLTRDGGED	TKN....KTE	
00BW2127_2		QIVNMWQGVG	RAIYAPPIAG	NITCNSSITG	LLLLRDGGTE	TENN...RTE	
00BW2128_3		QIINLWQEVG	RAMYAPPIEG	NITCKSNITG	LLLTRDGGTN	..N...NTE	
00BW2276_7		QIINMWQGVG	RAIYASPIEG	SITCKSNITG	LLLVDHGG..	NSNT...STE	
00BW3819_3		QIINMWQEVG	RAIYAPPIAG	NITCTSNTG	LLLTRDGEPS	TE.....	
00BW3842_8		QVINMWQRVG	QAIYAPPIEG	IITCNSSITG	LLLVRDGD..	NQ...TSDTE	
00BW3871_3		QIINMWQEVG	RAIYAPPIRG	IITCTSNTG	LLLTRDGGNT	GGN....TTE	
00BW3876_9		QIINMWQEVG	RAMYAPPIAG	NITCTSNTG	LLLTRDGG.N	GG...NTE	
00BW3886_8		QFIRMWQRVG	QAMYAPPIAG	NITCRSNITG	LLLTRDG...KNDTE	
00BW3891_6		QIINMWQGVG	RAMYAPPIAG	RIICKSNITG	LLLVRDGGQD	N...VMNATE	
00BW3970_2		QIINMWQKVG	RAIYAPPIAG	KITCKSNITG	LLLVRDGGGG	NN....TATE	
00BW5031_1		QIINMWQGVG	RAMYAPPIAG	NIICKSNITG	VLLTYDGGEE	N.....E	
96BW01B21		QIINMWQGVG	RAMYAPPIKG	SITCRSNITG	LLLTRDGGLN	RS...TEEPE	
96BW0407		QIINMWQGVG	RAIYAPPIAG	NITCVSNITG	LLLTWDGGHQ	SN.....E	
96BW0502		QIINMWQKVG	RAMYAPPIAG	NLTCESDITG	LLLTRDGGKT	G....PNDTE	
96BW06_J4		QIINMWQEVG	RAIYAPPIAG	NITCKSNITG	LLLTRDGGLN	NDS.....E	
96BW11_06		QFINLWQEVG	RAMYAPPIAG	NIICKSNITG	LLLTRDG...	.D...KNDSE	
96BW1210		QIINRWQEVG	RAMFAPPIAG	NITCKSNITG	ILLVRDGGNT	SEN.....IE	
96BW15B03		QIINMWQKVG	RAIYAPPIEG	NITCSSSITG	LLLRDGG..	LD...NVTE	
96BW16_26		QIINMWQGVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGTE	ENN...TGTE	
96BW17A09		QIINMWQGXG	QAMYVPPIAC	NITCRSNITG	LLLTRDGGK.	...VTGNTTE	
96BWM01_5		QIINMWQGVG	RAMYASPIAG	NITCKSNITG	LLLTRDGG..	NE...TSGIE	
96BWM03_2		QIINTWQEVG	RAIYAPPIAG	NIICISNITG	LLLTRDGGKT	ND...TNDTE	
98BWMC12_2		QIINMWQEVG	RAMYAPPIAG	NITCRSNITG	LLLTRD.GGN	TTE....TKE	
98BWMC13_4		QIINMWQGVG	RAMYAPPIAG	NITCISNITG	LILTRDGG..	VN...RSDTE	
98BWMC14_a		QIINMWQEVG	RAIYAPPIKG	NITCESNITG	LLLTRDGGSN	DTT.....E	
98BWM014_1		QIINMWQGVG	QAMYAPPIAG	NITCKSNITG	ILLTRDGGIN	NTN....GTE	
98BWM018_d		QIINMWQKVG	RAIYAPPIAG	NITCSSRITG	LLLTRDGGKNDTHE	
98BWM036_a		QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGNN	NTT.....E	
98BWM037_d		QIINMWQKVG	RAMYANPIEG	NITCRSNITG	LLLENDG...	N.....M	
99BW3932_1		QIINMWQKVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGTA	TD.....E	
99BW4642_4		QIINMWQEVG	RAMYAPPIAG	NITCQSNITG	LLLTRDGGTE	TD...NKTE	
99BW4745_8		QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGGK	N...ATNDTE	
99BW4754_7		QIINMWQEVG	RAMYAPPIAG	RIICNSTITG	LILTRDGGNT	N.....NTE	
99BWMC16_8		QIINRWQEVG	RAMYAPPIAG	NITCTSNTG	LLLVRDGGRT	SD....STKE	
A2_CD_97CD		QIINMWQRVG	RAMYAPPIAG	VIKTSNITG	MILTRDG..G	KNS....INE	
A2_CY_94CY		QIINMWQRVG	RAMYAPPIAG	IIKTSNITG	IILTRDG..G	NNG....TNE	
A2D_97KR		QIVNMWQRVG	RAMYAPPING	TIKTSNITG	MILTRDGNNG	GNA....TNE	
A2G_CD_97C		QIINMWQRVG	RAMYAPPIAG	IINCTSNITG	IILTRDGEKG	GDN....TIE	
A_BY_97BL0		QIINMWQRVG	QAMYAXPIKX	SIRCESNITG	LLLTRDGXGX	TXN....SNE	
A_KE_Q23_A		QIINMWQRVG	QAMYAPPIPG	VIKCESNITG	LLLTRDGGKD	NN....VNE	
A_SE_SE659		QIINMWQRVG	KAMYAPPIQG	VIRCESNITG	LILTRDG.GD	AG.....ENE	
A_SE_SE725		QIINMWQRVG	QAIYAPPIPG	IIRCESNITG	LLLTRDG.GV	VNS....TNE	

A_SE_SE753	QIINMWQVRG	QAMYAPPIRG	AIRCKSNITG	LLLTRDGGNS	NSS....TNE
A_SE_SE853	QIINMWQRAG	KAIYAPPIPG	IIKCVSNITG	LILTRDG.GS	NNS....TNE
A_SE_SE889	QIINMWQRAG	QAIYAPPIQG	VIRCESNITG	LILTRDG.GN	DNN....ESE
A_SE_UGSE8	QIINMWQRTG	QATYAPPIPG	VIQCRSNITG	LLLTRDGGVT	NNT....NNE
A_UG_92UG0	QIINMWQVRG	QAMYAPPIQG	VIKCESNITG	LILTRDG.GV	NSS....DSE
A_UG_U455_	QIINMWQVRG	QAMYAPPIQG	VIRCESNITG	LLLTRDG.GT	NNT....KNE
AC_IN_2130	QIINMWQVRG	QAMYAPPIQG	IIKCVSNITG	LILTRDGK.S	SNS....TDE
AC_RW_92RW	QIINMWQRTG	QAMYAPPIQG	VISCVSNITG	LLLTRDG.GN	NNT....TTE
AC_SE_SE94	QIIRMWQRTG	QAIYAPPIPG	EINCVSNITG	LLLTRDG..G	NNI....TNE
ACD_SE_SE8	QIINMWQVRG	QAMYALPIRG	VIRCESNITG	LILTRDG.GN	NTS....TNE
ACG_BE_VI1	QIINMWQEVG	RAMYANPIAG	NITCNSNITG	LLLTRDGGVN	ET....TETE
AD_SE_SE69	QIINMWQRAG	RAIYAPPIQG	VINCVSDITG	LILTRDGGVN	.NT.N....E
AD_SE_SE71	QIINMWQVRG	QAMYAPPIQG	VIKCTSNITG	LILTRDG.GG	NNS....INA
ADHK_NO_97	QIVNMWQVRG	QAMYAPPIKG	NITCVSNITG	LILTIDXG..	.N.MSAENF
ADK_CD_MAL	QIINMWQKTG	KAMYAPPIAG	VINCLSNITG	LILTRDGGNS	.SD.NS.DNE
AG_BE_VI11	QIVRMWQVRG	QAMYAPPIAG	KITCRSNITG	LILTRDGGNP	N....NTNNE
AG_NG_92NG	QIVRMWQVRG	QAMYAPPIAG	DITCRSNITG	LLLTRDGGVN	N....TGNE
AGHU_GA_VI	QIVNMWQVRG	RAMYAPPIAG	NITCRSNITG	IILTRDGG..	.SN.NESTNE
AGU_CD_Z32	QIVNMWQVRG	QAMYAPPIKG	VIKCESNITG	ILLTRDGVG.	NNT....ANE
AJ_BW_BW21	QIVRMWQVRG	QAIYAPPIAG	NITCTSNITG	LLLTRDGGYT	.N.NTNGTE
B_AU_VH_AF	QIINMWQKVG	KAMYAPPING	QIRCSSNITG	LILTRDGGNQENKTE
B_CN_RL42_	QIVNMWQEVG	KAMYAPPIEG	QIRCSSNITG	LLLTRDGGNN	.E..S.KPTE
B_DE_D31_U	QIINMWQEVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGKN	.K..D.NETE
B_DE_HAN_U	QIINMWQEVG	KAMYAPPIGG	LIRCSSNITG	LILTRDGGND	.N..S.STTE
B_FR_HXB2_	QIINMWQKVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGNS	.N..N..ESE
B_GA_OYI_	QIVNMWQEVG	KAMYAPPISG	QIRCSSKITG	LLLTRDGGKNTTNGIE
B_GB_CAM1_	QIINRWQEVG	KAMYAPPITG	TISCSSNITG	LLLTRDGGRG	.E..N..ETE
B_GB_GB8_C	QIVNMWQEVG	KAMYAPPITG	QIRCASHITG	LLLTRDGGRE	.N..NTNETE
B_GB_MANC_	QILNLWQEVG	KAMYAPPISG	QISCSSNITG	LLLTRDGGNT	.NT.TGNTTE
B_KR_WK_AF	QIINRWQEVG	KAMYAPPISG	LIRCSSNITG	LLLTRDGGNE	.NN.GTNGTE
B_NL_3202A	QIINMWQGVG	KAMYAPPISG	QIRCSSNITG	LLLTRDGGKD	.E..NKTCTE
B_TW_TWCYS	QIINMWQVRG	KAMYAPPIEG	LIKCSSNITG	LMLTRDGGTN	.D....SEVE
B_US_BC_L0	QIINMWQEVG	KAMYAPPISG	QIRCTSNITG	LLLTRDGGTS	.D..T.NTTE
B_US_DH123	QIINMWQEVG	KAMYAPPISG	QIWCSSNITG	LLLTRDGGKNSSTE
B_US_JRCSF	QIINMWQEVG	KAMYAPPIKG	QIRCSSNITG	LLLTRDGGK.NESEIE
B_US_MNCG_	QIINMWQEVG	KAMYAPPIEG	QIRCSSNITG	LLLTRDGGKD	.T..DTNDTE
B_US_P896_	QIINMWQKVG	KAMYAPPITG	QIRCSSNITG	LLLTRDGGNSTETETE
B_US_RF_M1	QIVNMWQEVG	KAMYAPPISG	QIKCISNITG	LLLTRDGGED	.T..T.NTTE
B_US_SF2_K	QIINMWQEVG	KAMYAPPIGG	QISCSSNITG	LLLTRDGGTN	.V..T.NDTE
B_US_WEAU1	QIINRWQEVG	KAMYAPPIEG	QIRCLSNITG	LLLTRDGGSS	.E..E.NQTE
B_US_WR27_	QIINMWQEVG	KAMYAPPIDG	QIRCSSNITG	LLLTRDGGN.SNETTE
B_US_YU2_M	QIINMWQEVG	KAMYAPPIRG	QIRCSSNITG	LLLTRDGGK.DTNGTE
BF1_BR_93B	QIVNMWQEVG	RAMYAAPPIAG	NITCSSNITG	LLLTRDGG..	Q...NNQTEE
C_BR_92BR0	QIINMWQGVG	RAMYAPPIEG	ILTCRSNITG	LLLTRDGGTGMHDTE
C_BW_96BW0	QIINMWQGVG	RAIYAPPIAG	NITCISNITG	LLLTRDGGTT	RNN....BSE
C_BW_96BW1	QFINLWQEVG	RAMYAPPIAG	NIICKSNITG	LLLTRDG...	.D...KNDSE
C_BW_96BW1	QIINRWQEVG	RAMFAPPIAG	NITCKSNITG	ILLVRDGGNT	SEN....IE
C_BW_96BW1	QIINMWQKVG	RAIYAPPIEG	NITCSSSITG	LLLRDGG..	LD...NVTTE
C_ET_ETH22	QIINMWQGVG	RAMYAPPIEG	IIMCRSNITG	LLLTRDGAKE	PH...STKE
C_IN_93IN1	QIINMWQEVG	RAMYAPPIAG	NITCTSNITG	LLLVRDGGIK	EN.DTENKTE
C_IN_93IN9	QIINMWQEVG	RAMYAPPIEG	NITCKSNITG	LLLVRDGGAE	AK...TNNTE
C_IN_93IN9	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	LLLVRDGGRG	ND..TENNTE
C_IN_94IN1	QIINMWQEVG	RAMYAPPIAG	NITCKSNITG	ILLERDG..G	SG...SNGTE
C_IN_95IN2	QIINMWQEVG	RAMYAPPIEG	KITCRSNITG	LLLVRDGGED	KNNTEKNTE
CRF01_AE_C	QVNMWQEVG	KAMYAPPISE	AVNCVSNITG	IILTRDGGNA	TNET.....
CRF01_AE_C	QIVNMWQEVG	RAMYAPPISE	VINCVSNITG	ILLTRDGGIN	QNQTNK...NE
CRF01_AE_C	QVIKMWQEVG	QAMYAPPIDE	AINCVSNITG	ILLVRDGGKI	ENET....IE
CRF01_AE_T	QIINMWQGTG	QAMYAPPIDG	KINCVSNITG	ILLTRDGG..	ANNTS...NE
CRF01_AE_T	QIIRMWQGAG	QAMYAPPISG	IINCVSNITG	ILLTRDGGG.	ANNTN...NE
CRF01_AE_T	QIINMWQGVG	QAMYNPPISG	NINCVSNITG	ILLTRDGGGG	NGTNN...BE

CRF01_AE_T	QIINMWQEVG	QAMYAPPITG	KINCVSNITG	ILLTRDGG..	ANNKS...SE
CRF01_AE_T	QIINMWQAG	QAMYAPPISG	RINCVSNITG	ILLTRDGG..	VNNTD...NE
CRF01_AE_T	QIINMWQAG	QAMYAPPING	TINCISNITG	ILLTRDGGD.	NNNTI...NE
CRF02_AG_F	QIVNMWQKVG	LAMYAPPISG	EIRCKSNITG	LLLTRDGG.S	NNS....TNE
CRF02_AG_F	QIVNMWQKVG	RAMYAPPPIG	EIRCESNITG	LLLTRDGG.S	NNS....TNE
CRF02_AG_G	QIINMWQKVG	QAMYAPPIQG	VIRCDSNITG	LLLTRDGG.S	NNN....TPE
CRF02_AG_N	QIVNMWQKVG	QAMYAPPIQG	IIRCDSNITG	LLLTRDGG.G	NNS....TNE
CRF02_AG_S	QIVRMWQKVG	QAMYAPPPIG	EIRCESNITG	LLLTRDGG.GN	DNN....NTE
CRF02_AG_S	QIINMWQKVG	QAIYAPPIEG	VIRCDSNITG	ILLTRDGG.GD	NTN....GDE
CRF03_AB_R	QIINMWQEVG	KARYAPPIAG	QIRCSSNITG	LLLTRDGGNQ	.S....NVTE
CRF03_AB_R	QIINMWQEVG	KAMYAPPIAG	QIRCSSNITG	LLLTRDGGNQ	.N....NVTE
CRF04_cpx_	QFVRMWQEVG	QAMYASPIAG	SINCSSDITG	IILTRDGG...GTNNT
CRF04_cpx_	QIVRMWQGVG	QAMYAPPIAG	SINCSSDITG	IILTRDGGIS	NNN.ETNDNE
CRF04_cpx_	QIVNRWQEVG	QAIYAPPLQG	SLTATQVITG	IILTRDGG..	.NR.SDTGNE
CRF05_DF_B	QIVRMWQGVG	QAMYAAPPIAG	NIACNSTITG	ILLARDGGNG	.ND.SSNDTE
CRF05_DF_B	QIINMWQGVG	QAMYAAPPIAG	NITCNSNITG	ILLTRDGG..G	.VN.ITNDTE
CRF06_cpx_	QIVRMWQRVG	QAMYAPPIAG	NITCVSNITG	IILTRDGG.N	EN....VSE
CRF06_cpx_	QIVRMWQVA	QAMYAPPIAG	NIICTSNITG	LLLTRDGGRN	DS....NSE
CRF06_cpx_	QIVRMWQRVG	QAIYAPPIAG	NITCISNITG	LLLTRDGG.N	NT....TSE
CRF06_cpx_	QIIRMWQRVG	QAMYAPPIAG	NITCTSNITG	LLLTRDGGH.N	D.....TE
CRF11_cpx_	QIVRMWQRVG	QAMYAPPIQG	EIRCDSNITG	LLLTRDGG..LNSTNE
CRF11_cpx_	QIINMWQEVG	QAVYAPPIQG	ELRCDSNITG	LLLTRDGGEG	.N.DTIGKE
D_CD_84ZR0	QIINMWQEVG	KAMYAPPIEG	QINCSSNITG	LLLTRDGGAN	.NT.Q...ND
D_CD_ELI_K	QIIKMWQAG.	.AIYAPPIER	NILCSSNITG	LLLTRDGGIN	.NS.T...NE
D_CD_NDK_M	QIVNLWQRVG	KAMYAPPIEG	LIKCSSNITG	LLLTRDGGAN	.NS.S...HE
D_UG_94UG1	QIINMWQEVG	KAMYAPPIEG	FINCSSNITG	LLLTRDGGAI	.NS.SQ..NE
F1_BE_VI85	QIVNMWQVCV	RAMYTSPPIAG	NITCNSNITG	LLLTRDGG..NESNIE
F1_BR_93BR	QIVNMWQEVG	RAMYANPIAG	NITCNSNITG	LLLTRDGG..LNSTNE
F1_FI_FIN9	QFVNMWQEVG	RAMYAAPPIAG	NITCNSNITG	LLLTRDGG..	QS..NNSDSE
F1_FR_MP41	QIINMWQGVG	QAMYSAPIAG	RINCNSTITG	LLLTRDGG..	QSN.DTNRTE
F2_CM_MP25	QIVNMWQRVG	QAMYAPPIAG	KIQCNSNITG	LLLTIDGG..EGNESE
F2KU_BE_VI	QIINRWQGVG	QAMYAPPIAG	NITCRSNITG	MILTRDGGNS	N...DTIDNE
G_BE_DRCBL	QIVRMWQRVG	QAMYAPPIAG	NITCRSNITG	LILTRDGGDN	N....STSE
G_NG_92NG0	QIVRMWQKVG	QAMYALPIAG	NLVCKSNITG	LILTRDGGNN	N....DSTEE
G_SE_SE616	QIVRMWQRVG	QAMYAPPIAG	NIECNSSITG	LILTRDGGNN	NNT.NTSESE
H_BE_VI991	QIVNMWQRVG	QAMYAPPIRG	NITCISNITG	LILTFD....	..R.NNTNNV
H_BE_VI997	QIVNMWQRVG	QAMYAPPIKG	SITCVSNITG	LILTYDED..	..K.GNNDNV
H_CF_90CF0	QIVNMWQRVG	RAMYAPPIQG	NIMCVSNITG	LILTIDEG..	..N.ASAENY
J_SE_SE702	QIVRMWQRTG	QAIYAPPIAG	NITCKSNITG	LLLTRDGGNR	.NG.SENGTE
J_SE_SE788	QIVRMWQRTG	QAIYAPPIAG	NITCTSNITG	LLLTRDGGNR	GNG.SENGTE
K_CD_EQTB1	QIINMWQKVG	QAIYAPPTAG	NITCRSNITG	MILTRDGGND	N...NTRTEE
K_CM_MP535	QIINMWQKVG	KAIYAPPIAG	SINCSSNITG	MILTRDGGNNTHNE
N_CM_YBF30	QIVNLWTRVG	KGIYAPPIRG	VLNCTSNITG	LVLEYSGGPDTKET
O_CM_ANT70	QVVRSWIRGQ	SGLYAPPIKG	NLTCSNITG	MILQMDNTWN	SSNN....NV
O_CM_MVP51	QLVRSWMKGE	SRIYAPPIPG	NLTCHSNITG	MILQLDQPN	STGE....N
O_SN_99SE_	QVVRSWIQGG	SGLYAPPRKG	NLTCSNITG	MILQLDMPWN	STNNS...NA
O_SN_99SE_	QVVRSWIQGG	YLTCSNITG	MILQLDKTWN	RTNNS...ES	
U_CD___83C	QVVRTWQGVG	QAMYAPPIEG	TIRCSSNITG	LLLTRDGGNG	N....ATQNE

551

600

00BW0762_1	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGI	APTSAKRRVV	EREKR.....
00BW0768_2	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
00BW0874_2	IFRPQGGNMK	DNWRSELYKY	KVVEVKPLGV	APTKAKRRVV	EREKR.....
00BW1471_2	IFRPGGGNMR	DNWRSELYKY	KVVEIKPLGV	APNKAKRRVV	EREK.R....
00BW1616_2	TFRPAGGEMR	DNWRSELYKY	KVVEVKPLGI	APTEAKRRVV	QREKR.....
00BW1686_8	TFRPGGGDMR	NNWRSELYKY	KVVEIRPLGV	APTEARRRVV	EREK.R....
00BW1759_3	IFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTKAQRVV	KREKR.....
00BW1773_2	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW1783_5	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTSAKRRVV	EREK.R....
00BW1795_6	IFRPIGGDMR	DNWRSELYKY	KVVEIKPLGL	APTESKRRVV	EREK.R....
00BW1811_3	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGL	APTEAKRRVV	EREK.R....
00BW1859_5	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGL	APTGAQRVV	EREK.R....
00BW1880_2	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREKR.....
00BW1921_1	IFRPEGGDMK	NNWRSELYKY	KVVEIRPLGV	APTKAKRRVV	EREK.....
00BW2036_1	TFRPEGGNMR	DNWRSELYKY	KVVEIKPLGV	APTEAQRVV	EKQK.R....
00BW2063_6	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
00BW2087_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW2127_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
00BW2128_3	TFRPVGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	KREK.R....
00BW2276_7	IFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTEAKRRVV	EREK.R....
00BW3819_3	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTGAQRVV	EREK.R....
00BW3842_8	TFRPQGGEMR	DNWRSELYKY	KVVEIKPLGV	APTTAKRRVV	EREK.R....
00BW3871_3	IFRPEGGDMR	NNWRSELYKY	KVVEIKPLGI	APTGAQRVV	EREK.R....
00BW3876_9	TFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
00BW3886_8	TFRPGGGNMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
00BW3891_6	TFRPGCGDMR	DNWRSELYKY	KVVEIKPLGV	APTSAKRRVV	EREK.....
00BW3970_2	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGI	APTGAQRVV	GREK.R....
00BW5031_1	TFRPAGGNMK	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.....
96BW01B21	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGV	APTGAQRVV	EREK.R....
96BW0407	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEARRRVV	EREKR.....
96BW0502	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
96BW06_J4	TFRPIGGEMR	NNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW11_06	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
96BW1210	TFRPGGGNMK	DNWRSELYKY	KVVEVKPLGI	APTRAKRRVV	EREK.R....
96BW15B03	IFRPQGGDMK	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
96BW16_26	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
96BW17A09	TFRPGGGNMR	DNWRSELYKY	KVVEVKPLGV	APTAQRVV	EREK.R....
96BWM01_5	IFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKSKRRVV	GREK.R....
96BWM03_2	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
98BWMC12_2	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTEAKRRVV	ERGKR.....
98BWMC13_4	IFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
98BWMC14_a	TFRPEGGDMR	NNWRSELYKY	KVVEIRPLGI	APTGAQRVV	NREK.R....
98BWM014_1	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGI	APTKAQRVV	EREK.R....
98BWM018_d	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGV	APSEAKRRVV	EREK.....
98BWM036_a	TFRPGGGNMK	DNWRSELYKY	KVVEIKPLGI	APTGAQRVV	EREK.R....
98BWM037_d	TFRPGGGDMK	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
99BW3932_1	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREK.R....
99BW4642_4	TFRPGGGDMR	DSWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
99BW4745_8	IFRPEGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	DKEK.....
99BW4754_7	IFRPIGGNMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREKR.....
99BWMC16_8	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEAKRRVV	EREKR.....
A2_CD_97CD	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTEARRRVV	QREK.R....
A2_CY_94CY	TFRPGGDMR	DNWRSELYKY	KVVKLEPLGV	APTRAKRRVV	EREK.R....
A2D_97KR	TFRPGGGDMR	DNWRSELYKY	KVVKLEPLGV	APTRARRRVV	EREK.....
A2G_CD_97C	VFRPVGGDMR	DNWRSELYKY	KVVKIKPLGI	APTRARRRVV	EKEK.R....
A_BY_97BL0	TFRPIXGDXR	NNWRSELYKY	KVVKIEPIXV	APTRAKRRXX	EREK.R....
A_KE_Q23_A	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRAKRRVV	EREK.R....
A_SE_SE659	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTQARRRVV	KREK.R....
A_SE_SE725	TFRPGGGNMK	DNWRSELYKY	KVVKIEPLGV	APTRARRRVV	QREK.R....

A_SE_SE753	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_SE853	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_SE889	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R....
A_SE_UGSE8	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAQRVV	KREK.R....
A_UG_92UG0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	EREK.R....
A_UG_U455_	TFRPGGGDMR	DNWKSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
AC_IN_2130	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRARRAV	GREK.R....
AC_RW_92RW	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
AC_SE_SE94	TFRPGGGDMQ	DNWRSELYKY	KVVQIEPLGV	APTKARRRVV	EREK.R....
ACD_SE_SE8	TIRPAGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	EREK.R....
ACG_BE_VI1	IFRPGGGNMK	DNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R....
AD_SE_SE69	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R...V
AD_SE_SE71	TFRPGGGDMR	DNWRSELYKY	KVVKIEPVGI	APNRAKRRVV	EREK.R....
ADHK_NO_97	TFRPGGGDMR	DNWRSELYKY	KVVXXXPLGV	APTXARRRVV	QREK.R....
ADK_CD_MAL	TLRPGGGDMR	DNWISELYKY	KVVRIEPLGV	APTKAKRRVV	EREK.R...A
AG_BE_VI11	TFRPGGGDMR	DNWRSELYQY	KVVKIKSLGV	APTKARRRVV	EREK.R...A
AG_NG_92NG	TFRPGGGDMR	DNWRSELYKY	KIVKIKPLGI	APTKARRRVV	ERGK.R...A
AGHU_GA_VI	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRARRRVV	EREK.R...A
AGU_CD_Z32	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	AREK.R....
AJ_BW_BW21	IFTPTGRNMR	DNWRSELYKY	KVVKIEPIGV	APTRAKRRVV	GREK.R...A
B_AU_VH_AF	IFRPGGGDMR	DNWRSELYKY	KVVRIEPLGV	APTKAKRRVV	QREK.R...A
B_CN_RL42_	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	QREK.R...A
B_DE_D31_U	TFRPGGGNMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_DE_HAN_U	IFRPGGGNMR	DNWRNELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_FR_HXB2_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GA_OYI_	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKARRRVV	QREK.R...A
B_GB_CAM1_	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GB_GB8_C	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_GB_MANC_	TFRPGGGNMR	DNWRSELYKY	KVVKVEPLGI	APTKAKRRVV	QREK.R...A
B_KR_WK_AF	TFRPEGGNMK	DNWRSKLYKY	KVVRIEPLGI	APTRARRRVV	QREK.R...A
B_NL_3202A	IFRPGGGDMK	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	QREK.R...A
B_TW_TWCYS	VFRPGGGDMK	DIWRNELYKY	KVVKVEPLGL	APTRARRRVV	QREK.R...A
B_US_BC_L0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTTAKRRVV	QREK.R...A
B_US_DH123	IFRPGGGDMR	DNWRSELYKY	KVVVEPLGI	APTKAKRRVV	QREK.R...A
B_US_JRCSF	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R....
B_US_MNCG_	IFRPGGGDMR	DNWRSELYKY	KVVTIEPLGV	APTKAKRRVV	QREK.R....
B_US_P896_	IFRPGGGDMR	DNWRSELYKY	KVVRIEPIGV	APTRAKRRTV	QREK.R....
B_US_RF_M1	IFRLGGGNMR	DNWRSELYKY	KVVRIEPLGV	APTRAKRRVV	QREK.R...A
B_US_SF2_K	VFRPGGGDMR	DNWRSELYKY	KVIEKIEPLGI	APTKAKRRVV	QREK.R...A
B_US_WEAU1	IFRPGGGNMK	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
B_US_WR27_	IFRPGGGDMR	DNWRSXLYKY	KVVXIEPLGV	APTKXKRRVX	XREK.R...X
B_US_YU2_M	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
BF1_BR_93B	TFRPGGGNMK	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	KREK.R...A
C_BR_92BR0	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGI	APTKAKRRVV	EREK.R....
C_BW_96BW0	IFGPGGGDMR	DNWRSELYKY	KVVEIKPLGI	APTEARRRVV	EREKR....
C_BW_96BW1	TFRPAGGDMR	DNWRSELYKY	KVVEIKPLGL	APTKAKRRVV	EREK.R....
C_BW_96BW1	TFRPGGGNMK	DNWRSELYKY	KVVEVKPLGI	APTRAKRRVV	EREK.R....
C_BW_96BW1	IFRPGGGDMK	DNWRNELYKY	KVVEIKPLGV	APTEAKRRVV	EREK.R....
C_ET_BTH22	IFRPEGGDMR	DNWRSELYKY	KVVEIKPLGV	APTKPKRRVV	EREK.R....
C_IN_93IN1	IFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTAARRRVV	EREK.R....
C_IN_93IN9	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTTAKRRVV	EREK.R....
C_IN_93IN9	IFRPGGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREKRA....
C_IN_94IN1	TFRPGGGDMR	NNWRSELYKY	KVVEIQPLGV	APTEAKRRVV	ERGK.R....
C_IN_95IN2	TFRPGGGDMR	DNWRSELYKY	KVVEVKPLGV	APTTAKRRVV	EREK.R....
CRF01_AE_C	.FRPGGGNMK	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	EREK.R....
CRF01_AE_C	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTKARRRVV	EREK.R....
CRF01_AE_C	TFRPGGGNMK	DNWRSELYKY	KVVQIEPLGV	APTGAARRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPEGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNMK	DNWRNELYKY	KVVEIEPLGI	APTKAKRRVV	EREK.R....

CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVEIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APTRAKRRVV	EREK.R....
CRF01_AE_T	TFRPGGGNIK	DNWRSELYKY	KVVQIEPLGI	APSKAKRRVV	EREK.R....
CRF02_AG_F	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRPKRRVV	EREK.R....
CRF02_AG_F	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTHAKRRVV	EREK.R....
CRF02_AG_G	IFRPGGGNMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
CRF02_AG_N	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....
CRF02_AG_S	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APSHAKRRVV	EREKRA....
CRF02_AG_S	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APSHAKRRVV	EREK.R....
CRF03_AB_R	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	QREK.R...A
CRF03_AB_R	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	QREK.R...A
CRF04_cpx	IFRPGGGDMR	DNWRSELYKY	KVVKIEPIGV	APNKARRRVV	QREK.....
CRF04_cpx	TLRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTGARRRVV	QKEK.R....
CRF04_cpx	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGV	APTRARRRVV	QREK.R....
CRF05_DF_B	IFRPGGGDMR	DNWRSELYKY	KVVEIQPLGI	APTRAKRQVV	KREK.R...A
CRF05_DF_B	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRAKRQVV	QREK.R...A
CRF06_cpx	TFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTWARRRVV	GREK.R...A
CRF06_cpx	TFRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTRARRRVV	GKEKRA...V
CRF06_cpx	IIRPGGGDMR	DNWRSELYKY	KVVKIKPLGI	APTEARRRVV	GREK.R...A
CRF06_cpx	IFRPGGGNMR	DNWRSELYKY	KVVKIKPLGI	APTKARRRVV	GREKRA...V
CRF11_cpx	TFRPGGGDMR	DNWRSELYKY	KVVEIKPLGV	APTRAKRRVV	EREK.R...A
CRF11_cpx	TFRPTGGDMR	NNWRSELYKY	KVVEIKPLGV	APTKAKRRVV	EREK.R...A
D_CD_84ZR0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRRVV	EREK.R...A
D_CD_ELI_K	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGV	APTRAKRRVV	EREK.R...A
D_CD_NDK_M	TFRPGGGDMR	DNWRSELYKY	KVVKIEPIGV	APTKARRRVV	EREK.R...A
D_UG_94UG1	TFRPGGGDMR	NNWRSELYKY	KVVKIEPIGL	APTKARRRVV	EREK.R...A
F1_BE_VI85	TFRPGGGNMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	QREK.R...A
F1_BR_93BR	TFRPGGGNMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRQVV	KRER.R...A
F1_FI_FIN9	TFRPGGGDMR	DNWRSELYKY	KVVEIEPLGV	APTRPKRPVV	RER.R...A
F1_FR_MP41	TFRPGGGNMR	DNWRSELYKY	KVVEIEPLGV	APTKARRRVV	QREK.R...A
F2_CM_MP25	TLRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKAKRQVV	QREK.R...A
F2KU_BE_VI	TFRPGGGNMR	DNWRSELYKY	KVVKIEPLGI	APTKARRRVV	QREK.R...G
G_BE_DRCBL	IFRPGGGDMR	NNWRSELYKY	KTVKIKSLGI	APTRARRRVV	EREK.R...A
G_NG_92NG0	TFRPGGGDMR	DNWRSELYKY	KTVKIKSLGV	APTRARRRVV	EREK.R...A
G_SE_SE616	IFRPGGGDMR	DNWRSELYKY	KTVKIKSLGV	APTRARRRVV	EREK.R...A
H_BE_VI991	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTEARRRVV	EREK.R....
H_BE_VI997	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTEARRRVV	EREK.R....
H_CF_90CF0	TFRPGGGDMR	DNWRSELYKY	KVVKIEPLGI	APTKTRRRVV	EREK.R....
J_SE_SE702	TFRPTGGNMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRRVV	EREK.R...A
J_SE_SE788	TFRPTGGNMR	DNWRSELYKY	KVVEIEPLGV	APTKAKRRVV	EREK.R...A
K_CD_EQTB1	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	QREK.R...A
K_CM_MP535	TFRPGGGDMR	DNWRSELYKY	KVVQIEPLGI	APTRARRRVV	QREK.R...A
N_CM_YBF30	IVYPSGGNMV	NLWRQELYKY	KVVSIEPIGV	APGKAKRRTV	SREK.R...A
O_CM_ANT70	TFRPIGGDMK	DIWRTBLFNY	KVVRVKPFSV	APTARIARPI	STRTHR.EKR
O_CM_MVP51	TLRPVGGDMK	DIWRTKLYNY	KVVQIKPFSV	APTMSRPII	NIHTPHREKR
O_SN_99SE	TFRPTGGDMK	DIWRTBLFKY	KVVVKPFSV	APTARIARPI	GTGTQR.EKR
O_SN_99SE	TFRPIGGDMK	DIWRTBLFKY	KVVKIKPFSV	APTARIARPI	GTGTRR.EKR
U_CD_83C	TFRPGGGDMK	DNWRSELYKY	KVVKIEPLGV	APTRAKRRVV	EREK.R....

601					650
00BW0762_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLMVQ	ARQLLSGIVQ	QQNNLLRAIE
00BW0768_2	AVGIGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQVLSGIVQ	QQSNLLRAIE
00BW0874_2	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1471_2	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLMRAIE
00BW1616_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
00BW1686_8	AVGIGAVLLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1759_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1773_2	AVGIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1783_5	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1795_6	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQNNLLRAIE
00BW1811_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW1859_5	AVGIGAVFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLKAIE
00BW1880_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQVLSGIVQ	QQSNLLRAIE
00BW1921_1	RAALGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW2036_1	AVGMGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
00BW2063_6	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW2087_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW2127_2	AVGMGAVILG	.FLGAAGSTM	GAASITLTVQ	TKQLLSGIVQ	QQSNLLKAIE
00BW2128_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ	QQNNLLRAIK
00BW2276_7	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3819_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLFGIVQ	QQSNLLRAIE
00BW3842_8	AVGMGAMILG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3871_3	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3876_9	AVEIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3886_8	AVGIGAVILG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3891_6	RAAIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
00BW3970_2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARKLLSGIVQ	QQSNLLRAIE
00BW5031_1	RAALGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
96BW01B21	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW0407	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW0502	AVGIGAVCLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW06_J4	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARLLLSGIVQ	QQNNLLRAIE
96BW11_06	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	AKQLLSGIVQ	QQSNLLKAIE
96BW1210	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW15B03	AVGIGAVIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW16_26	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BW17A09	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLQAIE
96BWM01_5	AVTFGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
96BWM03_2	AVGIGAVLLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QQSNLLRAIE
98BWM012_2	AAGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQVLSGIVQ	QQSNLLRAIE
98BWM013_4	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
98BWM014_a	AVGVAAVFLG	.FLSAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QQSNLLRAIE
98BWM014_1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQSLSGIVQ	QQSNLLRAIE
98BWM018_d	RAALGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
98BWM036_a	AVTLGAMFLG	.FLGAAGSTM	GAASITLTVQ	TRKLLSGIVQ	QQSNLLKAIE
98BWM037_d	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
99BW3932_1	AVGLGAVFLG	.FLGAAGSTM	GAASITLMVQ	ARQLLSGIVQ	QQSNLLRAIE
99BW4642_4	AVGIGAVLLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQNNLLRAIE
99BW4745_8	RAIAGAVFLG	.FLGVAGSTM	GAASVALTVQ	ARQLLSGIVQ	QQSNLLRAIE
99BW4754_7	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
99BWM016_8	AVTIGAMFLG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
A2_CD_97CD	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLRAIE
A2_CY_94CY	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLTGIVQ	QQSNLLKAIE
A2D_97KR	RAAVGLFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLQAIE
A2G_CD_97C	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE
A_BY_97BL0	AIGLXAAFLX	.FLGAAXSTX	GAASMTLTVQ	ARQLLSGIVQ	QQNNLLKAIE
A_KE_Q23_A	AVGIGAVFLG	.FLGAAGSTM	GATSITLTVQ	ARQLLSGIVQ	QQSNLLXAIX
A_SE_SE659	AVGLGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVR	QQNNLLRAIE
A_SE_SE725	AVGLGALFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQSNLLKAIE

A_SE_SE753	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
A_SE_SE853	AIGIGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSXIVQ	QOSNLLRAIE
A_SE_SE889	AIGIGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLMAIE
A_SE_UGSE8	AVGLAAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
A_UG_92UG0	AVTLGAVFIG	.FLGTAGSTM	GAASITLTVQ	ARKLLSGIVQ	QOSNLLRAIE
A_UG_U455	AVGLGAIFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
AC_IN_2130	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
AC_RW_92RW	AVGLGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
AC_SE_SE94	AVGMGAVFIG	.FLGAAGSTM	GAASVTLTVQ	ARQLLSGIVR	QOSNLLRAIE
ACD_SE_SE8	AVGIGAVFLG	.FLGAAGSAM	GAAAATLTVQ	ARQLLSGIVQ	QOSNLLKAIE
ACG_BE_VI1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
AD_SE_SE69	AG.LGAVFIG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLKAIE
AD_SE_SE71	AVGIGVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
ADHK_NO_97	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLKAIQ
ADK_CD_MAL	IG.LGAMFLG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QONNLLRAIE
AG_BE_VI11	VGLG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLRAIE
AG_NG_92NG	VGLG.AVFLG	.FLGAAGSTM	GAGSITLTVQ	VRQLLSGIVQ	QOSNLLRAIE
AGHU_GA_VI	IVGVGAVFLG	.FLGVAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLKAIE
AGU_CD_Z32	AIGMGAFLLG	.FLGAAGSTM	GAASITLTVH	VRQLLSGIVQ	QOSNLLRAIE
AJ_BW_BW21	VGIMGAMFLG	.FLGTAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLKAIE
B_AU_VH_AF	VGMIGAMILG	.FLGAAGSTM	GAASLTLTVQ	TRQLLSGIVQ	QONNLLRAIE
B_CN_RL42	VGTIGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QQRNLLRAIE
B_DE_D31_U	VGLLGAVFLG	.FLGAAGSTM	GARSMALTVQ	ARQLLSGIVQ	QONNLLRAIE
B_DE_HAN_U	VGMLGAMFLG	.FLGAAGSTM	GARSLTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_FR_HXB2	VG.IGALFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_GA_OYI	VGMLGAMFLG	.FLGAAGSTM	GARSMTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_GB_CAM1	VGAIGALFLG	.FLGAAGSTM	GAVALTLTVQ	TRQLLSGIVQ	QONNLLRAIE
B_GB_GBB_C	VGMIGAMFLG	.FLGAAGSTM	GAASLTLTVQ	ARLLLSGIVQ	QONNLLRAIE
B_GB_MANC	VGMLGAMFLG	.FLGAAGSTM	GARSITLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_KR_WK_AF	VT.FGALFLG	.FLGAAGSTM	GCTSMTLTVQ	ARLLLSGIVQ	QONNLLRAIE
B_NL_3202A	VG.IGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_TW_TWCYS	VG.IGALFLG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_US_BC_L0	VG.IGALFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_US_DH123	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_US_JRCSF	AVGIGALFLG	.FLGAAGSTM	GARSMTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_US_MNCG	RAAIGALFLG	.FLGAAGSTM	GAASVTLTVQ	ARLLLSGIVQ	QONNLLRAIE
B_US_P896	AVGIGAVFLG	.FLGAAGSTM	GAASVTLTVQ	ARLLLSGIVQ	QONNLLRAIE
B_US_RF_M1	VGTIGAMFLG	.FLGAAGSTM	GAGSITLTVQ	ARHLLSGIVQ	QONNLLRAIE
B_US_SF2_K	VGIVGAMFLG	.FLGAAGSTM	GAVALTLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_US_WBAU1	VGMLGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARLLLSGIVQ	QONNLLRAIE
B_US_WR27	VGIVGVMFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
B_US_YU2_M	VG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
BF1_BR_93B	VG.MGALFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QONNLLRAIE
C_BR_92BR0	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLRAIE
C_BW_96BW0	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
C_BW_96BW1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARRLLSGIVQ	QOSNLLRAIE
C_BW_96BW1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
C_BW_96BW1	AVGIGAVIFC	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QOSNLLRAIE
C_ET_ETH22	RAALGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLKAIE
C_IN_93IN1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTAQ	ARQLLSGIVQ	QOSNLLRAIE
C_IN_93IN9	AVGIGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
C_IN_93IN9	VVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
C_IN_94IN1	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
C_IN_95IN2	AVGIGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASLTLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF01_AE_C	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRTIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE

CRF01_AE_T	AVGIGALIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
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CRF01_AE_T	AVGIGAMIFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF02_AG_F	AVGLGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
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CRF02_AG_S	LVGLGAFFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLKAIE
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CRF03_AB_R	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
CRF03_AB_R	VG.IGAVFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
CRF04_cpx	AVGIGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF04_cpx	AVGLGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF04_cpx	AVGIGAVFPG	LFLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
CRF05_DF_B	MG.IGAMFLG	.FLAAAGSTM	GAASIALTVQ	ARQLLSGIVQ	QONNLLQAIE
CRF05_DF_B	VG.VGALLIG	.FLGAAGSTM	GAASMTLTVQ	ARQLLSGIVQ	QONNLLQAIE
CRF06_cpx	VGLG.AMFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLRAIE
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CRF11_cpx	VGIG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLKAIE
CRF11_cpx	VGIG.AVLLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLKAIE
D_CD_84ZR0	IG.LGAMFLG	.FLGAAGSTM	GAASMTLTVQ	ARQVLSGIVQ	QONNLLRAIE
D_CD_ELI_K	IG.LGAMFLG	.FLGAAGSTM	GARSVTLTVQ	ARQLMSGIVQ	QONNLLRAIE
D_CD_NDK_M	IG.LGAVFLG	.FLGAAGSTM	GAASVTLTVQ	ARQLMSGIVH	QONNLLRAIE
D_UG_94UG1	IG.LGALFLG	.FLGTAGSTM	GAVSLTLTVQ	ARQVLSGIVQ	QONNLLRAIE
F1_BE_VI85	AG.LGALFLG	.FLGDSREHM	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
F1_BR_93BR	VG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
F1_FI_FIN9	VA.IGAVFLG	.FLSAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QONNLLQAIE
F1_FR_MP41	VG.IGALFLR	.FLGAAGSNI	GAASITLTVQ	ARQLLSGIVQ	QONNLLRAIE
F2_CM_MP25	VG.MGAMFLG	.FLGAAGSTM	GAASITLTVQ	ARNLLSGIVQ	QOSNLLKAIE
F2KU_BE_VI	AG.LGALFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSDLLRAIE
G_BE_DRCBL	VGVG.AIFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLRAIE
G_NG_92NG0	VGLG.AVFLG	.FLGAAGSTM	GAASITLTAQ	VRQLLSGIVQ	QOSNLLRAIE
G_SE_SE616	VGLG.AVFLG	.FLGAAGSTM	GAASITLTVQ	VRQLLSGIVQ	QONNLLRAIE
H_BE_VI991	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIQ
H_BE_VI997	AVGMGAFFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIQ
H_CF_90CF0	AVGMGASFLG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIQ
J_SE_SE702	VGIG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLKAIX
J_SE_SE788	VGIG.AVFLG	.FLGTAGSTM	GAASITLTVQ	VRQLLSGIVQ	QOSNLLKAIE
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K_CM_MP535	VG.LGAVFFG	.FLGAAGSTM	GAASITLTVQ	ARQLLSGIVQ	QOSNLLRAIE
N_CM_YBF30	AFGLGALFLG	.FLGAAGSTM	GAASITLTVQ	ARTLLSGIVQ	QONILLRAIE
O_CM_ANT70	AVGLGMLFLG	.VLSAAGSTM	GAAATTLAVQ	THTLLKGIVQ	QODNLLRAIQ
O_CM_MVP51	AVGLGMLFLG	.VLSAAGSTM	GAAATALTVR	THSVLKGIVQ	QODNLLRAIQ
O_SN_99SE	AVGLGMLFLG	.VLSAAGSTM	GAAATALAVQ	TQSLMKGIVQ	QODNLLRAIQ
O_SN_99SE	AVGLGMLFLG	.VLSAAGSTM	GAAATTLAVQ	THTLMKGIVQ	QODNLLRAIQ
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00BW1759_3	AQQHMLQLTV	WGINQLQTRV	LAIERYLKDQ	QLLGIWGCSG
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00BW1783_5	AQQHMLQLTV	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG
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96BW06_J4	AQQHMLQLTV	WGIKQLQTKV	LAIERYLKDQ	QLLGFWGCSG
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99BWMC16_8	AQQHMLQLTV	WGIKQLQTRV	LAIERYLKDQ	QLLGIWGYSG
A2_CD_97CD	AQQQMLRLTV	WGIKQLQARV	LALERYLQDQ	QLLGIWGCSG
A2_CY_94CY	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG
A2D_97KR	AQQHMLRLTV	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG
A2G_CD_97C	AQQHLLKLTV	WGIKQLQARV	LALERYLQDQ	QLLGLWGCSG
A_BY_97BL0	AQQXLLKLTV	XGIKQLQARX	LAVEXYLKQ	QXLRXGCSX
A_KE_Q23_A	AQQHLLKLTV	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG
A_SE_SE659	AQQHLLKLTV	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG
A_SE_SE725	AQQHLLKLTV	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG

A_SE_SE753	VQQHLLKLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
A_SE_SE853	AQQHLLKLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
A_SE_SE889	AQQHLLKLT	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTTVPW
A_SE_UGSE8	AQQHMLRLT	WGIKQLQARV	MAVERYLKDQ	QLLGIWGCSG	KIICTTAVPW
A_UG_92UG0	AQQHLLKLT	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICPTNVPW
A_UG_U455	AQQHLLKLT	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTTVPW
AC_IN_2130	AQQHLLKLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AC_RW_92RW	AQQHLLKLT	WGIKQLQARV	LALERYLRDQ	QLLGIWGCSG	KLICTTNVPW
AC_SE_SE94	AQQHLLKLT	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KIICTTNVPW
ACD_SE_SE8	AQQHLLKLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
ACG_BE_VI1	AQQHMLQLT	WGIKQLQTRV	LAIERYLQVQ	QLLGIWGCSG	KLICATNVPW
AD_SE_SE69	AQQHLLKLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTSVPW
AD_SE_SE71	AQQHLLKLT	WGIKQLQARV	LALERYLKDQ	QLLGIWGCSG	KLICPTTVPW
ADHK_NO_97	AQQHMLQLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
ADK_CD_MAL	AQQHLLQLT	WGIKQLQARV	LAVERYLQDQ	RLLGMWGCSG	KHICTTFVPW
AG_BE_VI11	AQQHMLQLT	WGIKQLQARV	LAVERFLKDQ	QLLGIWGCSG	KLICTTNVPW
AG_NG_92NG	AQQHLLQLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AGHU_GA_VI	AQQHLLQLT	WGIKQLQARV	LAIERYLKDQ	QLLGIWGCSG	KLICTTNVPW
AGU_CD_Z32	AQQHLLKLT	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KIICPTNVPW
AJ_BW_BW21	AQQHLLRLT	WGIKQLQAKI	LAVERYLQDQ	QLLGIWGCSG	KFICTTTVP
B_AU_VH_AF	AQQHLLQLT	WGIKQLQARI	LAVERYLEDQ	QLLGIWGCSG	KLICTTSVPW
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B_DE_HAN_U	AQQHLLQLT	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTVPW
B_FR_HXB2	AQQHLLQLT	WGIKQLQARI	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_GA_OYI	AQQHLLQLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
B_GB_CAM1	AQQHLLQLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTAVPW
B_GB_GB8_C	AQQHLLRLT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
B_GB_MANC	AQQHLLQLT	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTAVPW
B_KR_WK_AF	AQQHLLQLT	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICTTNVPW
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B_TW_TWCYS	AQQHMLQLT	WGIKQLQARV	LAVERYLRDQ	QLLGIWGCSG	KLICNTNVPW
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B_US_DH123	AQQHMLQLT	WGIKQLQARV	LAVERYLQDQ	QLLGIWGCSG	KLICTTTVPW
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B_US_MNCG	AQQHMLQLT	WGIKQLQARV	LAVERYLKDQ	QLLGFWGCSG	KLICTTTVPW
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B_US_WEAU1	AQQHLLFELT	WGIKQLQARV	LAVERYLKDQ	QLLGIWGCSG	KLICTTTVPW
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B_US_DH123	NTWSN....	KSLDTIWGN.	.MTWMQWEKE	INNYTGLIYN	LIEBSNQOQE
B_US_JRCSF	NTWSN....	KSLDSIWNN.	.MTWMEWERE	INNYTNTIYT	LIEBSQIQQE
B_US_MNCG	NASWSN....	KSLDDIWNN.	.MTWMQWERE	IDNYTSLIYS	LLEBSQTQQE
B_US_P896	NVWSN....	KSVDDIWNN.	.MTWMEWERE	IDNYTDYIYD	LLEBSQTQQE
B_US_RF_M1	NASWSN....	KSLNMIWNN.	.MTWMQWERE	IDNYTGIIYN	LIEBSNQOQE
B_US_SF2_K	NASWSN....	KSLEDIWDN.	.MTWMQWERE	IDNYTNTIYT	LIEBSNQOQE
B_US_WEAU1	NASWSN....	RSQDYIWNN.	.MTWMEWERE	INNYTGLIYN	LIEBSNQOQE
B_US_WR27	NATWSN....	KSLDKIWQN.	.MTWMEWERE	IDNYTELIYS	LLEBSNQOQE
B_US_YU2_M	NTWSN....	KSLNEIWDN.	.MTWMKWERE	IDNYTHIYS	LIEBSNQOQE
BF1_BR_93B	NSSWSN....	KSQEKIWGN.	.MTWMEWERE	ISNYSNEIYR	LIEBSNQOQE
C_BR_92BR0	NSSWSN....	RSQEDIWNN.	.MTWMQWDRE	ISNYTNTIYR	LLEBSNQOQE
C_BW_96BW0	NNSWSN....	KSLDYIWGN.	.MTWMEWDRE	ISNYSNTIYR	LLEBSNQOQE
C_BW_96BW1	NASWSN....	KSQEBIWGN.	.MTWMQWDRE	ISNYTDTIYR	LLEBSNQOQE
C_BW_96BW1	NSSWSN....	KTENEIWEN.	.MTWMQWERE	IDNYTDTIYR	LLEBSNQOQE
C_BW_96BW1	NSSWSN....	KTQGEIWEN.	.MTWMQWDKE	ISNYTGIIYR	LLEBSNQOQE
C_ET_ETH22	NSSWSN....	KSQEBIWDN.	.MTWMQWDRE	ISNYTDIIYN	LLEBSNQOQE
C_IN_93IN1	NSSWSN....	KTQSEIWNN.	.MTWMQWDRE	VSNYTNIYS	LLEBSNQOQE
C_IN_93IN9	NSSWSN....	RSQQDIWDN.	.MTWMQWDRE	ISNYTNTIYR	LLEBSNQOQE
C_IN_93IN9	NSSWSN....	KSQEBIWEN.	.MTWMQWDRE	INNYTQTIYR	LLEBSNQOQE
C_IN_94IN1	NSSWSN....	RTQEBIWNN.	.MTWMQWDRE	INNYTNTIYR	LLEBSNQOQE
C_IN_95IN2	NSSWSN....	RTQKEIWDN.	.MTWMQWDRE	INNYTNTIYR	LLEBSNQOQE
CRF01_AB_C	NTWSN....	KSYAEIWDN.	.MTWIEWDKE	INNYTNQIYE	LLEBSNQOQE
CRF01_AB_C	NSSWSN....	KSYAEIWNN.	.MTWIEWDRE	INNYTNQIYE	LLEBSNQOQE
CRF01_AB_C	NSSWSN....	KSYNEIWNN.	.MTWIEWDRE	INNYTNQIYE	LLEBSNQOQE
CRF01_AB_T	NSTWSN....	RSFEEIWNN.	.MTWIEWERE	ISNYTNQIYE	LLEBSNQOQE
CRF01_AB_T	NSTWSN....	RSYEEIWNN.	.MTWIEWERE	ISNYTNQIYE	LLEBSNQOQE
CRF01_AB_T	.STWSN....	RSYEEIWDN.	.MTWIEWERE	ISNYTNQIYE	LLEBSNQOQE

CRF01_AE_T	NSTWSN....	KSFDEIWNN.	.MTWIEWERE	ISNYTNKIYD	ILTESQNQQD
CRF01_AE_T	NSTWSN....	RSFEEIWNN.	.MTWIEWERE	ISNYTNQIYE	ILTESQNQQD
CRF01_AE_T	NSTWSN....	KSYEEIWDK.	.MTWTQWERE	ISNYTSTIYE	ILTESQNQQD
CRF02_AG_F	NSSWSN....	KTYNDIWDN.	.MTWLQWDKE	VSNYTDIIYN	LIEESQNQQE
CRF02_AG_F	NASWSN....	KTYNDIWDN.	.MTWLQWDKE	ISNYTDIIYN	LIEESQNQQE
CRF02_AG_G	NSSWSN....	RTFEDIWEN.	.MTWLQWEKE	ISNYTDTIYA	LIEDSQNQQE
CRF02_AG_N	NSSWSN....	KTFNDIWDN.	.MTWIQWEKE	ISNYTDIIYN	LIEESQNRQE
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CRF03_AB_R	NTWSN....	KPLDEINN..	.MTWMEWERE	INNYTGLIYN	LIEESQNQQE
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CRF04_cpx	NSSWSN....	KSYNDIWDN.	.MTWLQWDKE	INNYTQIIYG	LLEESQNQQE
CRF04_cpx	NSSWNN....	KSYNDIWGN.	.MTWLQWDKE	INNYTQIIYE	LLEESQIQQE
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CRF05_DF_B	NSSWSN....	KSEGEIWDN.	.MTWMEWEKE	ISNYSSTIYR	LIEQSQIQQE
CRF05_DF_B	NSSWSN....	KSQEEIWEN.	.MTWMQWEKE	IGQYSNTIYR	LIEQSQNQQE
CRF06_cpx	NTWSN....	KTYDEIWGN.	.MTWIEWDRE	INNYTQQIYS	LIELSQTQQE
CRF06_cpx	NASWSN....	KTYNEIWDN.	.MTWIEWDRE	INNYTQQIYS	LIEESQNQQE
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CRF06_cpx	NISWSN....	KTYSEIWDN.	.MTWIEWDRE	INNYTQQIYN	LIEESQNQQE
CRF11_cpx	NISWSN....	KSYDEIWDN.	.MTWIEWERE	IDNYTQTIYT	LLEESQTQQE
CRF11_cpx	NVWSN....	KTYNEIWENE	NMTWIKWERE	IDNYTQTIYT	LIEESQNQQE
D_CD_84ZR0	NSSWSN....	RSVEYIWGN.	.MTWMQWERE	IDNYTGLIYN	LIEESQIQQE
D_CD_ELI_K	NSSWSN....	RSLNEIWQN.	.MTWMEWERE	IDNYTGLIYS	LIEESQTQQE
D_CD_NDK_M	NSSWSN....	RSLDEIWQN.	.MTWMEWERE	IDNYTGLIYS	LIEESQIQQE
D_UG_94UG1	NSSWSN....	RSVDEIWNN.	.MTWMEWERE	IDNYTELVYS	LLEVSQIQQE
F1_BE_VI85	NSSWSN....	KSQEEIWNN.	.MTWMEWEKE	ISNYSNIIYK	LIEESQNQQE
F1_BR_93BR	NSSWSN....	KSLEEIWGN.	.MTWMEWEKE	VSNYSKEIYR	LIEDSQNQQE
F1_FI_FIN9	NSSWSN....	KSQDEIWNN.	.MTWMQWEKE	ISNYSKTIYM	LIEKSQSQQE
F1_FR_MP41	NTWSN....	KSHDEIWNN.	.MTWMQWEKE	INNYSNTIYR	LIEESQNQQE
F2_CM_MP25	NLSWSN....	KSQDEIWGN.	.MTWMEWEKE	IGNYTDTIYR	LIESAQNQQE
F2KU_BE_VI	NSSWSN....	RSQDEIWNN.	.MTWMEWENE	INNYTGIIYQ	LIEQSQNQQE
G_BE_DRCBL	NTWSN....	KSYNEIWEN.	.MTWIEWERE	IDNYTYHIYS	LIEQSQIQQE
G_NG_92NG0	NTWSN....	KSYNEIWDN.	.MTWLEWERE	IHNYTQHIYS	LIEESQNQQE
G_SE_SE616	NVWSN....	KSYNEIWDN.	.MTWIEWERE	INNYTYQIYS	LLEESQNQQE
H_BE_VI991	NSSWSN....	KSLDEIWDN.	.MTWMEWDKQ	INNYTDEIYR	LLEVSQNQQE
H_BE_VI997	NSTWSN....	KSLAEIWDN.	.MTWMEWDRQ	IDNYTEVIYR	LLELSQTQQE
H_CF_90CF0	NSSWSN....	KSQSEIWDN.	.MTWMEWDKQ	ISNYTEEIYR	LLEVSQTQQE
J_SE_SE702	NASWSN....	KSYEDIWEN.	.MTWIEWERE	INNYTGIIYS	LIEEAQNQQE
J_SE_SE788	NASWSN....	KSYEDIWEN.	.MTWIEWERE	INNYTGIIYS	LIEEAQNQQE
K_CD_EQTB1	NSSWSN....	KSQSEIWEN.	.MTWMQWEKE	ISNHTSTIYR	LIEESQIQQE
K_CM_MP535	NSSWSN....	KSWEEIWNN.	.MTWMEWEKE	IGNYSDTIYK	LIEESQTQQE
N_CM_YBF30	NETWSN....	TSYDTIWNN.	.LTWQQWDEK	VRNYSGVIFG	LIEQAQEQQN
O_CM_ANT70	NRTWIG....	NES..IWDI.	.LTWQEWDRQ	ISNISSTIYE	BIQKAQVQQE
O_CM_MVP51	NTWSWGRYN.	DDS..IWDN.	.LTWQQWDQH	INNVSSIIYD	BIQAAQDQQE
O_SN_99SE	NTTWTNCTNT	NKLDIWDK.	.LTWQQWDQQ	ISNVSSIIYE	BIRNAQVQQE
O_SN_99SE	NRTWTN..NN	TDLDTIWGN.	.LTWQEWDDQ	ISNISATIYD	BIQKAQVQQE
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98BWM012_2	ENEKDLLALD	SWKNLWNWFD	ITNWLWYIKI FIMIVGGLIG LRIIFAVLSI
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98BWM014_a	QNEKDLLALD	KWKDLRNWFD	ISNWLWYIRI FIMIVGGLIG LRIIFAVLSI
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A2D_97KR	KNEKDLLALD	KWASLWNWFD	ISNWLWYIKI FIMIVGGLIG LRIVMAITSV
A2G_CD_97C	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI FIMIVGGLIG LRIVFAVLSI
A_BY_97BL0	KNEQDLLALD	KAG.LXSXXD	ISNWLWYIKI FIIIVGGLIX LRIIFAVLSI
A_KE_Q23_A	KNEKELLELD	KWANLWSWFD	ISNWLWYIKI FIIIVGGLIG LRIVFAVLSV
A_SE_SE659	MNEQDLLALD	KWANLWNWFD	ITNWLWYIRI FIMIVGGLIG LRIVFAVLSI
A_SE_SE725	KNEQDLLALD	KWANLWNWFD	ITKWLWYIKI FIMIVGGLIG LRIVFAVFSV

A_SE_SE753	KNEQDLMLD	KWTNLWTWFS	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLAI
A_SE_SE853	KNEQDLLALD	KWASLWNWFD	ISRWLWYIRI	FIMIVGGLIG	LRIVFAVLVS
A_SE_SE889	KNEQDLLALD	KWANLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVIAVISI
A_SE_UGSE8	KNEKELLELD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLTV
A_UG_92UG0	RNEKDLELD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVLVS
A_UG_U455	KNELDLLALD	KWANLN.WFN	ISNWLWYIRL	FVIIVGGLIG	LRIVFTVLSI
AC_IN_2130	KNEQDLLALD	KWADLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLVS
AC_RW_92RW	KNEQDLLALD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
AC_SE_SE94	KNEQDLLALD	KWASLWNWFD	ISKWLWYIRI	FIMIVGGLIG	LRIVFAVLVS
ACD_SE_SE8	KNEQDLLALD	KWGSLSWNWFE	ISKWLWYIRI	FIMIVGGLIG	LRIVFAVLVS
ACG_BE_VI1	QNEKDLLALD	KWQNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAILS
AD_SE_SE69	KNEQDLLALD	KWANLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLVS
AD_SE_SE71	MNEQDLLQLD	KWASLWNWFD	ITNWLWYIRI	FIIIVGGLIG	LRIVFAVLVS
ADHK_NO_97	XNEQDLLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGVIG	LRIVFAVLVS
ADK_CD_MAL	KNEKELLELD	KWASLWNWFS	ISKWLWYIRI	FIIIVGGLIG	LRIIFAVLSL
AC_BE_VI11	KNEQDLLSLD	KWASLWTWFD	IANWLWYIRI	FIMIVGGLIG	LRVVFVAVLN
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B_AU_VH_AF	KNEQELLALD	KWASLWNWFS	ITKWLWYIKI	FIMIVGGLVG	LRIVFAVLVS
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B_GB_CAM1	KNEKDLLELD	TWASLWNWFD	ITNWLWYIKI	FIMIIGGLIG	LRIVFTILSL
B_GB_GB8_C	KNEQELLELD	KWANLWNWFD	ITNWLWYIKI	FIMIIGGLIG	LRIIFAVIST
B_GB_MANC	KNEQELLELD	KWGSLSWSWFS	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVLVS
B_KR_WK_AF	KNEQELLELD	KWASLN.WFN	ITKWLWYIKI	FIMIVGGLVG	LRIIFFVLSI
B_NL_3202A	KNEQELLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLVG	LRIIFAVLSI
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B_US_BC_L0	KNEQELLELD	KWASLWNWFT	ITNWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
B_US_DH123	KNEQELLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFSVLSI
B_US_JRCSE	KNEQELLELD	KWASLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIVFSVLSI
B_US_MNCG	KNEQELLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVLVS
B_US_P896	KNEKELLELD	KWASLWNWFD	ITNWLWYIRL	FIMIVGGLIG	LRIVFAVLVS
B_US_RF_M1	KNEQELLELD	KWANLWNWFD	ITQWLWYIRI	FIMIVGGLVG	LKIVFAVLVS
B_US_SF2_K	KNEQELLELD	KWASLWNWFS	ITNWLWYIKI	FIMIVGGLVG	LRIVFAVLVS
B_US_WEAU1	KNEQELLELD	KWASLWTWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFTVLSI
B_US_WR27	KNEQELLELD	KWASLWNWFD	ITQWLWYIKI	FXMIVGGLIG	LRIVFAVLVS
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BF1_BR_93B	KNEQELLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVLVS
C_BR_92BR0	KNEQDLLALD	KWQNLWTWFG	ITNWLWYIKI	FIKIVGGLIG	LRIIFAVLSI
C_BW_96BW0	KNEKDLLALD	SWNNLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAALSI
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C_BW_96BW1	QNEKDLLALD	SWNNLWSWFD	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_ET_ETH22	KNEKDLLALD	KWENLWNWFD	ITNWLWYIKI	FIMIVGGVIG	LRIIFAVLSI
C_IN_93IN1	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_93IN9	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_93IN9	RNEKDLLALD	SWESLWNWFS	ISKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_94IN1	KNEKDLLALD	SWKNLWSWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
C_IN_95IN2	ENEKDLLALD	SWKNLWNWFD	ITKWLWYIKI	FIIIVGGLIG	LRIIFAVISI
CRF01_AE_C	KNEQDLLALD	KWANLWNWFS	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLVS
CRF01_AE_C	RNEKDLLALD	KWASLWNWFD	ITRWLWYIKI	FIIIVGGLIG	LRIVFAVLVS
CRF01_AE_C	RNEKDLELD	KWTSLSWNWFD	ITRWLWYIRI	FIMIVGGLIG	LRIVFAVLVS
CRF01_AE_T	RNEKDLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDLELD	KWANLWNWFS	ISNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDLELD	KWASLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIIFAVLSI

CRF01_AE_T	KNEKDLELD	KWASLWNWFD	ITSWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIIFAVLSI
CRF01_AE_T	RNEKDLLKLD	KWASLWNWFD	ISRWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_F	KNEQDLLALD	QWANLWNWFG	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_F	KNEKDLLALD	KWESLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_G	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_N	KNEQDLLALD	KWASLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_S	KNEQDLLALD	KWASLWNWFD	ISSWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF02_AG_S	KNEQDLLALD	KWASLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF03_AB_R	KNEQEILALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF03_AB_R	KNEQELLALD	KWASLWNWFD	ISKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF04_cpx	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF04_cpx	KNEQDLLAFD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF04_cpx	KNEQDLLALD	KWANLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF05_DF_B	KNEQELLALD	QWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF05_DF_B	KNEKDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF06_cpx	KNEQDLLALD	KWANLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF06_cpx	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
CRF06_cpx	KNEQDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF06_cpx	KNEQELLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF11_cpx	KNEQDLLALD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
CRF11_cpx	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
D_CD_84ZRO	KNEKELLELD	KWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
D_CD_ELI_K	KNEKELLELD	KWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
D_CD_NDK_M	KNEKELLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
D_UG_94UG1	KNEQELLKLD	TWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_BE_VI85	KNEQELLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_BR_93BR	KNEQELLALD	KWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_FI_FIN9	RNEQELLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F1_FR_MP41	KNEQELLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F2_CM_MP25	KNEQDLLALD	KWASLWNWFD	ITRWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
F2_KU_BE_VI	KNEQDLLALD	KWASLWNWFD	ITQWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
G_BE_DRCBL	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
G_NG_92NG0	KNEQDLLALD	KWASLWNWFD	ISNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
G_SE_SE616	KNEQDLLALD	KWASLWNWFD	ITRWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
H_BE_VI991	KNEQDLLALD	KWANLWNWFD	ITNWLWYIRI	FIMIVGGLIG	LRIVFAVLSI
H_BE_VI997	KNEQDLLALD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
H_CF_90CF0	KNEQDLLALD	KWASLWNWFD	ISHWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
J_SE_SE702	TNEKDLELD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
J_SE_SE788	NNEKDLELD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
K_CD_EQTB1	KNEQDLLALD	KWASLWNWFD	ISNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
K_CM_MP535	KNEQDLLALD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
N_CM_YBF30	TNEKLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
O_CM_ANT70	KNEKLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
O_CM_MVP51	KNEKLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
O_SN_99SE	KNEKLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
O_SN_99SE	HNEKLELD	KWASLWNWFD	ITKWLWYIKI	FIMIVGGLIG	LRIVFAVLSI
U_CD_83C	KSEKLELD	KWASLWNWFD	ITNWLWYIKI	FIMIVGGLIG	LRIVFAVLSI

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850

00BW0762_1 VNRVRQGYSP LSFQTLTP.. NQR.GPDRLG GIEEEGGEQD RDRSIRLVSG
 00BW0768_2 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLG RIEEEGGEQD KDRSIRLVSG
 00BW0874_2 VNRVRQGYSP LSFQTLTP.. SPR.EPDRLG RIEEEGGEQD KDRSIRLVGG
 00BW1471_2 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLE RIEEEGGEQD RGRSVRLVSG
 00BW1616_2 VNRVRQGYSP LSFQTLTP.. NPR.ELDRLG RIEEEGGEQD RDRSIRLVSG
 00BW1686_8 VNRVRQGYSP LSLQTLTP.. NPR.GPDRPR GIEEEGGEQD KDRSIRLVNG
 00BW1759_3 VNRVRQGYSP SSFQTLIP.. NPE.GPDRLR RIEEEGGEQD RDRSIRLVNG
 00BW1773_2 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLG RIEEEGGEQD RDRSVRLVSG
 00BW1783_5 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLE RIEEEGGEQD RDRSIRLVSG
 00BW1795_6 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLG RIEEEGGEQD RDRSIRLVSG
 00BW1811_3 VNRVRQGYSP LSFQTLIP.. NPG.GPDRLG RIEEEGGEQD RDRSVRLVNG
 00BW1859_5 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLG GIEEEGGEQD RDRSIRLVNG
 00BW1880_2 VNRVRQGYSP LSLQTLSP.. NQR.GLDRLG RIEEEGGEQD RDKSIRLVSG
 00BW1921_1 VNRVRQGYSP LSLQTLTP.. NPR.ELDRLG RIEEEGGEQD RGRSIRLVNG
 00BW2036_1 VNRVRQGYSP LSFQTLTP.. NPR.GLDRLG RIEEEGGEQD RGRSIRLVQG
 00BW2063_6 VNRVRQGYSP LSFQTLTP.. NPR.GPDKLE RIEEEGGEQD RNRSIRLVSG
 00BW2087_2 VNRVRQGYSP LSFQTLTP.. NPR.EPDRLG RIEEEGGEQD RERSIRLVSG
 00BW2127_2 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLG RTEEGGGEQD NDRSIRLASG
 00BW2128_3 VKRVRQGYSP LSFQTLTP.. NPG.GPDRLG RIEEEGGEQD REKSVRLVNG
 00BW2276_7 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLG GIEEEGGEQD RDRSIRLVSG
 00BW3819_3 VNRVRQGYSP LSLQTLTP.. SPR.GPDGLR GIEEEGGEQD KDRSIRLVNG
 00BW3842_8 VNRVRQGYSP LSLQTLTP.. NPR.ELDRLG RIEEEGGEQD RDRSIRLVNG
 00BW3871_3 VNRVRQGYSP LSLQTLTP.. NPR.ELDRLG RIEEEGGEQD KDRSIRLVNG
 00BW3876_9 VNRVRQGYSP LSFQTLTP.. NPR.EPDRPG RIEKEGGEQD KRSRIRLVSG
 00BW3886_8 VNRVRQGYSP LSFQTLTP.. NTR.ELDRLG RIEEEGGEQD RDRSIRLLNG
 00BW3891_6 VNRVRQGYSP LSFQTLIP.. NPR.GLDRLG RIEEEGGEQD RDRSIRLVNG
 00BW3970_2 VNRVRQGYSP LSLQTLTP.. NQR.EPDRLG RIEEEGGEQD RKRSIRLVSG
 00BW5031_1 VNRVRQGYSP LSFQTLTP.. SQR.ELDRLG RIEEEGGEQD RDRSIRLANG
 96BW01B21 VNRVRQGYSP LSFQTLTP.. NPG.GPDGLG RIEEEGGEQD KDRSIRLVNG
 96BW0407 VNRVRQGYSP LSFQTLIP.. NPR.RSDRLG RIEEEGGEQD RGRSIRLVSG
 96BW0502 VNRVRQGYSP LSFQTLTP.. NPR.EPDRLG RIEEEGGEQD RGRSIRLVSG
 96BW06_J4 VNRVRQGYSP LSFQTLPP.. NPR.GIDRLG RIEEGGGEQD RDRSIRLVNG
 96BW11_06 VKRVRQGYSP LSFQTLTP.. NPR.GPDRLE RIEEEGGEQD RNRSIRLVSG
 96BW1210 VNRVRQGYSP LSFQTLIP.. SPR.EPDKLE RIEEEGGEQD RDRSIRLVSG
 96BW15B03 VNRVRQGYSP LSFQTLTP.. NPR.GLDRLG RIEEEGGEQD RDRSIRLVQG
 96BW16_26 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLG RIEEEGGEQD RDRSVRLVHG
 96BW17A09 VNRVRQGYSP LSLQTLTP.. NPR.GPDGLE RIEEGGGEQD RGRSIRLVSG
 96BWM01_5 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLE GIEEEGGEQD KDRSIRLVSG
 96BWM03_2 VNRVRQGYSP LSFQTLTP.. NPR.ELDRLG RIEEEGGEQD RDRSIRLVSG
 98BWM012_2 VNRVRQGYSP LSFQTLNP.. NPR.GLDRLG RIEEEGGEQD KSTSIRLVNG
 98BWM013_4 VNRVRQGYSP LSFQTLTP.. NPR.GPDRLE RIEEEGGEQD RDRSIRLVNG
 98BWM014_a VNRVRQGYSL TSLQTHLP.. NAG.GLDRLD RIEEGGGEQD RHRSIRLVSG
 98BWM014_1 VNRVRQGYSP LSFQTLTP.. VPR.EPDRLG GIEEEGGEQD RDRSVRLVNG
 98BWM018_d VNRVRQGYSP LSFQTLTP.. NPR.GPDRLG RIEEEGGEQD RDRSIRLVSG
 98BWM036_a VNRVRQGYSP LSFQTLTP.. TPR.DPDRLR GIEEEGGEQD RDRSIRLVSC
 98BWM037_d VNRVRQGYSL TSFQTVIP.. NPR.GPDRPR GIEEEGGEQD RDRSIRLVSG
 99BW3932_1 VNRVRQGYSL LSFQTLTP.. NPR.GPDRLG GIEEEGGEQD RDRSIRLVNG
 99BW4642_4 VNRVRQGYSP LSFQTLTP.. NPR.ELDRLG RIEEEGGEQD RDRSVRLVNG
 99BW4745_8 VNRVRQGYSP LSLQTLTP.. SPR.RPDRLG GIEEEGGEQD RTRSVRLVNG
 99BW4754_7 VNRVRQGYSP LSFQTLTP.. NQR.GPDRLG EIEEEGGEQD RDRSIRLVNG
 99BWM016_8 VNRVRQGYSP LSFQTLAP.. NPG.GLDRLG RIEEEGGEQD RGRSIRLVNG
 A2_CD_97CD VKRVRQGYSP LSFQIPTP.. NPE.GLDRPG RIEEEGGEQD RDRSIRLVSG
 A2_CY_94CY VNRVRQGYSP VSFQIPTP.. SPE.GPDRPR GTEEGGGEQD RDRSIRLVNG
 A2D_97KR VNRVRQGYSP VSFQIPPP.. TPE.DPDRHG RIEDGGGEQD RDRSVRLVSG
 A2G_CD_97C VNRVRQGYSP LSFQTLTH.. HQR.EPDRPE RIEEGGGEQD RDRSVRLVSG
 A_BY_97BLO INRARXXYSP LSLQTLTP.. HPE.RPDRPX RIKEECXEQD RDRSIRLVSG
 A_KE_Q23_A INRVRQGYSP LSFQTHTP.. NPR.GLDRPE RIEEEDGEQD RGRSIRLVSG
 A_SE_SE659 INRVRQGYSP LSFQTHTP.. NPG.GLDRPG RIEEEGGEQD RDRSIRLVSG
 A_SE_SE725 INRVRQGYSP LSFQTHTP.. DPR.GLDRPR RIEEEGGEQD RGRSIRLVSG

A_SE_SE753 INNRVQGYSP LSFQIHTP.. NPR.DPDRPG RIEEEGGGEQ RDRSIRLASG
 A_SE_SE853 INNRVQGYSP LSFQIHTP.. NPG.DLDRPG RIEEEGGGEQD RGRSIRLVSG
 A_SE_SE889 INNRVQGYSP LSFQIHTP.. SPG.GLDRPG RIEEEGGGEQD RNRSIRLVNG
 A_SE_UGSE8 IKRVQGYSP LSFQIHTP.. SPR.DPDRPG RIEEEGGGEQ RDRSIRLVSG
 A_UG_92UG0 INNRVQGYSP LSFQTHTP.. NPR.GLDRPG RIEEEGGGEQD RGRSIRLVSG
 A_UG_U455_ INNRVQGYSP LSFQTLAP.. IPE.GLGRPG RIEEEGGGEQ KDRSIRLVSG
 AC_IN_2130 INNRVQGYSP LSFRTHTP.. NPG.GLDRPG RIEEEGGGEQ KDRSIRLVSG
 AC_RW_92RW VNRVRQGYSP LSFQTLIP.. NPR.GPDRLG GIEEEGGGEQD RGRSIRLVSG
 AC_SE_SE94 INNRVQGYSP LSFQIHTP.. NPG.GPDRPG RTEEEGGGEQD RDRSIRLVSG
 ACD_SE_SE8 INNRVQGYSP LSFQTHTP.. NPE.GVDRPG RIEEEGGGEQ RDRSIRLVSG
 ACG_BE_VI1 VNRVRQGYSP LSFQTLIP.. NPR.GPDRPG EIEEEGGGEQD RDTSTRLVSG
 AD_SE_SE69 VNRVRQGYSP LSFQTLIP.. APRGP.DRPE GIEEEGGGEQ RGRSIRLVNG
 AD_SE_SE71 INNRVQGYSP LSFQTHTP.. NPR.DLDRPE RIEEEGGGEQD RTRSIRLVSG
 ADHK_NO_97 VNRVRQGYSP LSFQTLIP.. NPRGA.DRPE GIEEEGGGEQD XNRSIRLVNG
 ADK_CD_MAL VNRVRQGYSP LSLQTLIP.. TPRGPPDRPE GIEEEGGGEQ RGRSIRLVNG
 AG_BE_VI11 INNRVQGYSP LSFQILTP.. HQRPD.DRPG RIEEEGGGEQD RDTSRRLVGG
 AG_NG_92NG VNRVRQGYSP LSFQTLTH.. HQREP.DRPE RIEEEGGGEQD RDRSVRLVSG
 AGHU_GA_VI VNRVRQGYSP LSFQTLFP.. NQREP.DRPE GIEEEGGGEQ RSRIRLVNG
 AGU_CD_Z32 INNRVQGYSP LSFQTLTH.. HQR.EPDRPE GIEEEGGGEQD RDRSIRLVSG
 AJ_BW_BW21 VNRVRQGYSP LSLQTLIP.. NPTEV.DRPG GIEEEGGGEQ KTRSIRLVNG
 B_AU_VH_AF VKKVREGYSP LSLQIRPP.. APRGP.DRPE GIEEEGGGEQD RDKSVRLVDG
 B_CN_RL42 VNRVRQGYSP LSLQTRFP.. AQRGP.GRPE GIEEEGGGERD RDRSERLVGT
 B_DE_D31_U VNSVRQGYSP LSFQTRLIP.. APRGP.DRPE GIEEEGGGERD RDRSNRLVKG
 B_DE_HAN_U VNRVRQGYSP LSFQTLIP.. ATRGP.RQPE EIEEEGGGERD RGRSVRLVSG
 B_FR_HXB2_ VNRVRQGYSP LSFQTHLP.. TPRGP.DRPE GIEEEGGGERD RDRSIRLVNG
 B_GA_OYI_ VNRVRQGYSP LSFQTRLIP.. TORGP.DRPE GIEEEGGGERD RDRSGRLVDG
 B_GB_CAM1_ VNRVRQGYSP LSFQTRFP.. VPRGP.DRPE GIEEEGGGERD RDTSGRLVTG
 B_GB_GB8_C VNRVRQGYSP LSLQTHLP.. TPRGP.DRPE GIEEEGGGEQD RDRSIRLVNG
 B_GB_MANC_ VNRVRQGYPP LSFQTHLP.. APRGP.DRPG GIEEEGGGED RDRSSRLVHG
 B_KR_WK_AF VNRVRQGYSP LSFQTHFP.. SPRGP.DRPG GIEEGGGEGD SGGSSHLVDG
 B_NL_3202A VNRVRQGYSP LSFQTRLIP.. APRGP.DRPE GIEEEGGGERD RDRSGRLVNG
 B_TW_TWCYS VNRVRQGYSP LSFQTHLP.. TPRGP.DRPE GIDEEGGERD RDRSERSVDG
 B_US_BC_L0 VNRVRQGYSP LSFQTHLP.. TPRGP.DRPE GIEEEGGGERD RDRSGRLVNG
 B_US_DH123 VNRVRQGYSP LSFQTRFP.. ASRGP.DRPE GIEEEGGGERD RDRSSPLVDG
 B_US_JRCSE VNRVRQGYSP LSFQTLIP.. ATRGP.DRPE GIEEEGGGERD RDRSGQLVNG
 B_US_MNCG_ VNRVRQGYSP LSLQTRPP.. VPRGP.DRPE GIEEEGGGERD RDTSGRLVHG
 B_US_P896_ VNRVRQGYSP LSFQTLIP.. ASRGP.DRPE GIEEEGGGERD RDRSGPLVNG
 B_US_RF_M1 VNRVRQGYSP LSFQTHLP.. APRGP.DRPE GIEEGGGGERD RDRSGGAVNG
 B_US_SF2_K VNRVRQGYSP LSFQTRLIP.. VPRGP.DRPG GIEEEGGGERD RDRSVRLVDG
 B_US_WEAU1 VNRVRQGYSP LSFQTHLP.. APRGP.DRPE GIEEEGGGERD RDRSGRLVDG
 B_US_WR27_ XNRVRQGXSP LSFQTLIP.. VPRGP.DRPE GIEEEGGGERD RDRSNRLVHG
 B_US_YU2_M VNRVRQGYSP LSFQTHLP.. AQRGP.DRPG GIEEEGGGERD RDRSGPLVDG
 BF1_BR_93B VNRVRQGYSP LSLQTRFP.. SPREP.DRPE GIEEGGGEPG KDRSVRLVNG
 C_BR_92BR0 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLG GIEEEGGGEQD RDRSIRLVSG
 C_BW_96BW0 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLG GIEEEGGGEQD RDRSIRLVSG
 C_BW_96BW1 VNRVRQGYSP LSFQTLIP.. NPR.GPDRLE RIEEEGGGEQD RNRSIRLVSG
 C_BW_96BW1 VNRVRQGYSP LSFQTLIP.. SPR.EPDKLE RIEEEGGGEQD RDRSIRLVSG
 C_ET_ETH22 VNRVRQGYSP LSFQTLIP.. NPR.GLDRLG RIEEEGGGEQD RDRSIRLVQ
 C_IN_93IN1 VNRVRQGYSP LSFQTLIP.. HPR.GPDRLG GIEEEGGGEQ RDRSIRLVNG
 C_IN_93IN9 VNRVRQGYSP LSFQTPTP.. NPR.GPDRLG RIEEEGGGEQ KDRSIRLVNG
 C_IN_93IN9 VNRVRQGYSP LSFQTLIP.. NPG.GPDRLG RIEEEGGGEQD KDRSIRLVNG
 C_IN_94IN1 VNRVRQGYSP LSFQTPTP.. NPG.GPDRLG RIEEEGGGEQD KDRSIRLVNG
 C_IN_95IN2 VNRVRQGYSP LSFQTLIP.. NPG.GPDRLG RIEEEGGGEQD KDRSIRLVSG
 CRF01_AE_C VNRVRQGYSP LSFQTLTH.. HQR.EPDRPE RIEEGGGEEG KDRSIRLVSG
 CRF01_AE_C VNRVRQGYSP LSFQTLTH.. QQR.EPDRPE RIEEESGEQ RDRSIRLVSG
 CRF01_AE_C VNRVRQGYSP LSFQTLTH.. HQR.EPDRPE RIEEGGGGEQD KDRSVRLVSG
 CRF01_AE_T VNRVRQGYSP LSFQTPH.. HQR.EPDRPE RIEEGGGGEQ RDRSVRLVSG
 CRF01_AE_T VNRVRQGYSP LSLQTPH.. HQR.EPDRPE RIEEGGGGEQ RDRSVRLVSG
 CRF01_AE_T VNRVRQGYSP LSFQTPH.. HQRGEPDRPE RIEEGGGGEQ RDRSVRLVSG

CRF01_AE_T	VNRVRQGYSP	LSFQTPH..	HQR.EPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTPSH..	HOK.EPDRPE	GIEEGGGEQG	RDRSVRLVSG
CRF01_AE_T	VNRVRQGYSP	LSFQTLTH..	HQR.DPDRPE	RIEEGGGEQG	RDRSVRLVSG
CRF02_AG_F	INRVRQGYSP	LSFQTLTH..	HQR.GPDRPE	RIEEGGGEQD	RDRSGRLVSG
CRF02_AG_F	IKRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF02_AG_G	INRVRQGYSP	LSFQILTP..	NPR.GPDRPE	GIEEGGGEQD	RDRSIRLVSG
CRF02_AG_N	INRVRQGYSP	LSFQTLTH..	HQR.EPDRPE	RIEEGGGEQD	KDRSVRLVSG
CRF02_AG_S	INRVRQGYSP	LSFQTLTH..	HQR.EPGRPE	RIEEGGGGQD	RDRSVRLVSG
CRF02_AG_S	INRVRQGYSP	LSFQTLTH..	HQR.GADRPE	GIEEGGGEQD	RDRSVRLVSG
CRF03_AB_R	VNRGRQGYSP	LSFQTRLP..	AQRGP.DRPE	GIEEEDGERD	RDTSIRLVNR
CRF03_AB_R	VNRVRQGYSP	LSFQTRLP..	TQRGP.DRPE	GIEEEGGERD	RDTSIRLVNG
CRF04_cpx	VNRVRQGYSP	LSLQTLIPT.	TQRGL.DRPG	GTEEGGGEQD	RSRSIRLVNG
CRF04_cpx	VNRVRQGYSP	LSFQTLIP..	TQREP.GRPE	GTEEGGGEQD	RSRSIRLVNG
CRF04_cpx	VKRVRQGYSP	LSSQTLIPT.	TQRGP.DRPE	GTEGGGGEQD	RIESIRLVNG
CRF05_DF_B	VNRVRKGYSP	LSFQTPFP..	APRGP.DRPE	ETEEGGGGEQD	RGRSIRLVNG
CRF05_DF_B	VNRVRKGYSP	LSFQTLIP..	GPRGP.DRPE	GTEEGGGEQD	RDRSVRLVSG
CRF06_cpx	VNRVRQGYSP	LSLQTLIP..	NPTGA.DRPG	EIEEGGGEQD	RTRSIRLVNG
CRF06_cpx	VNRVRQGYSP	LSLQTLIP..	NPTGA.DRPG	EIEEGGGEQD	RTRSIRLVNG
CRF06_cpx	VNRVRQGYSP	LSLQTLIP..	NPAEV.DRPG	GIEEGGGEQD	RNRSIRLVNG
CRF06_cpx	VKRVRQGYSP	LSLQTLIP..	NSAGV.DRPG	EIEGGGGEQD	RTRSIRLVNG
CRF11_cpx	VNRVRQGYSP	LSFQTLNP..	TQGEA.DRPG	GIEEGGGEQD	RTRSIRLVSG
CRF11_cpx	VNRVRQGYSP	LSFQALTP..	SQGEA.DRPG	GTKEGGGEQD	RTSSIRLVSG
D_CD_84ZR0	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GIEEGGGEQD	RGRSIRLVNG
D_CD_ELI_K	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GTEEGGGERG	RDRSVRLVNG
D_CD_NDK_M	VNRVRQGYSP	LSFQTLIP..	VPRGP.DRPE	EIEEGGGERG	RDRSVRLVNG
D_UG_94UG1	VNRVRQGYSP	LSFQTLIP..	APRGP.DRPE	GIEEGGGERD	RGRSIRLVNG
F1_BE_VI85	VNRVRKGYSP	LSLQTLIP..	SPRGP.DRPE	GIEEGGGEQD	KDRSVRLVSG
F1_BR_93BR	VNRVRKGYSP	LSFQTHIP..	SPRGP.DRPE	GIEEGGGEQD	KDRSVRLVSG
F1_FI_FIN9	VNRVRKGYSP	LSLQTLIP..	APTEP.DRPE	GIEEGGGEQD	KDRSVRLVNG
F1_FR_MP41	VNRVRKGYSP	LSLQTLIP..	SPRGP.DRPE	GIEEGGGEQD	RNRSVRLVNG
F2_CM_MP25	INRVRQGYSP	LSLQTLIP..	NSRGP.ERPG	GIEEGGGEQD	KDRSVRLVSG
F2KU_BE_VI	VNRVRQGYSP	LSFQTLIP..	SPRGP.DRPE	GTEEGGGEQD	RDRSVRLVSG
G_BE_DRCBL	VNRVRQGYSP	LSFQTLIP..	HQREP.DRPA	GIEEGGGEQD	RDRSVRLVSG
G_NG_92NG0	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPA	KTEEGGGEQD	RDRSVRLVSG
G_SE_SE616	VNRVRQGYSP	LSFQTLTH..	HQREP.DRPE	GIEEGGGEQD	RGRSVRLVSG
H_BE_VI991	VNRVRQGYSP	LSLQTLIP..	NQRGP.DRPR	EIEEGGGEQD	RDRSVRLVNG
H_BE_VI997	VGRVRQGYSP	LSFQTLIP..	NPRGP.DRPE	GIEEGGGEQD	RGRSVRLVNG
H_CF_90CF0	VNRVRQGYSP	LSFQTLVP..	NPRGP.DRPE	GTEEGGGEQD	RDRSVRLVNG
J_SE_SE702	VNRVRQGYSP	LSFQTLIP..	NPTEA.DRPG	GIEEGGGEQD	RTRSIRLVNG
J_SE_SE788	VNRVRQGYSP	LSFQTLIP..	NPTEA.DRPG	GIEEGGGEQD	RTRSIRLVNG
K_CD_EQTB1	VNRVRQGYSP	LSFQTLTP..	SPRGP.DRPE	GIEEGGGEQD	KDRSVRLVSG
K_CM_MP535	VNRVRQGYSP	LSFQTLIP..	TSRGA.DRPE	GIEEGGGEQD	KDRSVRLVSG
N_CM_YBF30	IARVRQGYSP	LSLQTLIPT.	ARG..PDRPE	ETEGGVGEQD	RGRSVRLVSG
O_CM_ANT70	VKNIRQGYQP	LSLQIPNH..	QEE..AGTPG	RTGGGGGEEG	RPRWIPSPQG
O_CM_MVP51	VKNIRQGYQP	LSLQIPVPH.	RQE..AETPG	RTGEGGGEGD	RPKWTALPPG
O_SN_99SE_	VKNIRQGYQP	LSFKTHIHH.	QPE..AEAPG	GTGEGGGGERG	MPTLIPWPQG
O_SN_99SE_	VRNIRHGYP	LSFQTPTHHQ	QPE..AQAPG	GTGEGGGGERD	RGRSVRLVSG
U_CD_83C	INRVRQGYSP	LSFQTLIP..	TPR.GPDRPG	RTBEGGGEED	RNRSVRLVNG

	851		900
00BW0762_1	FLALFWDDLR	SLCLFSYHRL	RDFILVAARA VELLGRSSLK GLQRGWEILK
00BW0768_2	FLALVWDDLR	RLCLFSYHRL	RDFILVATRA VELLGHSSLR GLQRGWEALK
00BW0874_2	FLALAWDDLR	SLCLFSYHRL	RDFILIAART VELLGRSSLR GLQRGWEILK
00BW1471_2	FLTLAWDDLR	SLCIFLYRLL	SDFISIAART VNLLGQNSLR GLQRGWEALK
00BW1616_2	FLALAWDDLR	SLCLFSYHRL	RDFTLIAARA VETLGR.... .RGWEALK
00BW1686_8	FLALAWDDLR	SLCLFSYHQL	RDFILIVARA VELLGRNSLR GLQRGWEILK
00BW1759_3	FLALFWDDLR	SLCLFSYHRL	RDLILVTARA VELLG.... .QRGWEALK
00BW1773_2	FLALTWDDLR	SLCLFSYHRL	RDFILIAARV VELLGRSSLR GLQKGWEALK
00BW1783_5	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA VELLGRSSLR GLQRGWEILK
00BW1795_6	FLALAWDDLR	SLCLFCYRRL	RDFILVTARA VELLGRSSLK GLQRGWEILK
00BW1811_3	FFALAWDDLR	SLCLFCYHRL	RDFILVTARA VELLGHSSLK GLQRGWEILK
00BW1859_5	FLALAWDDLR	SLCLFSYHRL	RDCILIAARA VELLGHSSLR GLQRGWEVLK
00BW1880_2	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA VELLGRSGLK GLQRGWEILK
00BW1921_1	FLPLVWEDLR	SLCLFSYHRL	RDLILVVARA VELLGRSSLR GLQKGWETLK
00BW2036_1	FLALAWDDLR	NLCLFSYHQL	RDLILVTTRV VELLGRSSLR GLQRGWEALK
00BW2063_6	FLALAWDDLR	SLCLFCYHRL	KDFVLVTARV VELLGLSSLK GLQRGWEILK
00BW2087_2	FLPLFWDDLR	SLCLFSYHRL	RDLILIAARA VELLGRSSLR GLQRGWEILK
00BW2127_2	FLAPAWDDLR	SLCLFSYHRL	RDLILVTARV VELLGRS.... .GWEALK
00BW2128_3	FLALFWDDLR	SLCLFSYHRL	RDFILIAARV VELLGRSSLR GLQRGWETLK
00BW2276_7	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA VELLGRSSLR GLQRGWEVLK
00BW3819_3	FLALAWDDLR	SLCLFSYHRL	RDLTLVTARG IELMGRSSLR GLQKGWEALK
00BW3842_8	FLALAWEDLR	SLCLFSYHRL	RDLILVTARA VELLGRSSLR GLQRGWEALK
00BW3871_3	FLALAWDDLR	SLCLFSYHRL	RDFILIVARV VELLGRSSLR GLQKGWETLK
00BW3876_9	FLALAWDDPR	SLCLFSYHRL	RDFILVVVRA VELLGRSSLK GLKRGWEALE
00BW3886_8	FLAIAWDDLR	SLCLFSYHRL	RDFILLIARA VELLGRSSLK GLQRGWEALK
00BW3891_6	FLALAWEDLR	SLCLFSYHRL	RDFILVTARA VELLGRSSLR GLQRGWEALK
00BW3970_2	FLALAWDDLR	SLCLFSYHHL	RDFILIAARV VELLGR.... .RGWDILK
00BW5031_1	FLALAWEDLR	SLCLFSYRHL	RDFILIVVRA VELLGRSSLR GIQKGWDALK
96BW01B21	FLPLVWDDLR	NLCLFSYHRL	RDFILVIARA VELLGRSSLR GLQRGWETLK
96BW0407	FLALAWDDLR	SLCLFSYHRL	RDFILIAARA AELLGRSGLR GLQKGWETLK
96BW0502	FLALAWDDLR	SLCLFSYHRL	RDFILIAARV LELLG.... .QRGWEALK
96BW06_J4	FLALAWDDLR	SLCLFSYHQL	RDFILVVARA VELLGRSSLR GLQRGWEALK
96BW11_06	FLALAWDDLR	SLCLFCYHRL	RDFTLVATRA VELLGRSSLK GLQRGWEILK
96BW1210	FLALAWDDLR	SLCLFSYHRL	RDSILVAART VELLGRSSLR GLQRGWEALK
96BW15B03	FLALAWDDLR	SLCLFSYHRL	RDLILVTARV VELLGRSSLR GLQRGWEALK
96BW16_26	FLALAWDDLR	SLCLFSYHRL	RDFILVAVRV VELLGR.... .RGWEALK
96BW17A09	FLALAWDDLR	SLCIFLYHHL	RDFILIAART VNLLGQSSLR GLQRGWEALK
96BWM01_5	FLALAWDDLR	SLCLFCYHRL	RDFILVTARA VELLGRSSLK GLQRGWEILK
96BWM03_2	FLALAWDDLR	SLCLFSYHRL	RDFILVTARA AELLGRSSLR GLQRGWEALK
98BWM012_2	FLAIAWDDLR	SLCLFSYHRL	RDFILIAARA VELLGRSSLR GLQRGWEALK
98BWM013_4	FLALAWDDLR	NLCLFCYHRL	RDFILVTARA VELLGRSSLT GLQRGWEILK
98BWM014_a	LLALAWDDLR	SVRLFYHQL	RNFILIVARA VELLGR.... .RGWETLK
98BWM014_1	FLALFWDDLR	SLCLFSYHRL	RDLILIAVRA VELLGRSSLW GLQKGWEALK
98BWM018_d	FLALAWDDLR	SLCLFSYHRL	RDFILIAARA VELLGHSLR GLQRGWEILK
98BWM036_a	FLALAWDDLR	SLCLFSYHRL	RDFILVTARV VELMGRSSLK GLQRVWEILK
98BWM037_d	FLALAWDDLR	SLCLFSYHQL	RDFILLIARV VERLGYSSLR GLQRGWEALK
99BW3932_1	FFSLAWDDLR	SLCLFSYHRL	RDLILVTVRV VELMGRCSLR GLQRGWEALK
99BW4642_4	FLALAWDDLR	SLCLFSCHRL	RDCILIAVRA VELLGRSSLK GLQRGWEALK
99BW4745_8	FLALAWDDLR	SLCLFSYHHL	RDFILVTARA VELLGRSSLR GLQRVWEALK
99BW4754_7	FLAIVWDDLR	SLCLFSYHRL	RDFILIAVTRA VELLGRSSLK GLQRGWEILK
99BWM016_8	FLAIAWEDLR	SLCLFSYHRL	RDLTLIVTRA VELLGRSSLK GLQRGWEALK
A2_CD_97CD	FLALAWDDLR	SLCLFSYHRL	RDCILIAARI VELVGHSSLK GLRLGWEGLK
A2_CY_94CY	FFALAWDDLR	SLCLFSYHRL	RDCILIAART VELLGHCSLK GLRLGWEGLK
A2D_97KR	FLALVWEDLR	SLCLFSYHRL	RDCISIAART VELLGHSSLK GLRLGWEGLK
A2G_CD_97C	FLALAWDDLR	SLCLFCYHRL	RDSILIAART VELLRHSSLK GLRLGWEGLK
A_BY_97BL0	FLALAXDDLX	SLCLFSYHRL	RDFISIAART XELLKRSSLX GLRLXXXGLK
A_KE_Q23_A	FLALAWDDLR	SLCLFSYHRL	RDFILIAART VELLGHSSLK GLRLGWEGIK
A_SE_SE659	FLALAWDDLR	SLCLFSYHHL	RDLILIAART VELLGHSSLK GLRLGWEGLK
A_SE_SE725	FLALAWDDLR	SLCLFSYHRL	RHFILIAATT VELLGHSSLK GLRLGWEGLK

A_SE_SE753	FLTLAWEDLR	SLCLFSYHRL	RDLILIAART	VELLGHSSLK	GLRLGWEGLK
A_SE_SE853	FLALAWDDL	SLCLFSYHRL	RDFILIAART	VELLGQR...GWEGLK
A_SE_SE889	FLALAWDDL	SLCLFCYRRL	RDFILIVART	VELLGHSSLR	GLRLGWEGLK
A_SE_UGSE8	FLALAWDDL	SLCRFSYHRL	RDFISIATRI	VELLG.....QGLK
A_UG_92UG0	FLALAWDDL	NLCLFSYHRL	RDFILIAART	VELPGHSSLK	GLRLGWEGLK
A_UG_U455_	FLAIAWDDL	NLCLFSYHRL	RDFALIVARA	VELLGRSSLK	GLRLGWEGLK
AC_IN_2130	FLALFWDDL	SLCLFSYHRL	RDFILIAKRT	VELLGHSSLK	GLRLGWEGLK
AC_RW_92RW	FLALAWDDL	SLCLFSYHRL	RDLILIAART	VELLGRSSLR	GLQRGWETLK
AC_SE_SE94	FLALAWDDL	SLCLFSYHRL	RDFILI....	...LG.HSSLK	GLRLGWEGLK
ACD_SE_SE8	FLALAWDDL	SLCLFSYHRL	RDLILIAARI	VELLGRR...GWEAIK
ACG_BE_VI1	FFALAWDDL	SLCIFLYHHL	RDLILIAART	VELLG.....QRGWEALK
AD_SE_SE69	FSALIWDDL	NLCLFSYHRL	RDLILIALRI	VELLGRR...GWEALK
AD_SE_SE71	FLAIAWDDL	SLCLFSYHRL	RDLILIAARI	VELLGRR...GWEALK
ADHK_NO_97	FLPLVWDDL	NLCLFSYHRL	RDLILILART	VELLGSR...GWETLK
ADK_CD_MAL	FSALIWDDL	NLCLFSYHRL	RDLILIAART	VELLGRR...GWEALK
AG_BE_VI11	FLTLVWDDL	NLCLFSYHRL	RDLVLIART	VELLGRR...GWEALK
AG_NG_92NG	FLALAWDDL	NLCLFSYHRL	RDLVLIART	VELLGRSSLR	GLRLGWEGLK
AGHU_GA_VI	FLPLIWDDL	NLCLFSYHRL	RDLILIVART	VELLGRR...GWEALK
AGU_CD_Z32	FLPLAWDDL	SLCLFCYHRL	RDCALIAARI	VELLGR...GWEALK
AJ_BW_BW21	FLALAWDDL	NLCLFSYHRL	RDFALIAART	VELLGR...GWEALK
B_AU_VH_AF	FLALIWDDL	SLCLFSYHRL	RDLILIAARI	VELLGR...GWEALK
B_CN_RL42_	FLSLIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_DE_D31_U	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_DE_HAN_U	FLALFWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_FR_HXB2_	SLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_GA_OYI_	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_GB_CAM1_	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_GB_GB8_C	FLALFWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_GB_MANC_	FLALVWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_KR_WK_AF	FLTLIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_NL_3202A	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_TW_TWCYS	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_BC_L0	FLALFWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_DH123	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_JRCSE	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_MNCG_	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_P896_	FLALFWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_RF_M1	FLTLIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_SF2_K	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_WEAU1	FLTLIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_WR27_	LLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
B_US_YU2_M	FLALIWDDL	SLCLFSYHRL	RDLILIVARI	VELLGR...GWEALK
BF1_BR_93B	FLALVWDDL	NLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
C_BR_92BR0	FLALAWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
C_BW_96BW0	FLALVWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
C_BW_96BW1	FLALAWDDL	SLCLFCYHRL	RDFILIAART	VELLGR...GWEALK
C_BW_96BW1	FLALAWDDL	SLCLFSYHRL	RDSILVART	VELLGR...GWEALK
C_BW_96BW1	FLALAWDDL	SLCLFSYHRL	RDLILVART	VELLGR...GWEALK
C_ET_ETH22	FLAIFWDDL	SLCLFSYHRL	RDLILIAART	VELLGR...GWEALK
C_IN_93IN1	FLALAWDDL	NLCLFSYHRL	RDFISVART	VELLGR...GWEALK
C_IN_93IN9	FLALAWDDL	NLCLFSYHRL	RDFILVART	VELLGR...GWEALK
C_IN_93IN9	FLALAWDDL	SLCLFSYHRL	RDFILVART	VELLGR...GWEALK
C_IN_94IN1	FLALAWDDL	SLCLFSYHRL	RDFILVART	VELLGR...GWEALK
C_IN_95IN2	FLALFWDDL	NLCLFSYHRL	RDFILVART	VELLGR...GWEALK
CRF01_AE_C	FLSLAWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
CRF01_AE_C	FLALAWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
CRF01_AE_C	FLALVWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
CRF01_AE_T	FLSLAWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
CRF01_AE_T	FLTLAWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK
CRF01_AE_T	FLALAWDDL	SLCLFSYHRL	RDFILIAART	VELLGR...GWEALK

CRF01_AE_T	FLALAWDDLR	SLCLFLYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFSYHRL	RDLTLIAART	VELLGHSSLK	GLRRGWEGLK
CRF01_AE_T	FLALAWDDLR	SLCLFLYHRL	RDFILIAART	VELLGHSSLK	GLRRGWEGLK
CRF02_AG_F	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGHSSLK	GLRLGWEALQ
CRF02_AG_F	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGHSSLK	GLRLGWEALQ
CRF02_AG_G	FLALAWDDLR	NLCLFSYHRL	RDLILIAART	VEILGHR...VWQILK
CRF02_AG_N	FLALAWDDLR	SLCLFSYHRL	RDLILIAART	VELLGHNCCLK	GLRLGWGALK
CRF02_AG_S	FLALAWDDLR	SLCLFSYHRL	RDFVSIVART	VELLGH...GWEALK
CRF02_AG_S	FLALAWDDLR	SLCLFLYHRL	RDFVLIIVRA	VELLGHSSLK	GLRLGWEALQ
CRF03_AB_R	FLALAWDDLR	SLCFFIYHHL	RDLILIAART	VELLGH...GWEALK
CRF03_AB_R	FLALAWDDLR	SLCFFIYHHL	RDLILIAART	VELLGH...GWEALK
CRF04_cpx_	FLPLIWDDLR	NLCLFSYHRL	RNLILLIVART	VELLGIR...GWEALK
CRF04_cpx_	FLPLIWDDLR	NLCLFSYHRL	RNLILLIVART	VELLGIR...GWEALK
CRF04_cpx_	FLPLIWDDLR	NLCLFSYHRL	RNLILLIVART	VELLGIR...GWEALK
CRF04_cpx_	FLPLIWDDLR	NLCLFSYHRL	RNLILLIVART	VELLGIR...GWEALK
CRF05_DF_B	FSALIWDDLR	NLCLFSYHRL	RDLTLIVVRI	VELLGH...GWEALK
CRF05_DF_B	FSALIWDDLR	NLCLFSYHRL	RDLTLIVVRI	VELLGH...GWEALK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFGLIAART	VEILGHR...GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFGLIAART	VEILGHR...GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGH...GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGH...GWEILK
CRF06_cpx_	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VELLGH...GWEILK
CRF11_cpx_	FLALAWDDLR	NLCLFSYHRL	RDFILIVARI	VETLGH...GWEILK
CRF11_cpx_	FLALAWDDLR	NLCLFSYHRL	RDFILIVARI	VETLGH...GWEILK
D_CD_84ZRO	FSALIWDDLR	NLCLFSYHRL	RDFILIVARI	VETLGH...GWEILK
D_CD_ELI_K	FSALIWDDLR	NLCLFSYHRL	RDFILIVARI	VETLGH...GWEILK
D_CD_NDK_M	FLALAWDDLR	SLCLFSYHRL	RDLILIAART	VELLGH...GWEILK
D_UG_94UG1	LSALIWDDLR	NLCLFSYHRL	RDLILIAART	VELLGH...GWEILK
F1_BE_VI85	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLRR...GWEALK
F1_BR_93BR	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLRR...GWEALK
F1_FI_FIN9	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLRR...GWEALK
F1_FR_MP41	FLALAWDDLR	NLCLFSYHRL	RDFILIAART	VDRGLRR...GWEALK
F2_CM_MP25	FLALAWDDLR	SLCVFSYHCL	RNFILIAART	VDKGLKR...GWEVLK
F2KU_BE_VI	FLALAWDDLR	NLCLFSYHRL	RDLILIVARI	LERGLRG...SWEILK
G_BE_DRCBL	FLALAWDDLR	SLCLFSYHRL	RDFILIAART	VELLGRNSLK	GLRLGWEALQ
G_NG_92NG0	FLALAWDDLR	SLCLFSYHRL	RDLVLIIVRA	VELLGRSSLK	GLRLGWEALQ
G_SE_SE616	FLPLIWDDLR	SLCLFSYHRL	RDSILIVART	VELLGRSSLK	GLRLGWEALQ
H_BE_VI991	FLPLIWDDLR	NLCLFSYHRL	RDLILIVART	VELLGR...GWEALK
H_BE_VI997	FLPLIWDDLR	SLCLFSYHRL	RDSLLIVART	VELLGR...GWEALK
H_CF_90CF0	FLPLIWDDLR	SLCLFSYHRL	RDLILIVART	VELLGR...GWEALK
J_SE_SE702	FLALAWDDLR	SLCLFSYHRL	RDFVLIIVRA	VGTLGLR...GWEILK
J_SE_SE788	FLALAWDDLR	NLCLFSYHRL	RDFVLIIVRA	VGTLGLR...GWEILK
K_CD_EQTB1	FLALAWDDLR	NLCLFSYHRL	RDLVLIIVRA	LDRGLKG...SWEALK
K_CM_MP535	FLALAWDDLR	NLCLFSYHRL	RNLILIVART	LERGLRG...GWEALK
N_CM_YBF30	FSALIWDDLR	NLCLFSYHRL	TDSLLIVART	LELLGQSLR	GLQLLNELRT
O_CM_ANT70	FLPLIWDDLR	TIILWYHLL	SNLASGIQV	ISYLRGLWI	LGQKIINVCR
O_CM_MVP51	FLQQLYTDLR	TIILWYHLL	SNLASGIQV	IDYLRGLWI	LGQKTIACR
O_SN_99SE_	FLPLIWDDLR	TIILWYHLL	SNLASGIQV	ISHLGLGLWT	LGQKIISACR
O_SN_99SE_	FLPLIWDDLR	TIILWYHLL	SNLASGIQV	ISHLGLGLWT	LGQKIISACR
U_CD_83C	FLALAWDDLR	SLCLFSYHRL	RDLILIVVKG	...LRR....GWEALK

	901		950
00BW0762_1	YLGILVQYWG	LELKKS AISL	FDTIAIAVAE GTDRIIEAIQ RICRAICNIP
00BW0768_2	YLGNLVLYWG	LELKKS AISL	LDSIAIAVAE GTDRILEAVQ RIWGAIRNIP
00BW0874_2	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIELIQ RICRAIYNIP
00BW1471_2	YLGSLGQYWG	QELKKSAINL	FDTIAIAVAE GTDRIIEAVQ RAVRAILHIP
00BW1616_2	YLGSLVQYWG	LELKKS AVSL	LDTIAIAVAE GTDRILEVTQ RICRVIRNIP
00BW1686_8	YLGSLIQYWG	LELKKS AISL	LDTIAIAVAG GTDRFIELIQ RIYRAIRNVP
00BW1759_3	YLGSLGQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIELIQ TICRAIRNIP
00BW1773_2	YLGNLVQDWG	LELKKS AISL	FDAIAIAVAE GTDRIIELIQ RTGRAICNIP
00BW1783_5	YLGTLVQYVW	LELKKS AISL	LDTAIAVAG GTDRIIELIQ RIGRAILSIP
00BW1795_6	YLGSLVQYWG	LELKKS AISL	LDTVAIAVAE GTDRIIELIQ RGYRAICNIP
00BW1811_3	YLGSLVQYWG	LELKKS AISL	LDTIAIAVGE GTDRIIEIIQ RICRAIRNTP
00BW1859_5	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIDLIQ RICRAILRIP
00BW1880_2	YLGSLIQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIEGIQ RICRIIRNIP
00BW1921_1	YLGSLIQYWG	LELKKS AISL	LDTIAIATAE GTDRIIEVIQ RICRVIRNIP
00BW2036_1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIELVQ RIGRGIYNIP
00BW2063_6	YLGSLVQYWG	LELKKS AISL	LNTTIAIAVAE GTDRVIELLQ RIGRAICNIP
00BW2087_2	YLGSLVQYWG	LELRKSASSL	LDTIAIAVAE GTDRIIEVIQ IICRAILHIP
00BW2127_2	YLGNLVLYWG	LELKKS AISL	FDTIAVAVAE GTDRILEVIQ RICRAIRNIP
00BW2128_3	YLGSLVQYWG	LELKKS AVSL	LNTIAIVVAE GTDRILELIQ RLRR AFLNIP
00BW2276_7	YLGSLVQYWG	LELKKS AISL	INTIAIAVGE RTDRIIELIQ TLCRAIHNIP
00BW3819_3	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIEFLQ RIFRAIRNIP
00BW3842_8	YLGSLVQYWG	LELKKS AISL	LDAIAIAVGE GTDRILELLO RIGRGICNIP
00BW3871_3	YLGSLIQYWG	LELKKSAINL	LDTTIAIAVAE GTDRFIELIQ RICRAVRNIP
00BW3876_9	YLGSLVQYWG	LELKKS AISL	LNTIAIAVAE GTDRVIEFVL RICRAIRHIP
00BW3886_8	YLGSLVQYWG	LELKKS SATSL	LDTIAIAVAE GTDRIIETVL RICRAILHIP
00BW3891_6	YLGSLVQYWG	LELKKS AISL	LDTIAIVVAE GTDRIIELVL GICRAIRNVP
00BW3970_2	YLGSLVQYWG	LELKKS AISL	LDSIAIAVAE GTDRIIAFIQ RLFRACNLP
00BW5031_1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE GTDRIIEVVQ RLYRAILNIP
96BW01B21	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRILELVQ GICRAIRNIP
96BW0407	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEIAQ RICRAICNVP
96BW0502	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEFIQ RICRAIRNIP
96BW06_J4	YLGSLIQYWG	LELKKS AISL	LDTVPIAVPE GTDRIIEIIQ RIWRAICNIP
96BW11_06	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEVLQ RIGRAIRNTP
96BW1210	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIELTQ RVFAIRNIP
96BW15B03	YLGSLVQYWG	LELKKS SATSL	LDSIAIAVAE GTDRIIEVIQ RIYRAFCNIP
96BW16_26	YLGSLVQYWG	LELKKSAINL	LDTIAIAVAE GTDRIIDFIL RICRAIRNIP
96BW17A09	YLGSLGQYWG	QELKKSAINL	LDTIAIAVAE GTDRIIEVLQ GAIIRAILNIP
96BWMO1_5	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEVLQ RVGRAIRNTP
96BWMO3_2	YLGSLVRYWG	LELKKS AISL	LDTIAIAVAE GTDRIIEVIQ GICRGIRNIP
98BWMC12_2	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEIVL RICRAICNVR
98BWMC13_4	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIELLQ RIGRAIRNTP
98BWMC14_a	YLGSLVQYWG	LELKKSAINL	LDTTIAIAVAE GTDRIIEIIQ RVCRAILNIP
98BWMO14_1	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEIIQ IICRAIRNIP
98BWMO18_d	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIELVQ RICRGVLNIP
98BWMO36_a	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEIIQ RICRAIYNIP
98BWMO37_d	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIEFIQ RICRAIRNLP
99BW3932_1	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRILEIIQ RIFRAICNIP
99BW4642_4	YLGSLVQYWG	LELKKS SATSL	IDAIAIAVAE GTDRIIDLIQ RICRAIRNIP
99BW4745_8	YLGSLVQYWG	LELKKS AISL	FDTIAIAVAE GTDRIIELVL RICGAIRNIP
99BW4754_7	YLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE GTDRIIELLR RFCRAIYSIP
99BWMC16_8	YLGSLGQYWG	QELKKS AISL	LDTTIAIAVAE GTDRIIEIIQ RTFRAICNIP
A2_CD_97CD	HLWNLLVYWG	QELKKS AISL	LDTTIAIAVAE WTDRIIEIIQ RACRAIRNIP
A2_CY_94CY	HLWNLLVYWG	RELKKS AISL	FDTIAIAVAE WTDRIIEIIQ RAFAIRNIP
A2D_97KR	YLGSLVQYWG	RELKKS AISL	FNATAIAVAE WTDRIIEIIQ RACRAIRNIP
A2G_CD_97C	YLGSLVQYWG	RELKKS AISL	LDTTIAIAVAE WTDRIIEIIQ GACRAIRNIP
A_BY_97BL0	YLGSLVQYWG	RELKKS AISL	FNATAIAVAE WTDRIIEIIQ RFCRAIRNIP
A_KE_Q23_A	YLGSLVQYWG	RELKKS AISL	FNATAIAVAE WTDRIIEIIQ RIGRAILHIP
A_SE_SE659	YLGSLVQYWG	RELKKS AISL	FNATAIAVAE WTDRIIEIIQ GIGRAFLHIP
A_SE_SE725	YLGSLVQYWG	RELKKS AISL	FNATAIAVAE WTDRIIEIIQ RIGRAILNIP

A_SE_SE753	YLWNLLLYWG	RELKSSAINL	VDTIAIAVAG	WTDRIIEIGL	RIGRAFLHIP
A_SE_SE853	YLWNLLVYWI	RELKISAIISL	LDTIAIAVAG	WTDREVIELGQ	RLCRAILHIP
A_SE_SE889	YLKNLLSYWG	RELKLSAINL	LDTIAIVVAG	WTDREVIEIGQ	GFCRAIFHP.
A_SE_UGSE8	YLGNNLLYWI	RELKISAIISL	FDTIAIAVAG	WTDREVIEIGQ	RIGRAILHIP
A_UG_92UG0	YLGNNLLYWG	RELKISAINL	LDTIAIAVAG	WTDREVIVTQ	RLGRAILNIP
A_UG_U455	YLWNLLLYWG	RELKISAITL	LDAVAVAVAG	WIDRVIEIGQ	TIGRAILNIP
AC_IN_2130	YLWNLLVYWG	RELKISAIKL	VDTIAIVVAG	WTDRIIEIGQ	GIGRAILHIP
AC_RW_92RW	YLGNLVQYWG	LELKRSAINL	LDTTIAIVVAE	GTDRRIELIQ	RISRATYNIP
AC_SE_SE94	YLWNLLLYWG	RELKRISAINL	LDTIAIATAS	WTDREVIELGQ	RICRAILNIP
ACD_SE_SE8	YLWNLLQYWI	QELKNSAINL	FNTIAIAVAE	GTDRVIEIGQ	RIGRAILNTP
ACG_BE_VI1	LLGNILLYWS	QELKNSAINL	LDTIAIAVAN	WTDREVIEIGQ	RAGRAFLNIP
AD_SE_SE69	YLWNLLQYWI	QELKNSAISL	VDTTIAIAVAE	GTDRVIETVQ	RAFRVLRIP
AD_SE_SE71	YLWNLLQYWI	QELKISAIISL	VDSIAIVVAG	WTDREVIEIGQ	GIGRAILHIP
ADHK_NO_97	YLGNNLLYWG	QELKNSAINL	LNTTIAIAVAE	GTDRRIEIVQ	RTGRAVLHIP
ADK_CD_MAL	YLWNLLQYWG	QELKNSAISL	LNTTIAIAVAE	CTDRVIEIGQ	RFGRAILHIP
AG_BE_VI11	YLWNLLVYWG	QELKNSAINL	LDTVAIAVAN	WTDREVIEIGQ	RAGRAILNIP
AG_NG_92NG	YLWNLLLYWG	RELKNSAINL	IDTIAIAVAN	WTDREVIEVQ	GACRAILNIP
AGHU_GA_VI	YLWNLLLYWG	QELKSSAISL	LDAVAIAVAN	WTDREVIEVQ	RVGRAILNIP
AGU_CD_Z32	YLGNLVYWG	QELKNSAINL	LDTVAIAVAD	WTDREVIEVQ	RAGRAFLNIP
AJ_BW_BW21	YLGNLALYWG	RELKNSAISL	LDTIAITVAE	ATDRIIEIAQ	RAFRAILHIP
B_AU_VH_AF	YWWNLLQYWS	QELQNSAISL	LNATAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_CN_RL42	YWWNLLQYWI	QELKNSAIGL	LNATAIAVAE	GTDRVIEVVQ	RAYRAILHIP
B_DE_D31_U	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	RAWRAILHIP
B_DE_HAN_U	YWWNLLQYWS	QELKNSAVSL	FNTIAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_FR_HXB2	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	GACRAIRHIP
B_GA_OYI	YWWNLLQYWS	QELKNSVISL	LNATAIAVAE	GTDRVIEIVQ	RAYRAFLNIP
B_GB_CAM1	YWWNLLQYWS	QELRNSAVSL	FDTIAIAVAE	GTDRVIEVVQ	RACRAILHIP
B_GB_GB8_C	YWWNLLQYWI	QELKNSAISL	LNTTIAIAVAE	GTDRVIEVVQ	RAYRAILHIP
B_GB_MANC	YWWNLLQYWS	QVLKNSAVSL	LNVTIAIAVAE	GTDRRIEIVQ	RVGRAILHIP
B_KR_WK_AF	YLWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRRIEILQ	RAYRAILNIP
B_NL_3202A	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIEVVQ	RACRAVLHIP
B_TW_TWCYS	YLWNLLQYWI	QELKNSAVSL	FNAIAIAVAE	GTDRVIEVVQ	RVFRAILHIP
B_US_BC_L0	YWWSLQYWS	QELKNSAVNL	LNVTIAIAVAE	GTDRVIEVVQ	RTYRAILHIP
B_US_DH123	YLWNLLQYWS	QELKNSAVSL	LNATAIAVGE	GTDRRIEILQ	RAGRAILNIP
B_US_JRCSF	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRRIEIVQ	RVYRAILHIP
B_US_MNCG	YWWNLLQYWS	QELKSSAVSL	LNATAIAVAE	GTDRVIEVLQ	RAGRAILHIP
B_US_P896	YWWNLLQYWS	QELKNSAVSL	LNATAIAVAE	GTDRVIKIVQ	RACRAIRNIP
B_US_RF_M1	YWWNLLQYWS	QELKNSAVSL	LNTTIAIAVAE	GTDRRIEVAQ	RILRAFLHIP
B_US_SF2_K	YWWSLQYWI	QELKNSAVSW	LNATAIAVTE	GTDRVIEVAQ	RAYRAILHIH
B_US_WEAU1
B_US_WR27	YWGNNLQYWG	QELRNSAISL	LNATAIAVAE	GTDRVIEVGQ	RIFRAILHIP
B_US_YU2_M	YWWNLLQYWI	QELKNSAVSL	LNATAIAVAE	GTDRVIEILQ	RAFRVLRHIP
BF1_BR_93B	LLGNLALYWS	QELKNSAISL	LNTTIAIVVAE	GTDRVIEALQ	RAGRAVLNVP
C_BR_92BR0	YLGGLVQYWS	LELKKS AISL	FDTIAIAVAE	GTDRRIEVIQ	GIWRAICNIP
C_BW_96BW0	FLGSLVQYWG	LELKKS AISL	LDTTIAIAVAE	GTDRRIEIAQ	RICRAICNIP
C_BW_96BW1	YLGSLVQYWG	LELKMS TISL	LDTTIAIAIAE	GTDRRIELIQ	RIGRAIRNTP
C_BW_96BW1	YLGSLVQYWG	LELKKS AISL	LDTIAIAVAE	GTDRRIELTQ	RVFRAIRNIP
C_BW_96BW1	YLGSLVQYWG	LELKKSATS L	LDSIAIAVAE	GTDRRIEVIQ	RIYRAPCNIP
C_ET_ETH22	YLGSLVQYWG	LELKKSAINL	LNTTIAIVVGE	GTDRPIELIQ	RIWRAFCNIP
C_IN_93IN1	YLGSLVQYWG	LELKKS AISL	FDSIAIVVAE	GTDRRIELVQ	GFCRAIRNIP
C_IN_93IN9	YLGSLVQYWG	LELKKS AISL	LDIIAIAVAE	GTDRRIELIQ	RTCRAIRNIP
C_IN_93IN9	YLGSLVQYWG	IELKRS AISL	LDFTAIAVAE	GTDRRIELVL	RICRAIRNIP
C_IN_94IN1	YLGSLVQYWG	LELKKS AIRL	LDIIAIAVAE	GTDRRIEIIQ	GTCAIRNIP
C_IN_95IN2	YLGSLVQYWG	LELKKSAINL	LDRIAIAVAE	GTDRILELVQ	RICRAIRNIP
CRF01_AE_C	YLGNNLSYWG	QELKTSAITL	FDAIAVAVAG	WTDREVIEVVQ	RAWRAILHIP
CRF01_AE_C	YLGNNLSYVW	QELRISAITL	LDATAITVAG	WTDREVIEIVQ	RAWRAILHIP
CRF01_AE_C	YLGSLLSYWG	QELKTSAITL	LDATAITVAG	WTDRAIEIAQ	RACRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	LNTTIAIAVAG	WTDREVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	LDATAIAVAG	WTDREVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLGNNLLYWG	QELKISAIISL	FDALAVVVAG	WTDREVIEVAQ	GAWRAILHIP

CRF01_AE_T	YLGNNLLLYWG	QELKISAIISL	LDAIAIAVAG	WTDRVIKVAQ	RAWRAILHIP
CRF01_AE_T	YLGNNLLLYWG	QELKISAIISL	LDATAIAAAG	WTDRVIEVAQ	GAWRAILHIP
CRF01_AE_T	YLWNLLVYWG	QELKISVISL	LNATAIVVAG	WTDRVIEVAQ	GAWRAILHIP
CRF02_AG_F	YLGNNLLLYWG	QELKNSAINL	LDTIALAVAN	WTDRVIEIGQ	RVGRAILNIP
CRF02_AG_F	YLGNNLLTYWG	QELKNSAINL	LDTIAIAVAN	WTDRVIEIGQ	RVGRAIRNIP
CRF02_AG_G	YLGNNLAQYWG	LELKNSAISL	LNTTAIVVAE	QTDRLLLEFLQ	RAGRAILHIP
CRF02_AG_N	YLWNLLISYVW	QELKNSAINL	LNTIAIVVAN	WTDRAIEIGQ	RVGRAIRNIP
CRF02_AG_S	YLWNLLSYWG	QELKNSAISL	LDTIAIVVAN	WTDRVIELVQ	RAGRAILNIP
CRF02_AG_S	HLWNLLSYWG	QELKNSAINL	LDTTAVAVAN	WTDRVIEIVQ	RTGRAICNIP
CRF03_AB_R	YWWNLLQYWI	QELKSSAINL	IGTIAIAVAG	WTDRVIEIGQ	RFCRAMRNIP
CRF03_AB_R	YWWNLLQYWI	QELKSSAINL	INTIAIAVAG	WTDRVIEIGQ	RFCRAIRNIP
CRF04_cpx_	YLWNFLLYWG	QELKNSAINL	FNTTAIAVAE	GTDRIEEAVQ	RACRAICNIP
CRF04_cpx_	YLWNLLLYWG	QELRNSAINL	LDTTAIAVAE	GTDRILEAVQ	RACRAIRNIP
CRF04_cpx_	YLWNLLLYWG	QEIRSSAISL	LDTTAVAVAE	GTDRIEEAVQ	RICRAILNIP
CRF05_DF_B	YLWSLPQYWS	RELKNSAISL	LNTTAVVVAE	GTDRVIEALQ	RAGRAILNIP
CRF05_DF_B	YLWSLLQYWS	QELKNSAISL	LNTTAVVVAE	GTDRILEALQ	RAGRAVLNIP
CRF06_cpx_	YLGNLICYWG	QELQNSAISL	FDAAIAIVAN	WTDRVAEVVQ	RIFRAFLNVP
CRF06_cpx_	YLGSLVWYWG	QELKNSAINL	LDTTAIAVAN	GTDRVIEIVQ	RAFRAVLNIP
CRF06_cpx_	YLWNLVQYWG	QELKNSAISL	IDTTAIAVAN	WTDRVIEVVQ	RAFRAVLNIP
CRF06_cpx_	YLGNLVQYWG	QELKNSAISL	LDTTAIAVAN	WTDRVIEIVQ	RVFRAFLNVP
CRF11_cpx_	YLGNLTYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEIVQ	RVLRGILHIP
CRF11_cpx_	YLGNNLAQYWG	QELKSSAISL	LNATAIAVAE	GTDRIEEVAH	RALRAILNIP
D_CD_84ZR0	YLWNLLQYWS	RELKNSAISL	VDATAIAVAE	GTDRIIDIVR	RACKAVLHIP
D_CD_ELI_K	YLWNLLQYWS	QELRNSASSL	FDAIAIAVAE	GTDRVIEIIQ	RACRAVLNIP
D_CD_NDK_M	YLWNLLQYWS	QELRNSASSL	LDTIAIAVAE	RTDRVIEVVQ	RACRAILNVP
D_UG_94UG1	YLWNLLQYWI	QELKNSAVSL	FNTIAIAVAE	GTDRVIEIVQ	RAVRAILNIP
F1_BE_VI85	YLGNNTRYWG	QELKNSAISL	FNTTAIVVAE	GTDRIEEVLQ	RAGRAVLNIP
F1_BR_93BR	YLGNNLTQYWG	QELKNSAISL	LNATAIAVAE	WTDRVIEALQ	RAGRAILNIP
F1_FI_FIN9	YLGNNIIQYWS	QELKNSAISL	FNTTAIVVAE	GTDRVIEALQ	RAVRAVLNIP
F1_FR_MP41	YLWNLAQYWS	QELKNSAISL	LNTTAIVVAE	GTDRVIEVLQ	RAGRAVLNVP
F2_CM_MP25	YLWNLAQYWG	QELKNSAISL	LDRTAIAVAE	GTDRIEEILQ	RAGRAVLNIP
F2KU_BE_VI	YLWSLVQYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEVFQ	RAGRAVLNIP
G_BE_DRCBL	YLWNLLLYWA	RELKNSAINL	LDTIAIAVAN	WTDRVIEVAQ	RAGRAVLNIP
G_NG_92NG0	YLWNLLLYWG	RELKNSAINL	LDTIAIATAN	GTDRVIEVAQ	RAYRAILNVP
G_SE_SE616	YLWNLLLYWG	RELKNSAISL	LDTVAIAVAN	WTDRVIEVAQ	RACRAILNIP
H_BE_VI991	LLGNLLLYWG	QELKNSATSL	LNTTAIAVAE	GTDRIEELVQ	RAWRAILHIP
H_BE_VI997	YLWNLLQYWG	QELKNSAINL	LNTTAIVVAE	GTDRIEEIVQ	RAWRAVLHIP
H_CF_90CF0	YLWNLLQYWG	QELKNSAIDL	LNTTAIAVAE	GTDGIIIVVQ	RAWRAILHIP
J_SE_SE702	YLVNVLVYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEIAQ	RAFRAILHIP
J_SE_SE788	YLVNVLVYWG	QELKNSAISL	LNTTAIAVAE	GTDRIEEIAQ	RAFRAILHIP
K_CD_EQTB1	YLWNLLLYWG	QELKNSAINL	LNTTAIAVAE	GTDRIEEIVQ	RAFRALLHIP
K_CM_MP535	YLWNLVQYWS	QELKNSAISL	LNTTAIAVAG	GTDRIEEIGQ	RAFRALLHIP
N_CM_YBF30	HLWGILAYWG	KELRDSAISL	LNTTAIVVAE	GTDRIEELAQ	RIGRGILHIP
O_CM_ANT70	ICAAVTQYWL	QELQNSATSL	LDTLAVAVAN	WTDGIIAGIQ	RIGTGIRNIP
O_CM_MVP51	LCGAVMQYWL	QELKNSATNL	LDTIAVSVAN	WTDGIIILGLQ	RIGQGFLHIP
O_SN_99SE_	LCIAVIQYWL	QELQNSATSL	LDTIAVAVAN	WTVTIILGIQ	RIGRGILNIP
O_SN_99SE_	ICIAVIQYWL	QELQNSATSL	LDTLAVAVAN	WTDGIIILGLQ	RIGRGILNIP
U_CD_83C	YLGNNLVLYWG	QELKNSAISL	LNATAIVVAE	GTDRIEEVGQ	RICRAILNIP

	951	962
00BW0762_1	RRIRQGFEEA	LQ
00BW0768_2	RRIRQGFEEA	LQ
00BW0874_2	RRIRQGFEEA	LQ
00BW1471_2	RRIEQTFEPP	LL
00BW1616_2	RRIRQGFEEA	LQ
00BW1686_8	RRIRQGFETA	LL
00BW1759_3	RRIRQGFEEA	LQ
00BW1773_2	RRIRQGFEEA	LQ
00BW1783_5	RRIRQGFEEA	LQ
00BW1795_6	TRIRQGFEEA	LQ
00BW1811_3	RRIRQGFEEA	LL
00BW1859_5	RRIRQGFEEA	LL
00BW1880_2	TRIRQGFEEA	LQ
00BW1921_1	TRIRQGFEEA	LQ
00BW2036_1	RRIRQGFEEA	LQ
00BW2063_6	RRVRQGFETA	LL
00BW2087_2	RRIRQGFEEA	LL
00BW2127_2	TRIRQGFEEA	LL
00BW2128_3	SSIRQGFEEA	LQ
00BW2276_7	RRIRQGFEEA	LL
00BW3819_3	TRIRQGFEEA	LL
00BW3842_8	RRIRQGFEEA	LQ
00BW3871_3	RRIRQGFEEA	LL
00BW3876_9	RRIRQGFEEA	LL
00BW3886_8	RRIRQGFEEA	LL
00BW3891_6	TRIRQGFEEA	LQ
00BW3970_2	RRIRQGFEEA	LL
00BW5031_1	RRIRQGFEEA	LQ
96BW01B21	RRIRQGFEEA	LQ
96BW0407	TRIRQGFEEA	LQ
96BW0502	RRIRQGFEEA	LQ
96BW06_J4	RRIRQGFEEA	LL
96BW11_06	RRIRQGFETA	LL
96BW1210	RRIRQGFEEA	LQ
96BW15B03	RRVRQGFEEA	LQ
96BW16_26	RRIRQGFEEA	LQ
96BW17A09	TRIRQGLEAA	LQ
96BWM01_5	RRIRQGFEEA	LL
96BWM03_2	RRIRQGFEEA	LL
98BWMC12_2GFEEA	LQ
98BWMC13_4	RRIRQGFETA	LL
98BWMC14_a	RRVRQGFEEA	LQ
98BWM014_1	TRIRQGLEAA	LL
98BWM018_d	RRIRQGFEEA	LQ
98BWM036_a	TRIRQGFEEA	LL
98BWM037_d	RRIRQGFEEA	LL
99BW3932_1	RRIRQGFETA	LL
99BW4642_4	RRIRQGFEEA	LQ
99BW4745_8	TRIRQGFEEA	LQ
99BW4754_7	RRIRQGFEEA	LQ
99BWMC16_8	RRIRQGFETA	LL
A2_CD_97CD	RRIRQGLERA	LL
A2_CY_94CY	RRIRQGLERA	LL
A2D_97KR	RRIRQGLERA	LL
A2G_CD_97C	RRIRQGLERA	LL
A_BY_97BL0	RRIRXGAEKA	LQ
A_KE_Q23_A	VRIRQGLERA	LL
A_SE_SE659	RRIRQGFEEA	LL
A_SE_SE725	RRIRQGFEEA	LL

A_SE_SE753	RRIRQGFERA	LL
A_SE_SE853	VRIRQGFERA	LL
A_SE_SE889	RRSKQGLKRA	LQ
A_SE_UGSE8	RRIRQGFER.	..
A_UG_92UG0	RRIRQGFERA	LL
A_UG_U455_	RRIRQGLERA	LL
AC_IN_2130	RRIRQGLERA	LL
AC_RW_92RW	SRIRQGFEEA	LQ
AC_SE_SE94	RRIRQGFERA	LL
ACD_SE_SE8	RRIRQGLERA	LL
ACG_BE_VI1	RRIRQGFERA	LL
AD_SE_SE69	ARIRQGLERV	LL
AD_SE_SE71	RRIRQGLERA	LL
ADHK_NO_97	RRIRQGFERX	LL
ADK_CD_MAL	RRIRQGFERA	LL
AG_BE_VI11	RRIRQGLERA	LL
AG_NG_92NG	RRIRQGLERA	LL
AGHU_GA_VI	RRIRQGLERA	LI
AGU_CD_Z32	RRIRQGLERA	LL
AJ_BW_BW21	VRIRQGFERA	LL
B_AU_VH_AF	RRIRQGLERL	LL
B_CN_RL42_	TRIRQGLERA	LL
B_DE_D31_U	VRIRQGLERA	LL
B_DE_HAN_U	RRVRQGLERA	LL
B_FR_HXB2_	RRIRQGLERI	LL
B_GA_OYI_	RRIRQGLERA	LL
B_GB_CAM1_	RRIRQGLERL	LL
B_GB_GB8_C	TRIRQGLERA	LQ
B_GB_MANC_	VRIRQGLERA	LL
B_KR_WK_AF	RRIRQGLERA	LL
B_NL_3202A	VRIRQGLERA	LL
B_TW_TWCYS	TRIRQGLERA	LL
B_US_BC_L0	RRIRQGLERL	LL
B_US_DH123	TRIRQGLERA	LL
B_US_JRCSE	TRIRQGLERA	LL
B_US_MNCG_	TRIRQGLERA	LL
B_US_P896_	TRIRQGLERA	LL
B_US_RF_M1	RRIRQGLERA	LL
B_US_SF2_K	RRIRQGLERL	LL
B_US_WEAU1
B_US_WR27_	RRIRQGLERV	LL
B_US_YU2_M	VRIRQGLERA	LL
BF1_BR_93B	RRIRQGLERA	LL
C_BR_92BR0	RRIRQGFEEA	LQ
C_BW_96BW0	TRIRQGFEEA	LQ
C_BW_96BW1	RRIRQGFETA	LL
C_BW_96BW1	RRIRQGFEEA	LQ
C_BW_96BW1	RRVRQGFEEA	LQ
C_ET_ETH22	RRIRQGLEAA	LQ
C_IN_93IN1	TRIRQGFEEA	LQ
C_IN_93IN9	RRIRQGFEEA	LQ
C_IN_93IN9	TRIRQGFETA	LQ
C_IN_94IN1	RRIRQGLEAA	LQ
C_IN_95IN2	RRIRQGFEEA	LQ
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_C	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERT	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERA	LL

CRF01_AE_T	RRIRQGLERA	LL
CRF01_AE_T	RRIRQGLERT	LL
CRF01_AE_T	RRIRQGLERA	LL
CRF02_AG_F	RRIRQGLERA	LL
CRF02_AG_F	VRIRQGLERA	LL
CRF02_AG_G	RRIRQGFERA	LL
CRF02_AG_N	RRIRQGFERA	LL
CRF02_AG_S	RRIRQGFERA	LL
CRF02_AG_S	RRIRQGLERA	LQ
CRF03_AB_R	RRIRQGAEKA	LQ
CRF03_AB_R	RRIRQGAEKA	LQ
CRF04_cpx_	RRIRQGLERA	LL
CRF04_cpx_	RRIRQGFeka	LL
CRF04_cpx_	RRIRQGLERA	LL
CRF05_DF_B	RRIRQGLERA	LL
CRF05_DF_B	RRIRQGLERA	LL
CRF06_cpx_	RRIRQGFERA	LL
CRF06_cpx_	TRIRQGFERA	LL
CRF06_cpx_	RRIRQGAERA	LI
CRF06_cpx_	RRIRQGFERA	LL
CRF11_cpx_	RRIRQGLERA	LL
CRF11_cpx_	RRIRQGFERA	LL
D_CD_84ZR0	TRIRQGLERA	LL
D_CD_ELI_K	RRIRQGLERS	LL
D_CD_NDK_M	RRIRQGLERL	LL
D_UG_94UG1	VRIRQGLERA	LL
F1_BE_VI85	RRIRQGAERA	LL
F1_BR_93BR	RRIRQGLERA	LL
F1_FI_FIN9	RRIRQVERA	LI
F1_FR_MP41	RRIRQGLERS	LL
F2_CM_MP25	RRIRQGLERA	LL
F2KU_BE_VI	RRIRQGFERA	LL
G_BE_DRCBL	RRIRQGLERA	LL
G_NG_92NG0	TRIRQGLERA	LL
G_SE_SE616	TRIRQGLERA	LL
H_BE_VI991	RRIRQGFERA	LL
H_BE_VI997	RRIRQGLERI	LL
H_CF_90CF0	RRIRQGFERS	LL
J_SE_SE702	RRIRQGLERA	LL
J_SE_SE788	RRIRQGLERA	LL
K_CD_EQTB1	RRIRQGFERL	LL
K_CM_MP535	RRIRQGLERA	LL
N_CM_YBF30	RRIRQGLERA	LI
O_CM_ANT70	RRIRQGLERS	LL
O_CM_MVP51	RRIRQGAERI	LV
O_SN_99SE_	RRIRQGLERS	LL
O_SN_99SE_	RRIRQGLERA	LL
U_CD___83C	RRIRQGFERA	LL

Table 13. HIV Nef Sequence Alignment

GCC Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	Len: 232	Check: 3461	Weight: 1.00
Name: 00BW0768_2	Len: 232	Check: 5650	Weight: 1.00
Name: 00BW0874_2	Len: 232	Check: 3483	Weight: 1.00
Name: 00BW1471_2	Len: 232	Check: 9491	Weight: 1.00
Name: 00BW1616_2	Len: 232	Check: 1504	Weight: 1.00
Name: 00BW1686_8	Len: 232	Check: 1380	Weight: 1.00
Name: 00BW1759_3	Len: 232	Check: 5319	Weight: 1.00
Name: 00BW1773_2	Len: 232	Check: 156	Weight: 1.00
Name: 00BW1783_5	Len: 232	Check: 8063	Weight: 1.00
Name: 00BW1795_6	Len: 232	Check: 3123	Weight: 1.00
Name: 00BW1811_3	Len: 232	Check: 4460	Weight: 1.00
Name: 00BW1859_5	Len: 232	Check: 9116	Weight: 1.00
Name: 00BW1880_2	Len: 232	Check: 4302	Weight: 1.00
Name: 00BW1921_1	Len: 232	Check: 2737	Weight: 1.00
Name: 00BW2036_1	Len: 232	Check: 4558	Weight: 1.00
Name: 00BW2063_6	Len: 232	Check: 1020	Weight: 1.00
Name: 00BW2087_2	Len: 232	Check: 7532	Weight: 1.00
Name: 00BW2127_2	Len: 232	Check: 3425	Weight: 1.00
Name: 00BW2128_3	Len: 232	Check: 5136	Weight: 1.00
Name: 00BW2276_7	Len: 232	Check: 3623	Weight: 1.00
Name: 00BW3819_3	Len: 232	Check: 993	Weight: 1.00
Name: 00BW3842_8	Len: 232	Check: 6030	Weight: 1.00
Name: 00BW3871_3	Len: 232	Check: 3547	Weight: 1.00
Name: 00BW3876_9	Len: 232	Check: 1951	Weight: 1.00
Name: 00BW3886_8	Len: 232	Check: 3786	Weight: 1.00
Name: 00BW3891_6	Len: 232	Check: 3655	Weight: 1.00
Name: 00BW3970_2	Len: 232	Check: 8913	Weight: 1.00
Name: 00BW5031_1	Len: 232	Check: 2223	Weight: 1.00
Name: 96BW01B21	Len: 232	Check: 2176	Weight: 1.00
Name: 96BW0407	Len: 232	Check: 5261	Weight: 1.00
Name: 96BW0502	Len: 232	Check: 333	Weight: 1.00
Name: 96BW06_J4	Len: 232	Check: 5784	Weight: 1.00
Name: 96BW11_06	Len: 232	Check: 4950	Weight: 1.00
Name: 96BW1210	Len: 232	Check: 6118	Weight: 1.00
Name: 96BW15B03	Len: 232	Check: 5089	Weight: 1.00
Name: 96BW16_26	Len: 232	Check: 3957	Weight: 1.00
Name: 96BW17A09	Len: 232	Check: 1945	Weight: 1.00
Name: 96BWMO1_5	Len: 232	Check: 5827	Weight: 1.00
Name: 96BWMO3_2	Len: 232	Check: 2303	Weight: 1.00
Name: 98BWMC12_2	Len: 232	Check: 2423	Weight: 1.00
Name: 98BWMC13_4	Len: 232	Check: 4043	Weight: 1.00
Name: 98BWMC14_a	Len: 232	Check: 3568	Weight: 1.00
Name: 98BWMO14_1	Len: 232	Check: 4909	Weight: 1.00
Name: 98BWMO18_d	Len: 232	Check: 3505	Weight: 1.00
Name: 98BWMO36_a	Len: 232	Check: 6393	Weight: 1.00
Name: 98BWMO37_d	Len: 232	Check: 1912	Weight: 1.00
Name: 99BW3932_1	Len: 232	Check: 19	Weight: 1.00
Name: 99BW4642_4	Len: 232	Check: 6848	Weight: 1.00
Name: 99BW4745_8	Len: 232	Check: 938	Weight: 1.00
Name: 99BW4754_7	Len: 232	Check: 1379	Weight: 1.00
Name: 99BWMC16_8	Len: 232	Check: 4222	Weight: 1.00
Name: A2_CD_97CD	Len: 232	Check: 2359	Weight: 1.00
Name: A2_CY_94CY	Len: 232	Check: 5163	Weight: 1.00
Name: A2D_97KR	Len: 232	Check: 9468	Weight: 1.00
Name: A2G_CD_97C	Len: 232	Check: 4189	Weight: 1.00
Name: A_BY_97BL0	Len: 232	Check: 2590	Weight: 1.00

Name: A_KE_Q23	Len: 232	Check: 2652	Weight: 1.00
Name: A_SE_SE659	Len: 232	Check: 9245	Weight: 1.00
Name: A_SE_SE725	Len: 232	Check: 985	Weight: 1.00
Name: A_SE_SE753	Len: 232	Check: 1638	Weight: 1.00
Name: A_SE_SE853	Len: 232	Check: 2503	Weight: 1.00
Name: A_SE_SB889	Len: 232	Check: 2327	Weight: 1.00
Name: A_SE_UGSE8	Len: 232	Check: 9538	Weight: 1.00
Name: A_UG_92UG0	Len: 232	Check: 2621	Weight: 1.00
Name: A_UG_U455	Len: 232	Check: 2084	Weight: 1.00
Name: AC_IN_2130	Len: 232	Check: 2406	Weight: 1.00
Name: AC_RW_92RW	Len: 232	Check: 3441	Weight: 1.00
Name: AC_SE_SE94	Len: 232	Check: 3488	Weight: 1.00
Name: ACD_SE_SE8	Len: 232	Check: 3016	Weight: 1.00
Name: ACG_BE_VI1	Len: 232	Check: 5006	Weight: 1.00
Name: AD_SE_SE69	Len: 232	Check: 3362	Weight: 1.00
Name: AD_SE_SE71	Len: 232	Check: 2262	Weight: 1.00
Name: ADHK_NO_97	Len: 232	Check: 8765	Weight: 1.00
Name: ADK_CD_MAL	Len: 232	Check: 6397	Weight: 1.00
Name: AG_BE_VI11	Len: 232	Check: 6471	Weight: 1.00
Name: AG_NG_92NG	Len: 232	Check: 2880	Weight: 1.00
Name: AGHU_GA_VI	Len: 232	Check: 9053	Weight: 1.00
Name: AGU_CD_Z32	Len: 232	Check: 523	Weight: 1.00
Name: AJ_BW_BW21	Len: 232	Check: 3842	Weight: 1.00
Name: B_AU_VH	Len: 232	Check: 8468	Weight: 1.00
Name: B_CN_RL42	Len: 232	Check: 9366	Weight: 1.00
Name: B_DE_D31	Len: 232	Check: 3989	Weight: 1.00
Name: B_DE_HAN	Len: 232	Check: 563	Weight: 1.00
Name: B_FR_HXB2	Len: 232	Check: 3184	Weight: 1.00
Name: B_GA_OYI	Len: 232	Check: 5511	Weight: 1.00
Name: B_GB_CAM1	Len: 232	Check: 4779	Weight: 1.00
Name: B_GB_GB8	Len: 232	Check: 1128	Weight: 1.00
Name: B_GB_MANC	Len: 232	Check: 2885	Weight: 1.00
Name: B_KR_WK	Len: 232	Check: 9915	Weight: 1.00
Name: B_NL_3202A	Len: 232	Check: 3135	Weight: 1.00
Name: B_TW_TWCYS	Len: 232	Check: 2211	Weight: 1.00
Name: B_US_BC	Len: 232	Check: 3145	Weight: 1.00
Name: B_US_DH123	Len: 232	Check: 7019	Weight: 1.00
Name: B_US_JRCSE	Len: 232	Check: 4099	Weight: 1.00
Name: B_US_MNCG	Len: 232	Check: 4137	Weight: 1.00
Name: B_US_P896	Len: 232	Check: 4405	Weight: 1.00
Name: B_US_RF	Len: 232	Check: 450	Weight: 1.00
Name: B_US_SF2	Len: 232	Check: 5413	Weight: 1.00
Name: B_US_WEAU1	Len: 232	Check: 5335	Weight: 1.00
Name: B_US_WR27	Len: 232	Check: 3720	Weight: 1.00
Name: B_US_YU2	Len: 232	Check: 9943	Weight: 1.00
Name: BF1_BR_93B	Len: 232	Check: 3598	Weight: 1.00
Name: C_BR_92BR0	Len: 232	Check: 3908	Weight: 1.00
Name: C_BW_96BW0	Len: 232	Check: 3880	Weight: 1.00
Name: C_BW_96BW1	Len: 232	Check: 4542	Weight: 1.00
Name: C_BW_96BW1	Len: 232	Check: 6118	Weight: 1.00
Name: C_BW_96BW1	Len: 232	Check: 5089	Weight: 1.00
Name: C_ET_ETH22	Len: 232	Check: 744	Weight: 1.00
Name: C_IN_93IN1	Len: 232	Check: 943	Weight: 1.00
Name: C_IN_93IN9	Len: 232	Check: 1241	Weight: 1.00
Name: C_IN_93IN9	Len: 232	Check: 9885	Weight: 1.00
Name: C_IN_94IN1	Len: 232	Check: 6448	Weight: 1.00
Name: C_IN_95IN2	Len: 232	Check: 5597	Weight: 1.00
Name: CRF01_AE_C	Len: 232	Check: 1052	Weight: 1.00
Name: CRF01_AE_C	Len: 232	Check: 744	Weight: 1.00
Name: CRF01_AE_C	Len: 232	Check: 1265	Weight: 1.00

Name: CRF01_AE_T	Len: 232	Check: 697	Weight: 1.00
Name: CRF01_AE_T	Len: 232	Check: 8468	Weight: 1.00
Name: CRF01_AE_T	Len: 232	Check: 9246	Weight: 1.00
Name: CRF01_AE_T	Len: 232	Check: 8105	Weight: 1.00
Name: CRF01_AE_T	Len: 232	Check: 9948	Weight: 1.00
Name: CRF01_AE_T	Len: 232	Check: 9460	Weight: 1.00
Name: CRF02_AG_F	Len: 232	Check: 925	Weight: 1.00
Name: CRF02_AG_F	Len: 232	Check: 9559	Weight: 1.00
Name: CRF02_AG_G	Len: 232	Check: 399	Weight: 1.00
Name: CRF02_AG_N	Len: 232	Check: 2782	Weight: 1.00
Name: CRF02_AG_S	Len: 232	Check: 538	Weight: 1.00
Name: CRF02_AG_S	Len: 232	Check: 6700	Weight: 1.00
Name: CRF03_AB_R	Len: 232	Check: 6784	Weight: 1.00
Name: CRF03_AB_R	Len: 232	Check: 3106	Weight: 1.00
Name: CRF04_cpx_	Len: 232	Check: 1551	Weight: 1.00
Name: CRF04_cpx_	Len: 232	Check: 5866	Weight: 1.00
Name: CRF04_cpx_	Len: 232	Check: 7925	Weight: 1.00
Name: CRF05_DF_B	Len: 232	Check: 3625	Weight: 1.00
Name: CRF05_DF_B	Len: 232	Check: 5585	Weight: 1.00
Name: CRF06_cpx_	Len: 232	Check: 3770	Weight: 1.00
Name: CRF06_cpx_	Len: 232	Check: 4202	Weight: 1.00
Name: CRF06_cpx_	Len: 232	Check: 5376	Weight: 1.00
Name: CRF06_cpx_	Len: 232	Check: 1869	Weight: 1.00
Name: CRF11_cpx_	Len: 232	Check: 3479	Weight: 1.00
Name: CRF11_cpx_	Len: 232	Check: 3712	Weight: 1.00
Name: D_CD_84ZR0	Len: 232	Check: 1380	Weight: 1.00
Name: D_CD_ELI	Len: 232	Check: 4418	Weight: 1.00
Name: D_CD_NDK	Len: 232	Check: 4588	Weight: 1.00
Name: D_UG_94UG1	Len: 232	Check: 2178	Weight: 1.00
Name: F1_BE_VI85	Len: 232	Check: 4350	Weight: 1.00
Name: F1_BR_93BR	Len: 232	Check: 7703	Weight: 1.00
Name: F1_FI_FIN9	Len: 232	Check: 5036	Weight: 1.00
Name: F1_FR_MP41	Len: 232	Check: 84	Weight: 1.00
Name: F2_CM_MP25	Len: 232	Check: 2622	Weight: 1.00
Name: F2KU_BE_VI	Len: 232	Check: 2193	Weight: 1.00
Name: G_BE_DRCBL	Len: 232	Check: 2548	Weight: 1.00
Name: G_NG_92NG0	Len: 232	Check: 3608	Weight: 1.00
Name: G_SE_SE616	Len: 232	Check: 2716	Weight: 1.00
Name: H_BE_VI991	Len: 232	Check: 1561	Weight: 1.00
Name: H_BE_VI997	Len: 232	Check: 663	Weight: 1.00
Name: H_CF_90CF0	Len: 232	Check: 1804	Weight: 1.00
Name: J_SE_SE702	Len: 232	Check: 1615	Weight: 1.00
Name: J_SE_SE788	Len: 232	Check: 1704	Weight: 1.00
Name: K_CD_EQTB1	Len: 232	Check: 4783	Weight: 1.00
Name: K_CM_MP535	Len: 232	Check: 2033	Weight: 1.00
Name: N_CM_YBF30	Len: 232	Check: 6419	Weight: 1.00
Name: O_CM_ANT70	Len: 232	Check: 8742	Weight: 1.00
Name: O_CM_MVP51	Len: 232	Check: 5835	Weight: 1.00
Name: O_SN_MP129	Len: 232	Check: 8625	Weight: 1.00
Name: O_SN_MP130	Len: 232	Check: 8793	Weight: 1.00
Name: U_CD_83C	Len: 232	Check: 1586	Weight: 1.00

1					50
00BW0762_1	MGGKWSKSS.	IVGWPAVRER	IR...RTDP	AAEGVG
00BW0768_2	MGGKWSKSSI	V.GWPEVRER	IRR..TEP..	AAEGVG
00BW0874_2	MGGKWSKSS.	LTGWPAVRER	IR...RTEP	AAEGVG
00BW1471_2	MGGKWSKSS.	IVGWPAVKER	IRR..TNPR.	TERAAVGVG
00BW1616_2	MGNKWSKSS.	IVGWPAVRDR	MRR..AEP..	AAEGVG
00BW1686_8	MGGKWSKRS.	KADWPAVREK	LR...TTEP	AAEGVG
00BW1759_3	MGNKWSKS..	...WPAVRER	IRR..TRPAR	GNEPAAEGVG

00BW1773_2	MGSKWSKSSI	V.GWPKVRET	IRR..TEP..AAEGVG
00BW1783_5	MGNKWSKS..	...WPAIRER	IRR..TNPAA	ERTRAAEGVG
00BW1795_6	MGGKWSKSS.	VVGWPAIRER	MRR.....TEPAAEGVG
00BW1811_3	MGGKWSKSC.	KIGWPAVRER	MRR.....TEPAVEGVG
00BW1859_5	MGGKWSKSG.	KVGWPEVRER	MRR..TRPAA	EGG.....	..DSAAEGVG
00BW1880_2	MGGKWSKSS.	LVGWPAVRER	IRT..TAP..
00BW1921_1	MGGKWSKSS.	IVGWPAVRER	MR....KTEPAAEGVG
00BW2036_1	MGGKWSKSS.	IVGWPAVRER	IRR.....TEPAAEGVG
00BW2063_6	MGGKWSKSSI	I.GWPAVRER	MRK..AEP..AAEGVG
00BW2087_2	MGSKWSKSS.	IVGWPAVRER	IRR..T....	RTEPAAEGVG
00BW2127_2	MGGKWSKSSI	I.GWPAIRER	IRR..TEP..AAEGVG
00BW2128_3	MGSKWSKCSI	I.GWPAVRER	IRR..AEP..AAVGVG
00BW2276_7	MGSKWSKC..	.SGWPDVRER	MRR..ATPAA	EAGRA...AP	AAEGAAPGVG
00BW3819_3	MGSKWSKCSI	V.GWPDVRER	MRR..ARPAV	RERRRQTEPA	AEGVAAEGVG
00BW3842_8	MGGKWSKGR.	IVGWPAVRER	MRR.....TEPAAEGVG
00BW3871_3	MGSKWSKRS.	IVEWPAVRER	LR....KTEPAAEGVG
00BW3876_9	MGGKWSKSS.	IVGWPAVRER	IRQ..TGAR.AAEGVG
00BW3886_8	MGGKWSKSS.	IVGWSAVRER	MK....RTEPAAEGVG
00BW3891_6	MGGKWSKSS.	IVGWPTVRER	MRR..TQP..AAEGVG
00BW3970_2	MGSKWSKRS.	TAGWPAVRER	MRR..TQPAA	EG.....	.TQSAAGVG
00BW5031_1	MGGKWSKSS.	LVGWPEVRDR	IRR..TDP..AAEGVG
96BW01B21	MGGKWSKSSI	V.GWPAVRER	IRR..TEP..AAEGVG
96BW0407	MGGKWSKSSI	V.GWPAVRER	MRR..AEP..AAEGVG
96BW0502	MGGKWSK..	CSGWPAVRER	MRR..TRPAV	EGR.....	.TESAAEGVG
96BW06_J4	MGGKWSKSS.	IVGWPAVRER	IR....RTDPPAEGVR
96BW11_06	MGGKWSKSSI	I.GWPAIRER	IRR..TEPAA	ER.....V	..GAAAEGVG
96BW1210	MGNKWSKG..	...WPAVRDR	IRR..TEPATEPAAEGVG
96BW15B03	MGGKWSKSS.	IVGWPAVRER	IRR.....TEPAAEGVG
96BW16_26	MGGKWSK..	...WPAVRER	MRR..TR....VG
96BW17A09	MGXKWSKRS.	IVGWPNVRER	IRR..TNPLT	ER.....	EAERAAVGVG
96BWMO1_5	MGSKWSKSSI	I.GWPAVRER	IRK..TEPRKTEPAAEGVG
96BWMO3_2	MGGKWSKSS.	IVGWPAVRER	MRR..TRPGA	AE.....GVG
98BWMC12_2	MGSKWSKSS.	IIGWPAVRER	MR....RTEPAAEGVG
98BWMC13_4	MGGKWSKSS.	IIGWPAVRER	MRR.....TEPAAEGVG
98BWMC14_a	MGGKWSKSS.	LVGWPDVRER	IR....KPRP	KP.....AAEGVG
98BWMO14_1	MGSKLSKSK.	IVGWPAIRER	LR.....	RTEPAAEGVG
98BWMO18_d	MGGKWSKSS.	IVGWPAVRER	IRQ..TDPRE	RI.....R	QTEPAAEGVG
98BWMO36_a	MGGKWSKSSI	V.GWPAVRER	IRR..TEPRRAEPAAECVG
98BWMO37_d	MGGKWSKSS.	IVGWPEVRER	LR....RTAPAAEGVG
99BW3932_1	MGGKWSKRKI	V.QWPTVRER	LRR..TEP..AEGVG
99BW4642_4	MGGKWSKSS.	IVGWPAVRER	IRR..TQPAA	EG.....VG
99BW4745_8	MGSKLSKSC.	TAGWPTVRER	IRQ..AEP..AAEGVG
99BW4754_7	MGGKWSKSS.	IVGWANVRER	MRR.....TEPAAVGVG
99BWMC16_8	MGNKWSKS..	...WPAVRER	IRR..TEPAV	RV.....R	RTEPAAEGVG
A2_CD_97CD	MGGKWSKRT.	IVGWPEIRER	MRR..TPPAA	EG.....VR	PTPPAAEGVG
A2_CY_94CY	MGGKWSKRS.	IPGWPAIRER	MRRTPPTAQR	TE.....	AVSPAAPGVG
A2D_97KR	MGGKWSKRS.	LPGWPAIRER	MRRTPPAAER	TP.....	PAA.AAEGVG
A2G_CD_97C	MGSKWSKSS.	IVGWPAVRAR	IR....QTPP.AAEGVG
A_BY_97BL0	XXGKWSKSS.	IXXWPQVXER	IRRAPAP...AARXVG
A_KE_Q23	MGGKWSKSS.	IVGWPEIRER	MRRAPP....AAPGVG
A_SE_SE659	MGGKWSKSS.	IVGWPEIRER	MRRAPS....AAPGVG
A_SE_SE725	MGSKWSKSS.	IVGWREVRER	LRQTLAAARGVG
A_SE_SE753	MGGRWSKSR.	IVGWPEVRER	IRRAPP....AATGVG
A_SE_SE853	MGGKWSKRS.	KEGWSEVRER	IRQT.....PPAAKGVG
A_SE_SE889	MGGKWSKSS.	IVGWPKVRER	MARTPP....AAKGVG
A_SE_UGSE8	MGNKWSK... .	.GWPEVRER	IRQARAPAHT	PAPTAATGVG
A_UG_92UG0	MGNKWSKSC.	IVGWPEVRER	IRQTPTAARE	RTR.....	QAPTAAGVG
A_UG_U455	MGGKWSKKS.	RVEWPEVRKR	MRETPA....AAKGVG
AC_IN_2130	MGGKWPCKSS.	VVGWPEVRER	IRRTPA....AAPGVG
AC_RW_92RW	MGSKWSKCSP	V.GWPAVRER	LRQ..TEP..AAEGVG

ACD_SE_SE94	MGGKWSKSS.	IIGWPQIRER	IRRTPP.	AATGVG
ACD_SE_SE8	MGGKWLKSSI	V.GWPAVRER	IRR..TEP.	AAEGVG
ACG_BE_VI1	MGGKWSKRS.	KVEWPQVRER	MRQ..TPIAA	EA.....	EG	AAAEGVG
AD_SE_SE69	MGGKWSKSS.	IVGWPAVRER	IKR..T....	DPAAEGVG
AD_SE_SE71	MGGKWSKSS.	IVGWPEVRER	MRRARAP.	SAAPGVG
ADHK_NO_97	MGGKWSKSS.	IVGWPAIRER	MRR..AEP.	AAEGVG
ADK_CD_MAL	MGGKWSKSS.	IVGWPKIRER	IRRTPTTETG	VGAVSQD
AG_BE_VI11	MGGKWSKSS.	PVGWSRVRE	MRR..TPPAA	EG.....	AAAEGVG
AG_NG_92NG	IGGKWSKSS.	IVGWPAVRER	IR...QTP.	PAEGVG
AGHU_GA_VI	MGGEWSRSS.	IVGWSTIRER	MRRAEP....	AAAGVG
AGU_CD_Z32	MGNKWSKG..	..WPAVRER	IRQ..TPPAP	P.....	AAEGVG
AJ_BW_BW21	MGSNWSKS.S	IIGWPQVRER	MKR....AP	A.....	P	AAEGVG
B_AU_VH	MGGKGSKRI.	RSEWPTVRER	IIQ..AEPAA	AG.....	VG
B_CN_RL42	MGGKWSKHS.	MFGWPSVRER	MKR..AEPAA	DG.....	VG
B_DE_D31	MGGKWSKSS.	VVGWPAIRER	MK.....	RAEPAAEGVG
B_DE_HAN	MGGKWSK..	CSGWPTVRER	MKQAP..	EPAADGVG
B_FR_HXB2	MGGKWSKSS.	VIGWPTVRER	MR.....	RAEPAADRVG
B_GA_OYI	MGGKWSKCS.	MKGWPTIRER	MKR..AELQP	PE.....	PAAEGVG
B_GB_CAM1	MGGKWSKRS.	LGGSASVRER	MQR..AEP.	RAEPAAEGVG
B_GB_GB8	MGGKLSKRS.	MFGWSRVDR	MQQ..AEP.	AAEGVG
B_GB_MANC	MGGKWSKSR.	KIGWPTVRER	MKQ..VDPAE	EGR....	KK	QAEPAAEGVG
B_KR_WK	MGGKWSKRS.	VPGWNTIRK	MRR..AEPAA	EG.....	VG
B_NL_3202A	MGGKWSKSS.	VVGWPAIRER	MK.....	RAEPAADGVG
B_TW_TWCYS	MGGKWSKRS.	IPGWSNIRER	IRQ..AEP.	AADGVG
B_US_BC	MGGKWSKRM.	EGGWHAVRER	MR.....	RAEPAADGVG
B_US_DH123	MGGKLSKCG.	GVGWSTVRER	MRR..AEPAA	DR.....	EP.AVGVG
B_US_JRCSP	MGGKWSKHS.	VPGWSTVRER	MRR..AEPAT	DR.....	VR	QTEPAAVGVG
B_US_MNCG	MGGKWSKR..	VTGWPTVRER	MRR..AEP.	AELAADGVG
B_US_P896	MGGKWSKRR.	AEGWQTIRER	MRRAEPA..	EPAADGVG
B_US_RF	MGGKWSKSK.	MGGWPAVRER	MQK..AEPAA	DG.....	VG
B_US_SF2	MGGKWSKRS.	MGGWSAIRER	MRR..AEP.	RAEPAADGVG
B_US_WEAU1	MGGIWSKRS.	SGGWPAIRER	MKR..AEPAA	EG.....	VG
B_US_WR27	MGGKWSKRS.	VGGWPAIRER	MX.....	RAEPAAEGVG
B_US_YU2	MGGKWSKRS.	MAGWPTVRER	MRR..AEPAA	ER.....	MR	RAEPAADGVG
BF1_BR_93B	MGSKWSKSS.	IVGWPAIRER	LRQ..TP.	PAAEGVG
C_BR_92BR0	MGNKWSKCST	V.GRPAIRER	MRR..AP.	AAEGVG
C_BW_96BW0	MGGKWSKSSI	V.GWPAVRER	MRR..TEP.	AAEGVG
C_BW_96BW1	MGGKWSKRSK	I.EWPTIRDR	MRR..TEPAA	EG.....	V	GAAAEVG
C_BW_96BW1	MGNKWSKG..	..WPAVRDR	IRR..TEPAT	EPAAEVG
C_BW_96BW1	MGGKWSKSS.	TVGWPAVRER	IRR.....	TEPAAEGVG
C_ET_ETH22	MGGTMSKCS	V.GWPAIRER	IRR..AAP.	AAEGVG
C_IN_93IN1	MGGKWSKCSI	V.GWPAIRER	MRR..AEP.	AAEGVG
C_IN_93IN9	MGGKWSKCSI	V.GWPDIRER	MRR..TQP.	AAEGVG
C_IN_93IN9	MGGKWSKCSI	V.GWPAVRER	MRR..TEP.	AAEGVG
C_IN_94IN1	MGGKWSKCSI	V.GWPEIRER	MRR..TQP.	AADGVG
C_IN_95IN2	MGGKWSKCSI	V.GWPDIRER	MRR..TEP.	AAEGVG
CRF01_AE_C	MGGKWSKN.R	IVGWPOVRER	IRR..TPAAA	EGVG
CRF01_AE_C	MGGKWSKSC.	IVGWPOVRER	IRQ..TPVAE	B.....	R	QTPAAAEVG
CRF01_AE_C	MGNKWSKS..	..WPQIRER	IRQ..TPVAT	EGVG
CRF01_AE_T	MGGKWSKS.S	IVGWPOVREK	IKQ..TPPAA	EGVG
CRF01_AE_T	MGGKWSKS.S	IVGWPOVREK	IKQ..TPPAA	EGVG
CRF01_AE_T	MGGKWSKS.S	IVGWPOVREK	IKQ..TPPAA	EGVG
CRF01_AE_T	MCAKWSKRG.	..WPQVRER	IRQ..TPPAA	EGVG
CRF01_AE_T	MGSKWSKS.S	IVGWPOVREK	IKQ..TPPAT	EGVG
CRF01_AE_T	MGNKWSKS..	..WPRVRER	IKQ..TPPAA	EGVG
CRF02_AG_F	MGGKWSKSS.	IVGWPKVRER	IR...QTPP.	AATGVG
CRF02_AG_F	MGGKWSKSS.	LVGWPKVRER	II...QTPP.	AATGVG
CRF02_AG_G	MGGKWSKSS.	IVGWPOVRER	IR...QTPT.	AAKGVG
CRF02_AG_N	MGGKWSKSS.	IVGWPKVMKR	MR...QTPT.	AATGVG
CRF02_AG_S	MGGKWSKSS.	IVGWQIRDR	IR...QTPP.	AARGVG

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CRF02_AG_S MGGKWSKSS. LVGWPOVRER IRRTOPTPS. .... AAIGVG
CRF03_AB_R MGGKWSKSS. IVGWPOVRER IRRAPAP... .... AARGVG
CRF03_AB_R MGGKWSKSS. IVGWPOVRER IRRAPAP... .... AARGVG
CRF04_cpx_ MGGKWSKSS. IVGWPEIRER MRR..ARAEP ERM...RA QAEPAAGVG
CRF04_cpx_ MGGKWSKSS. LVGWPAIRER MRR..ARAEP .....AA QAEPAAGVG
CRF04_cpx_ MGNKWSKS.. ...WPAVRER MRR..ARAEP .....A RAEPAAVGVG
CRF05_DF_B MGGKWSKSS. VVGWPAIREK MRR..TP... .... PAAEGVG
CRF05_DF_B MGGKWSKSS. IVGWPAIRER MRR..TPPAA ..... GAAAGVG
CRF06_cpx_ MGNKWSKS.. ...GWSQVRER MRR..TPPTE R..... AAEVG
CRF06_cpx_ MGGKWSKS.S IVGWPOVRER IRQ..TPPTE G..... AAKVG
CRF06_cpx_ MGGKWSKS.S LVGWPOVRER IRQ..TPPTE G..... AAEVG
CRF06_cpx_ MGGKWSKS.S IVGWPKVRER MRQ..TPPAA E.....R QTPPAAGVG
CRF11_cpx_ MGGKWSKS.S IVGWPEIRER LRR..... T PPAAGVG
CRF11_cpx_ MGNKWSKS.S IVGWPEIRER LRR..... T PPTAAAGVG
D_CD_84ZRO MGGKWSKSS. IVGWPAIRER IRK..TDPRE RR..... RPEPAAGVG
D_CD_ELI MGGKWSKSS. IVGWPAIRER IRR..T.... ..NPAAGVG
D_CD_NDK MGGKWSKSS. LVGWPAIRER IRK..T.... ..DPAAGVG
D_UG_94UG1 MGGKWSKSS. IVGWPAVRER MRR..T.... ..EPAAGVG
F1_BE_VI85 MGGKWSKSS. IVGWPAVRER MRQ..TP... ..TAAEGVG
F1_BR_93BR MGGKWSKSS. IVGWPAIRER MRR..TPPT. .... PPAAEGVG
F1_FI_FIN9 MGGKWSKSS. IVGWPAIRER MRR..PP... ..PAAAGVG
F1_FR_MP41 MGGKWSKSS. IVGWPAVRER MRR..TP... ..PAAEGVG
F2_CM_MP25 MGGKWSKSS. IVGWPAIRER IRR..TP... ..VAAEGVG
F2KU_BE_VI MGGKWSKS.. ...GWPSVRER IRR..TPPAA P..... AADGVG
G_BE_DRCBL MGNKWSKRK. VAGWPEVRER LR...QHPA. .... AAEVG
G_NG_92NG0 MGGKWSKSS. IVGWPOVRER IR...QTPV. .... AAEVG
G_SE_SE616 MGGKWSKSS. IVGWPEVRER IR...NTPT. .... AAEVG
H_BE_VI991 MGGKWSKGC. ISGWPAVRER IRQ..TBP.. .... AAEVG
H_BE_VI997 MGGKWSKSS. IVGWPAVRER IRR..AQF.. .... AADGVG
H_CF_90CF0 MGGKWSKSR. MGGWSTIRER MRR..AEP.. .... VARGVG
J_SE_SE702 MGNKWSKS.. ...WPQVRDR MRR..A..AP A.....P .... AADGVG
J_SE_SE788 MGNKWSKS.. ...WPQVRER MRR.....AP A.....P .... AADGVG
K_CD_EQTB1 MGGKWSKS.S IVGWSTVRER MR..... KTPPAAGVG
K_CM_MP535 MGGKWSKS.S IVGWPAIRER MRR..ARPA DR.....V GTQPAAGVG
N_CM_YBF30 MGKIWSKSS. LVGWPEIRER MRRQTQEP. .... AVEPAVGAG
O_CM_ANT70 MGNALRKKG. FEGWAAVRER MRRTRTF... ..P ESEPCAPVG
O_CM_MVP51 MGNAWSKSK. FAGWSEVRDR MRRSSS.... ..D PQQPCAPVG
O_SN_MP129 MGNVLGKDI. FKGWSAVRER MRGTS.... ..P DPEPCAPVG
O_SN_MP130 MGNVLGKDK. FKGWSAVRER MRKTS.... ..P EPEPCAPVG
U_CD_83C MGNKWSKQ.. ...WPAIRER MRR..ARPA E.....P .... AADGVG

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51

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00BW0762_1 AASQDLDRHG AITSSNTPTT NAACAWLEAQ EEDE...VGF PVRPQVPLRP
00BW0768_2 AASQDLDKYG ALTSSNTANT NAACAWLEAQ EKEE.E.VGF PVRPQVPLRP
00BW0874_2 EASQDLDKHG ALTTSNTAAN NADCAWLQAH EEED...EVGF PVRPQVPLRP
00BW1471_2 AASQDLDKYG ALTANNTPAN NADCARLQAH EEDN...EVGF PVRPQVPLRP
00BW1616_2 PASQDLGRHG ALTSSNTAHN NADCAWLEAQ EEED.G.VGF PVRPQVPLRP
00BW1686_8 AASQDLAKHG ALTSSNTAHN NADCAWLEAQ EEEE...VGF PVRPQVPLRP
00BW1759_3 AASQDLDKYG ALTSSNTPTT NAACAWLEAQ EEAE.E.VGF PVRPQVPLRP
00BW1773_2 AASQDLDKYG ALTSSNTDTN NADCAWLKAG EEEG.E.VGF PVRPQVPLRP
00BW1783_5 AASRDLDKHG ALTSSNTPAT NADCAWLEAQ EEEE.E.VGF PVRPQVPLRP
00BW1795_6 AASQDLDKYG ALTSSNTATN NADCAWLEAQ EEAD..DVGF PVRPQVPLRP
00BW1811_3 AASQDLDRHG ALTSSNTATN NADCAWLEAQ EEGB..EVGF PVRPQVPLRP
00BW1859_5 AASRDLARHG ALTSSNTATT NAACAWLEAQ EEAD..EVGS PVRPQVPLRP
00BW1880_2 ..... AAT NDACARLKEQ EEEG.E.VGF PVRPQVPLRP
00BW1921_1 AASRDLDKYG ALTSSNTVTT NAACAWLEAQ EKEG..GVGF PVRPQVPLRP
00BW2036_1 AASQDLDKHG ALTSSNTSST NDACAWLEAQ EEAD..DVGF PVRPQVPLRP
00BW2063_6 AASQDLDKHG ALTSSNTANN NADCAWLEAQ EEEE...VGF PVRPQVPLRP
00BW2087_2 AASQDLDKHG ALTPSNTAGN NSTCAWLQAH EEEE..EVGF PVRPQVPLRP
00BW2127_2 AASQDLDKHG ALTSSNTATN NADCAWLQAH EEES.EGVGF PVRPQVPLRP

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00BW2128_3	AASQDLDKYG	ALTSSNTDTN	NAACAWLRAQ	EEEE.E.VGF	PVX....TS
00BW2276_7	AASRDLDHRG	ALTSSNTPTN	NADCAWLQAQ	EEEE.BEVGF	PVRPQVPLRP
00BW3819_3	TASQDLAKHG	ALTSSNTPAN	NAACAWLQAQ	EEEE.D.VGF	PVRPQVPLRP
00BW3842_8	AASRDLDKHG	ALTSSNTAEN	NADCAWLEAQ	EETE..EVGF	PVRPQVPLRP
00BW3871_3	AASQDLDKHG	ALTSSNTAQN	NAACAWLEAQ	EEAE.GEVGF	PVRPQVPLRP
00BW3876_9	AASQDLDRHG	ALTSSNTGAT	NSDVAWLEAQ	EEEG.E.VGF	PVRPQVPLGP
00BW3886_8	AASQDLDKHG	ALTSSNTPAN	NADCAWLETQ	EEAD..EVGF	PVRPQVPLRP
00BW3891_6	AASQDLDKYG	ALTSSNTADT	NADCAWLQAQ	EEEG.E.VGF	PVRPQVPLRP
00BW3970_2	AASQDLDKHG	ALTSSNTAAT	NADCAWLEAQ	EEDG..DVGF	PVRPQVPLRP
00BW5031_1	AASQDLDKHG	ALTSSNTAAT	NKDCAWLEAQ	EEEG.E.VGF	PVRPQVPLRP
96BW01B21	AASQDLDKYG	ALTSSNTDPN	NAACAWLRAQ	EEEG.E.VGF	PVRPQVPLRP
96BW0407	TASRDLDKYG	ALTSSNTPTN	NAACAWLEPQ	EEEE.E.VGF	PVRPQVPLRP
96BW0502	AASQDLDKYG	ALTSSNTSTN	NADCAWLEAQ	EEEG..DVGF	PVRPQVPLRP
96BW06_J4	APSQDLDKHG	ALTSSNTPAN	NADVAWLEPQ	EEEG..AVGF	PLRPQVPLKP
96BW11_06	AASQDLDKHG	ALTSSNTAAN	NADCAWLEAQ	EEEE..VGF	PVRPQVPLRP
96BW1210	SASKDLEKHG	ALTSSNTAAN	NPHCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
96BW15B03	AASQDLDKYG	AFTSSNTASN	NADCAWLEAQ	EEAD..EVGF	PVRPQVPLRP
96BW16_26	AEYQDLDKDR	ALTSSNTDTN	NAACAQ...Q	EEEE.E.VGF	PVRPQVPLRP
96BW17A09	AASQDLDKHG	ALTSSNTPAN	NADCAWLQAQ	EEDE..EVGF	PVRPQVPLRP
96BWM01_5	AVSQDLQDHG	AITSSNTATN	.ADCACLEAQ	EEEA.E.LGF	PVRPQMPLKP
96BWM03_2	AASQDLDKYG	ALTSSNTASN	NADCAWLEAQ	EEAN..EVGF	PVRPQVPLRP
98BWMC12_2	AASQDLDKYG	AMTSSNTAHN	NGDCAWLQAQ	EEEE..EVGF	PVRPQVPLRP
98BWMC13_4	AASQDLDKHG	ALTSSNTATT	NADCAWLEAQ	AEAE..KVGF	PVRPQVPLRP
98BWMC14_a	AASQDLDKYG	ALTSSNTATN	NAACAWLEAQ	EEAG..EVGF	PVKPQVPLRP
98BWM014_1	AASQDLDKHG	ALTSSNTASN	NAACAWLQAQ	EEDN.GDVGF	PVRPQVPLRP
98BWM018_d	AASRDLERHG	AITSSNTAAN	NPACAWLEAQ	EEDG.D.VGF	PVRPQVPLRP
98BWM036_a	AASQDLDKHG	ALTSSNTASN	NADCAWLEAQ	EEEE.E.VGF	PVKPQVPLRP
98BWM037_d	AASQDLAKHG	AITSSNTATT	NADCAWLEAQ	EEGE..EVGF	PVRPQVPLRP
99BW3932_1	AASQDLANHG	ALTSSNTATN	NADCAWLQAQ	EEEE..VGF	PVRPQVPLRP
99BW4642_4	AASQDLDRHG	AITSSNTAAT	NADCAWLEAQ	EEAD..EVGF	PVRPQX...P
99BW4745_8	AASKDLDKHG	ALTSSNTAGT	NADCAWLQAQ	EEEG.E.VGF	PVRPQVPLRP
99BW4754_7	AASQDLDKYG	ALTSSNTAAT	NADCARLEAQ	EETE..EVGF	PVRPQVPLRP
99BWMC16_8	AASKDLEKHG	ALTSSNTVHN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
A2_CD_97CD	AVSQDLARHG	AVTSSNTAAN	NPDCAWLEAQ	EEE...EVGF	PVRPQVPLRA
A2_CY_94CY	AVSQDLATHG	AVTSSNTAAT	NPDCAWVEAQ	EEES..EVGF	PVRPQVPLRP
A2D_97KR	AVSQDLATRG	AVTINNTAAT	NADSAWLEAQ	EEEE..EVGF	PVRPQVPLRP
A2G_CD_97C	AVSQDLARHG	AITSSNTAAN	NPDCAWLEAQ	QEDS..EVGF	PVRPQVPLRP
A_BY_97BL0	PVSQDXDKHG	AVTSSNTAAN	NADCAWLEAQ	X...BXEVGF	PVRPQVPLRP
A_KE_Q23	AVSQDLDKHG	AVTSKNINH.	.PSYAWLEAQ	E...DEDVGF	PVRPQVPLRP
A_SE_SE659	AVSQDLAKHG	AVTSSNNIN.	.PSCVWLEAQ	E...EEEVGF	PVRPQVPLRP
A_SE_SE725	AVSQDLEKYG	AVTSSNVNH.	.PSCAWLEAQ	E...EEEVGF	PVRPHVPLRP
A_SE_SE753	AVSQDLDKYG	AITSSNNINH.	.PSCVWLEAQ	E...DEGVGF	PVRPQVPLRP
A_SE_SE853	AVSQDLDRHG	AITSSNNINH.	.PSCTWLEAQ	E...DEEVGF	PVKPQVPLRP
A_SE_SE889	AVSQDLDKHG	AVTSSNNINH.	.PSCAWVEAQ	E...EEEVGF	PVRPQVPLRP
A_SE_UGSE8	AVSQDLEKHG	AITSSNNINH.	.PSCTWLEAQ	AQE.DEEVGF	PVRPQVPLRP
A_UG_92UC0	AVSQDLDKHG	AVTSSNVNH.	.PSCVWLEAQ	E...EEEVGF	PVRPQVPLRP
A_UG_U455	AVSQDLDKYG	AVTSSNTSST	NASCAWLEAQ	E...EGDVGF	PVRPQVPLRP
AC_IN_2130	AVSQDLDKHG	AVTSSNVNH.	.PSCVWLDQAQ	E...EEEVGF	PVRPQVPLRP
AC_RW_92RW	AASQDLDKYG	ALTSSNTPSN	NADCAWLAAQ	EBEN.E.VGF	PVRPQVPLRP
AC_SE_SE94	AVSQDLDKHG	AITSSNNINH.	.PSNTWLAAQ	E.E.EEEVGF	PVRPQVPLRP
ACD_SE_SE8	AASQDLDKYG	ALTSSNTVTN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
ACG_BE_VI1	AVSQDLARHG	AVTSRNTSAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP
AD_SE_SE69	AASRDLGKHG	AITSSNTAQT	NPDCAWLEAQ	EED..GEVGF	PVRPQVPLRP
AD_SE_SE71	AVSQDLDKHG	AITSSNNINH.	.PSCVWLEAQ	E...DEDVGF	PVRPQVPLRP
ADHK_NO_97	AASRDLDRRG	AIXINNLPNS	NSDSAWLEAQ	EE...EEVGF	PVRPQVPLRP
ADK_CD_MAL	AVSQDLDKCG	AAASSSPAAN	NASCEPPEEE	EE....VGF	PVRPQVPLRP
AG_BE_VI11	AVSRDLAKHG	AITSSNTVAT	NADCAWLEAQ	KEG..EEVGF	PVRPQVPLRP
AG_NG_92NG	AAPQDLARHG	AITSSNTAQT	NPDCAWLEAQ	QENS..EVGF	PVRQQVPLRP
AGHU_GA_VI	AVSQDLDKRG	AITTNNTVKT	NADCAWLEAQ	EDE...EVGF	PVRPQLPLRP
AGU_CD_Z32	AASQDLAKHG	AISSSNTATN	NPDCAWLEAQ	ESEE..EVGF	PVRPQVPLRP

AJ_BW_BW21	AVSRDLKDHG	AITSSNTPTT	NADCAWLEAQ	TEAE.DEVGF	PVKPQVPLRP
B_AU_VH	AASRDLEKHG	AITSSN..IN	NADCVWLQAQ	EEE...EVGF	PVRPQVPLRP
B_CN_RL42	AVSRDLEKHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_DE_D31	AVSRDLEKHG	AITSSNTPAT	NAACAWLEAQ	EEE...EVGF	PVKPQVPLRP
B_DE_HAN	AASRDLEKHG	AITSSNTATN	NAACAWLEAQ	EEE...EEGF	PVRPQVPLRP
B_FR_HXB2	AASRDLEKHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVTPQVPLRP
B_GA_OYI	AASRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP
B_GB_CAM1	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_GB_GB8	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_GB_MANC	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_KR_WK	AASRDLEQRG	AITTSNTASN	NAACAWQEAQ	EEE...EVGF	PVRPQVPLRP
B_NL_3202A	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVKPQVPLRP
B_TW_TW2CYS	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_BC	AVSRDLEKHG	AITSSNTAAN	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_DH123	AASRDLEKHG	AITSSNTAAT	NADCAWLEAQ	QEE...BEVGF	PVRPQVPLRP
B_US_JRCSE	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EDE...EVGF	PVRPQVPLRP
B_US_MNCG	AASRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVKPQVPLRP
B_US_P896	AVSRDLARHG	AITSSN..TN	NADIAWLEAQ	EEG...EVGF	PVRPQVPLRP
B_US_RF	AASRDLEKHG	TITSSNTAAN	NAACTWLEAQ	EDED.EEVGF	PVRPQVPLRP
B_US_SF2	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_WEAU1	AVSRDLAKHG	AITSSN..EN	NADCVWLKAQ	EDE...EVGF	PVRPQVPLRP
B_US_WR27	AVSRDLEKHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
B_US_YU2	AVSRDLERHG	AITSSNTAAT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
BF1_BR_93B	AVSQDLERRG	AITSSNTGAN	NPDLAWLEAQ	EEEE...VGF	PVRPQVPLRP
C_BR_92BR0	PASQSDSKYG	ALTSSSTPAN	NADCAWLEAQ	QEEE.E.VGF	PVRPQVPLRP
C_BW_96BW0	TASQDLKDHG	ALTSSNTAAN	NAACAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_BW_96BW1	AASQDLKDHG	ALTSSNTAAN	NADCAWLEAQ	EEEE...VGF	PVRPQVPLRP
C_BW_96BW1	SASKDLEKHG	ALTSSNTAAN	NPHCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_BW_96BW1	AASQDLKDHG	AFTSSNTASN	NADCAWLEAQ	EEAD...EVGF	PVRPQVPLRP
C_ET_ETH22	AASRDLDKYG	ALTSSNTPAN	NPDCAWLEAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_93IN1	AASQDLKDHG	ALTSSNTDIT	NADCAWLRAQ	EEEG.E.VGF	PVTPQVPLRP
C_IN_93IN9	AASQDLKDHG	ALTSSNTDIT	NPDCAWLKAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_93IN9	AASQDLKDHG	ALTSSNTDIT	NADCAWLRAQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_94IN1	AASQDLKDHG	ALTSSNTDIT	NADCAWLRTQ	EEEE.E.VGF	PVRPQVPLRP
C_IN_95IN2	AASQDLKDHG	ALTSSNTDIT	NTE.....	.EEE.G.VGF	PVRPQVPLRP
CRF01_AE_C	AASQDLKDHG	AITSSNMNN.	.ADCAWLEAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_C	AVSQDLKDHG	AVTSSNNIN.	.ADNVWLEAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_C	AVSQDLKDHG	AVTSSNMNS.	.AASVWLEAQ	ED...EEVGF	PVRPQVPLRP
CRF01_AE_T	TVSQDLKDHG	AVTSSNMNN.	.DDCVWLQAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLKDHG	AVTSSNMNN.	.ADCEWLRAQ	EE...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLKDHG	AVTSSNMNN.	.ADCVWLRAQ	EE...EGVGF	PVRPQVPLRP
CRF01_AE_T	AVSRDLKDHG	AVTSSNMNN.	.ADSVWLRAQ	EED...EEVGF	PVRPQVPLRP
CRF01_AE_T	AVSQDLKDHG	AITSSNIDN.	.ADCVWLRAQ	ED...EEVGF	PVMPQVPLRP
CRF01_AE_T	AVSQDLKDHG	AVTSTNMDN.	.ADSVWLRAQ	EED...EEVGF	PVEPQVPLRP
CRF02_AG_F	AASQDLDRHG	AITSSNTADT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_F	AASQDLDRHG	AITSSNTAET	NADCAWLEAQ	EDE...EVGF	PVKPQVPLRP
CRF02_AG_G	AASQDLKDHG	AITSSNTAFT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_N	AASQDLDRHG	AITSSNTAQT	NPDCAWLEAQ	EDE...NVGF	PVRPQVPLRP
CRF02_AG_S	AASQDLDRHG	AITSSNTAAT	NAACAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF02_AG_S	AVSQDLDRHG	AITSRNTAHT	NADCAWLEAQ	EEE...EVGF	PVRPQVPLRP
CRF03_AB_R	PVSQDLKDHG	AVTSSNTAAN	NADCAWLEAQ	E...EEEVGF	PVRPQVPLRP
CRF03_AB_R	PVSQDLKDHG	AVTSSNTAAN	NADCAWLEAQ	K...EEEVGF	PVRPQVPLRP
CRF04_cpx	AVSQDLKDHG	AITINNTAAT	NPDKTWLEAQ	EEEE...EVGF	PVRPQVPLRP
CRF04_cpx	AVSRDLKDHG	AITSSNTAAT	NPDKAWLEAQ	EEDE...EVGF	PVRPQVPLRP
CRF04_cpx	AVSQDLKDHG	AITTSNTAAT	NPDKAWLEAQ	EEEE...EVGF	PVRPQVPLRP
CRF05_DF_B	AVFQDLNDRG	AVTIRNTVAT	NPDMAWVEAQ	EEEE...VGF	PVKPQVPLRP
CRF05_DF_B	SVSQDLERRG	AITSNNTAAT	NADLAWVEAQ	EEEE...VGF	PVRPQVPLRP
CRF06_cpx	AVSQDLKDHG	AITSSNTATT	NAACAWVEAQ	TBE...EVGF	PVRPQVPLRP
CRF06_cpx	AVSQDLKDHG	AITSNNTPTT	NAACAWLEEQ	TED...EVGF	PVRPQVPLRP
CRF06_cpx	AVSQDLKDHG	AITSSNTVTT	NAACAWLEAQ	TED...EVGF	PVRPQVPLRP

CRF06_cpx_	AASQDLAKHG	AITSSNTAAT	NADCAWLEAQ	SEDN.EEVGF	PVRPQVPLRP
CRF11_cpx_	AVSKDLEKFG	AITSSNTAHT	NDTCAWLEAQ	ED...EEVGF	PVRPQVPLRP
CRF11_cpx_	AASKDLERHG	AITSSNTSQN	NAACAWLEAQ	ED...EGVGF	PVRPQVPLRP
D_CD_84ZR0	AVSRDLERHG	AITSSNTATT	NAACAWVEAQ	EED...EEVGF	PVRPQVPLRP
D_CD_ELI	AVSRDLEKHG	AITSSNTAST	NADCAWLEAQ	EES...DEVGF	PVRPQVPLRP
D_CD_NDK	AVSRDLEKHG	AITSSNTAST	NDTCAWLEAQ	EES...EEVGF	PVRPQVPLRP
D_UG_94UG1	AASRDLEKHG	AITSSNTAQT	NDACAWLEAQ	EE...EEVGF	PVRPQVPLRP
F1_BE_VI85	AVSRDLDRRG	AITSSNTRTT	NPDLAWLEAQ	EEEE...VGF	PVRPQVPLRP
F1_BR_93BR	AVSQDLERRG	AITSSNTRAN	NPDLAWLEAQ	EED...VGF	PVRPQVPLRP
F1_FI_FIN9	AVSQDLERRG	AITSSNTGAT	NPDLAWLEAQ	EDEE...VGF	PVRPQVPLRP
F1_FR_MP41	AVSQDLDRRG	AVTSSNTAAT	NPDLAWLEAQ	EDEE...VGF	PVRPQVPLRP
F2_CM_MP25	AVSQDLDRRG	AVTSSNTAAT	NPDLAWLEAQ	EDEE...VGF	PVRPQVPLRP
F2_KU_BE_VI	AVSQDLAKHG	AITSSNTSST	NPDCAWLEAQ	EEE...EVGF	PVGPQVPLRP
G_BE_DRCBL	AVSQDLDRHG	AITSRNTAGT	NPDCAWLEAQ	EEDS...EVGF	PVRPQVPLRP
G_NG_92NG0	AVSQDLARHG	AITSSNTATN	NPDCAWLEAQ	EEDS...DVGF	PVRPQVPLRP
G_SE_SE616	AVSQDLDRHG	AITSSNTAAN	NPDCAWLEAQ	EEDS...EVGF	PVRPQVPLRP
H_BE_VI991	AVSQDLDRRG	AVTINNIAAN	NADSAWLEAQ	EEE...EEVGF	PVRPQVPLRP
H_BE_VI997	AVSRDLDRRG	AVTINNTAAT	NPDVAWLEAQ	EEA...EEVGF	PVRPQVPLRP
H_CF_90CF0	AVSRDLDRRG	AVTINNTAST	NRDAAWLEAQ	EDG...EEVGF	PVRPQVPLRP
J_SE_SE702	AVSQDLAKHG	AITSSNTAAT	NDDCAWLEAQ	T...E.EEVGF	PVRPQXPLRP
J_SE_SE788	AVSQDLAKHG	AITSSNTAAT	NADCAWLEAQ	T...E.EEVGF	PVKQPIPLRP
K_CD_EQTB1	AVSQDLDRHG	AVTSSNTAFN	NPDCAWLEAQ	ED...EDVGF	PVRPQVPLRP
K_CM_MP535	AVSQDLARHG	AVTSSNTSHN	NPDCAWLEAQ	EE...EBVGF	PVRPQVPLRP
N_CM_YBF30	AASQDLANRG	AITIRNTRDN	NESIAWLEAQ	EEEE...EVGF	PVRPQVPLRP
O_CM_ANT70	QISRELAARG	GIPSSHTPQN	NAALAFLESH	QEEE...VGF	PVAPQVPLRP
O_CM_MVP51	AVSRELATRG	GISSSHTPQN	NAALAFLDH	KDED...VGF	PVRPQVPLRP
O_SN_MP129	QISRELAARG	GIPSSYTPQN	NAALAFLESH	QDEE...VGF	PVRPQVPLRP
O_SN_MP130	QISRELAARG	GIPSSHTPQN	NAALAFLESH	QDED...VGF	PVRPQVPLRP
U_CD_83C	AASRDLEKYG	AITSSNTAET	NEACAQLEAA	QE.D.GEVGF	PVRPQVPLRP

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150

00BW0762_1	MTYKGALDLG	FFLK.EKGGL	EGLIYSTKRK	EILDWVYHT	QGYFPDWQNY
00BW0768_2	MTYKGAVDLS	WFLK.EKGGL	EGLIYSKKRQ	EILDWVYNT	QGYFPDWQNY
00BW0874_2	MTFKGAFDLG	FFLK.EKGGL	EGLIWSQKRQ	DILDWVYHT	QGYFPDWQNY
00BW1471_2	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	DILDWVYNT	QGYFPDWQNY
00BW1616_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW1686_8	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW1759_3	MTYKAAFDLG	FFLK.EKGGL	EGLIHSKQRQ	DILDWVYHT	QGYFPDWQNY
00BW1773_2	MTYKAAFDLS	FFLK.EXGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW1783_5	MTYKAAFDLS	FFLK.EKGGL	EGLIHSKQRQ	DILDWVYNT	QGYFPDWQNY
00BW1795_6	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKRQ	EILDWVYHT	QGYFPDWQNY
00BW1811_3	MTYKAAFDLS	FFLK.EKGGL	DGLIHSKKRQ	DILDWVYHT	QGYFPDWQNY
00BW1859_5	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW1880_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYNT	QGYFPDWQNY
00BW1921_1	MTYKAAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW2036_1	MTYKAAIDLS	FFLK.EKGGL	DGLIYSAKRQ	EILDWVYHT	QGYFPDWQNY
00BW2063_6	MTMKGAVDLS	FFLK.EKGGL	EGLIYSKRQ	EILDWVYHT	QGYFPDWQNY
00BW2087_2	MTYKAAFDLS	FFLK.EKGGL	DGLIYSQRQ	DILDWVYNT	QGYFPDWQNY
00BW2127_2	MTYKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW2128_3	GTFKAAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW2276_7	MTYKAAFDLS	FFLK.EKGGL	EGLIYSKRQ	EILDWVYHT	QGYFPDWQNY
00BW3819_3	MTYKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDWVYNT	QGYFPDWQNY
00BW3842_8	MTYKGAVDLS	FFLK.EKGGL	DGLIYSQKRQ	DILDWVYHT	QGYFPDWQNY
00BW3871_3	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW3876_9	MTYKGAVDLS	FFLK.EKGGL	ERLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW3886_8	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW3891_6	MTYKGAVDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW3970_2	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
00BW5031_1	MTYKGAFDLG	WFLK.EKGGL	DGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
96BW01B21	MTYKGAFDLG	FFLK.EKGGL	EGLIYSKKRQ	EILDWVYNT	QGYFPDWQNY

96BW0407	MTYKAAVDLS	FFLK. EKGGL	GGI IYSNKRQ	DILDLWVYNT	QGYFPDWQNY
96BW0502	MTYKGAFDLG	FFLK. EKGGL	EGLVYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BW06_J4	MTYKGAVDLG	FFLK. EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BW11_06	MTYKAAFDLS	FFLK. EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWHNY
96BW1210	MTYKGAFDLS	FFLK. EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQCY
96BW15B03	MTYKGAVDLS	FFLK. EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGYFPDWHNY
96BW16_26	MTYKEAFDLS	FFLK. EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGFLPDWQNY
96BW17A09	MTYKAAFDLS	FFLK. EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
96BWM01_5	VTYKAAFDLS	FFLK. KGGL	EGLIYSKKRQ	NILDLWVYHT	QGYFPDWHNY
96BWM03_2	MTQKGAFDLG	FFLK. EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
98BWMC12_2	MTFKGALDLG	FFLK. EKGGL	DGLIHSKRQ	DILDLWVYHT	QGYFPDWQNY
98BWMC13_4	MTYKGAVDLS	FFLK. EKGGL	DGLIYSKRQ	DILDLWVYNT	QGYFPDWQNY
98BWMC14_a	MTYKAAFDLG	FFLK. EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
98BWM014_1	MTYKAAFDLG	FFLK. EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
98BWM018_d	MTYKAAFDLS	FFLK. EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
98BWM036_a	ITYKAAFDLS	FFLK. EKGGL	EGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
98BWM037_d	MTYKGAFDLG	FFLK. EKGGL	DGLIHSKRQ	DILDLWVYHT	QGYFPDWQNY
99BW3932_1	MTYKAAFDLS	FFLK. EKGGL	EGLIYSKRQ	DILDLWVYNT	QGYFPDWHNY
99BW4642_4	MTYKAAFDLS	FFLK. EKGGL	DGLIYSRKRQ	DILDLWVYHT	QGYFPDWQNY
99BW4745_8	MTYKSAFDLS	FFLK. EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
99BW4754_7	MTYKAAFDLS	FFLK. EKGGL	DGLIHSKRQ	EILDLVHHT	QGYFPDWQNY
99BWMC16_8	MTYKAAVDLS	WFLK. EXGGL	DGLIHSQKRQ	EILDLWVYHT	QGYFPDWQNY
A2_CD_97CD	MTYKGAVDLS	HFLK. EKGGL	DGLIYSQRRQ	DILDLWVYNT	QGYFPDWQNY
A2_CY_94CY	MTFKGAFDLS	FFLK. EKGGL	DGLIYSKRQ	DILDMVYHT	QGYFPDWQNY
A2D_97KR	MTYKGAFDLS	HFLR. EKGGL	DGLIHSQKRQ	DILDLWVYHT	QGYFPDWQNY
A2G_CD_97C	MTYKSAFDLS	FFLK. EKGGL	DGLIYSKRQ	DILDLWVYNT	QGYFPDWQNY
A_BY_97BL0	MTXXXXDXS	HFXK. EKGGL	DGX IYSKKRQ	XILDLXVYHT	QGYFPDWQNY
A_KE_Q23	MTYKGAVDLS	HFLK. KGGL	DGLVYSRKRQ	EILDLWVYHT	QGYFPDWQNY
A_SE_SE659	MTYKAAVDLS	HFLK. EKGGL	DGLIYSRKRQ	EILDLVHHI	QGYFPDWQNY
A_SE_SE725	MTYKGALDLS	HFLK. EKGGL	DGLIYSRRRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_SE753	MTYKGALDLS	HFLK. EKGGL	DGLVYSKKRQ	EILDLVHHT	QGYFPDWQNY
A_SE_SE853	MTYKGAFDLS	HFLK. EKGGL	DGLIYSRKRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_SE889	MTYKGAVDLS	HFLK. EKGGL	DGLIYSRRRQ	EILDLWVYNT	QGYFPDWQNY
A_SE_UGSE8	MTYKGALDLS	HFLK. EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWHNY
A_UG_92UG0	MTYKAAFDLG	FFLK. EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
A_UG_U455	MTYKAAFDLS	FFLK. EKGGL	DGLIHSQKRQ	EILDLWVYHT	QGYFPDWQNY
AC_IN_2130	MTYKGALDLS	FFLK. EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWHNY
AC_RW_92RW	MTYKAAVDLS	FFLK. EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
AC_SE_SE94	MTYKGALDLS	HFLK. EKGGL	DGLIYSQRRQ	DILDLWVYNT	QGYFPDWQNY
ACD_SE_SE8	MTYKAAVDLS	FFLK. EKGGL	EGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
ACG_BE_VI1	MTFKGALDLS	HFLK. EKGGL	DGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
AD_SE_SE69	MTYKGAVDLS	HFLK. EKGGL	EGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
AD_SE_SE71	MTYKAAVDLS	HFLK. EKGGL	DGLIYSRKRQ	DILDLWVYHT	QGYFPDWQNY
ADHK_NO_97	MTYKAAVDLS	HFLK. EKGGL	DGLIYSKKRQ	EILDLVHNT	QGYFPDWQNY
ADK_CD_MAL	MTYKGAFDLS	HFLK. EKGGL	DGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
AG_BE_VI11	MTYKAALDLS	HFLK. EKGGL	EGLIYSQRRQ	DILDLWVYNT	QGYFPDWQNY
AG_NG_92NG	MTYKAAFDLS	FFLK. EKGGL	DGLIYSKKRQ	DILDLWVYNT	QGYFPDWQNY
AGHU_GA_VI	MTFKGAFDLG	FFLK. EKGGL	DGLIHSQKRQ	DILDLWVYHT	QGYFPDWQNY
AGU_CD_Z32	MTFKGAFDLS	FFLK. EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWHNY
AJ_BW_BW21	MTYKGAFDLS	FFLK. EKGGL	DGLIYSKKRQ	EILDLWVYNT	QGYFPDWQNY
B_AU_VH	MTFKAAHDL	FFLK. EQGGL	EGLIYSQRRQ	DILDLWYHT	QGYFPDWQNY
B_CN_RL42	MTYKGALDLS	HFLR. EKGGL	EGLIYSQRRQ	DILDLWVYHT	QGYFPDWQNY
B_DE_D31	MTYKAAVDLS	HFLK. EKGGL	EGLVHSQKRQ	EILDLWVYHT	QGYFPDWQNY
B_DE_HAN	MTYKGALDLS	HFLK. EKGGL	EGLIYSPKRQ	EILDLWVYHT	QGYFPDWQNY
B_FR_HXB2	MTYKAAVDLS	HFLK. EKGGL	EGLIHSQRRQ	DILDLWYHT	QGYFPD. ONY
B_GA_OYI	MTYKGALDLS	HFLK. EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_GB_CAM1	MTYKAAALDIS	HFLK. EKGGL	EGLIYSQRRQ	DILDLWYHT	QGYFPDWQNY
B_GB_GB8	MTYKAAVDLS	HFLK. EQGGL	D		

B_NL_3202A	MTYKGALDLS	HFLK.EKGGL	EGLIYSQRRQ	DILDLWIYHT	QGYFPDWQNY
B_TW_TWCYS	MDYKGALDLS	HFLR.KEGGL	EGLVYSQKKE	DILDLWIYHT	QGYFPDWQNY
B_US_BC	ITYKAAVDLS	HFLK.EKGGL	EGLIFSQRRQ	DILDLWTYHT	QGYFPDWQNY
B_US_DH123	MTYKAAALDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_JRCSF	MTYKAAIDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWIYHT	QGYFPDWQNY
B_US_MNCG	MTYKAAALDLS	HFLK.EKGGL	DGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_P896	MTYKAAVDLS	HFLK.EKGGL	EGLVHSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_RF	MTFKAAVDLS	HFLK.EKGGL	DGLVFSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_SF2	MTYKAAALDIS	HFLK.EKGGL	EGLIWSQRRQ	EILDLWIYHT	QGYFPDWQNY
B_US_WEAU1	MTYKAAHDL	HFK..EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_WR27	MTYKAAVDLS	HFLK.EKGGL	EGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
B_US_YU2	MTYKAAALDIS	HFLK.EKGGL	EGLIHSQRRQ	DILDLWVYHT	QGYFPDWQNY
BF1_BR_93B	MTYKGALDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_BR_92BR0	MTYKAVDLS	FFLE.EKGGL	EGLIYSKKRQ	DILDLWVYHT	QGYFPDWQNY
C_BW_96BW0	MTYKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	DILDLWVYHT	QGYFPDWQNY
C_BW_96BW1	MTYKAAAFDLS	FFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
C_BW_96BW1	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_BW_96BW1	MTYKGAVDLS	FFLK.EKGGL	DGLIYSPKRQ	EILDLWVYHT	QGYFPDWQNY
C_ET_ETH22	MTYKAAFDLS	LFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_93IN1	MTYKSAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_93IN9	MTFKAAVDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_93IN9	MTFKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_94IN1	MTFKGAFDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
C_IN_95IN2	MTFKGALDLS	FFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLS	FFLK.EKGGL	DGLIHSKRRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_C	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_T	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	EGLVYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_T	MTFKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF01_AE_T	MTYKGAFDLS	FFLE.EKGGL	DGLVYSKKRQ	EILDLWVYHT	QGYFPDWQNY
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CRF02_AG_F	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF02_AG_G	MTYKGALDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
CRF02_AG_N	MTYKGAVDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF02_AG_S	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF02_AG_S	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF03_AB_R	MTYKGAFDLS	HFLK..KGG	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF03_AB_R	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF04_cpx_	MTFKGALDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF04_cpx_	MTFKAAALDLS	HFLK.EKGGL	DGLIYSQKRQ	DILDLWVYHT	QGYFPDWQNY
CRF04_cpx_	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF05_DF_B	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	DILDLWVYHT	QGYFPDWQNY
CRF05_DF_B	MTFKGALDLS	HFLK.EKGGL	DGLIYSRKRQ	KILDLWVYHT	QGYFPDWQNY
CRF06_cpx_	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF06_cpx_	MTFKGAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF06_cpx_	MTFKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	DILDLWVYHT	QGYFPDWQNY
CRF06_cpx_	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
CRF11_cpx_	MTYKAAFDLG	FFLK.EKGGL	DGLIYSQKRQ	EILDLWVYHT	QGYFPDWQNY
CRF11_cpx_	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
D_CD_842R0	MTYKAAVDLS	HFLR.KGG	EGLVYSQKRQ	DILDLWVYHT	QGYFPDWQNY
D_CD_ELI	MTYKEALDLS	HFLK.EKGGL	EGLIWSKKRQ	EILDLWVYHT	QGYFPDWQNY
D_CD_NDK	MTYKEAVDLS	HFLK.EKGGL	EGLIWSKKRQ	EILDLWVYHT	QGYFPDWQNY
D_UG_94UG1	MTYKEAVDLS	HFLK.EKGGL	EGLVWSPKRQ	EILDLWVYHT	QGYFPDWQNY
F1_BE_VI85	MTYKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	DTLWVYHT	QGYFPDWQNY
F1_BR_93BR	MTYKGAVDLS	HFLK.EKGGL	EGLIYSRKRQ	EILDLWVYHT	QGYFPDWQNY
F1_FI_FIN9	MTYKGAFDLS	QFXX.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY
F1_FR_MP41	MTFKAAVDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDLWVYHT	QGYFPDWQNY

F2_CM_MP25	MTYKAALDLS	HFLK.EKGGL	EGLIYSKRQ	EILDWVYHT	QGYFPDWQNY
F2KU_BE_VI	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDWVYNT	QGYFPDWHNY
G_BE_DRCBL	MTYKAAFDLS	FFLK.EKGGL	DGLVYSKKRQ	EILDWVYHT	QGYFPDWQNY
G_NG_92NG0	MTYKAAFDLS	FFLK.EKGGL	DGLIYSKRQ	DILDWVYNT	QGYFPDWQNY
G_SE_SE616	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYNT	QGYFPDWQNY
H_BE_VI991	MTYKGAFDLS	HFLK.EKGGL	EGLIYSKKRQ	EILDWVYNT	QGYFPDWHNY
H_BE_VI997	MTYKAALDLS	HFLK.EKGGL	DGLIYSKKRQ	EILDWVYNT	QGYFPDWQNY
H_CF_90CF0	MTYKGAFDLS	HFLK.EKGGL	DGLIYSKRQ	DILDWVYNT	QGYFPDWQNY
J_SE_SE702	MTYKGAFDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDWVHNT	QGYFPDWQNY
J_SE_SE788	MTYKGAVDLS	FFLK.EKGGL	DGLIYSKKRQ	EILDWVHNT	QGYFPDWQNY
K_CD_EQTB1	MTYKGAFDLG	FFLK.EKGGL	DGLIYSKRQ	EILDWVYHT	QGYFPDWQNY
K_CM_MP535	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYHT	QGYFPDWQNY
N_CM_YBF30	ITYKQAFDLS	FFLK.DKGGL	EGLVWSKRQ	DILDWVYHT	QGYFPDWHNY
O_CM_ANT70	MTYKGAFDLS	FFLK.EKGGL	EGLIYSHKRA	EILDWVYNT	QGYFPDWQNY
O_CM_MVP51	MTYKGAFDLS	FFLK.EKGGL	DGLIYSHKRA	EILDWVYHT	QGYFPDWQNY
O_SN_MP129	MTYKGAFDLS	FFLK.EKGGL	DGLIYSHKRA	EILDWVYHT	QGYFPDWQNY
O_SN_MP130	MTYKGAFDLS	FFLK.EKGGL	DGLIYSPERA	EILDWVYHT	QGYFPDWQNY
U_CD_83C	MTYKAAFDLG	FFLK.EKGGL	DGLIYSKKRQ	EILDWVYNT	QGYFPDWQNY

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00BW0762_1	TPGPGTRYSL	TFGWPFKLVP	VD.PKEVEEA	NEGENNCLLH	PMSQHRIDDD
00BW0768_2	TPGPGVRYPL	TLGWCFKLVP	VD.PREAEVEE	TKGENSCLLH	PMSQHGMEDS
00BW0874_2	TPGPGVRYPL	TFGWPFKLVP	VD.PTEVEEA	NEGENNCLLH	PMSQHGMDDK
00BW1471_2	TPGPGVRYPL	TFGWCFKLVP	VD.PKEVDAN	.EGENNCLLH	PMSQHGMDDK
00BW1616_2	TPGPGTRLPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSQQGMEDK
00BW1686_8	TPGPGVRYPL	TFGWPFKLVP	VD.PREVQEA	NKGENNCLLH	PMSQHGMEDK
00BW1759_3	TPGPGIRYPL	TFGWCFKLVP	VD.PKEVEEA	NEGEDNCLLH	PMSLHGMEDD
00BW1773_2	TPGPGVRFPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PMSQHGMEDK
00BW1783_5	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGMEDK
00BW1795_6	TPGPGTRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGMEDK
00BW1811_3	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NKGENNCLLH	PMSLHGAEDI
00BW1859_5	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NEGEDNCLLH	PISQHGMDT
00BW1880_2	TPGPGIRYPL	TFGWCFKLVP	VD.PGEVEEA	NKGENNCLLH	PMSQYGMDDK
00BW1921_1	TPGPGVRYPL	TFGWPFKLVP	VD.PKEVEEA	NKGENNCLLH	PLSQQGMEDK
00BW2036_1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NQGENNCLLH	PMSQFGMDDK
00BW2063_6	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PISLHGMEDN
00BW2087_2	TPGPGVRYPL	TSGWCYKLVP	VD.PREVEEA	NEGESNSLLH	PISLHGMEDD
00BW2127_2	TPGPGVKYPL	TFGWCFKLVP	VD.PKEVEEA	NEGEDNCLLH	PMSQHGMDDK
00BW2128_3	TPGPGVRYPL	TFGWRYKLVP	VD.PQEVQQS	NEGEDNCLLH	PMSQHGMEDK
00BW2276_7	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PRSLHGIEDE
00BW3819_3	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEA	TEGENTCLLH	PMSQHGMEDK
00BW3842_8	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NQGENNCLLH	PMSQHGMDDK
00BW3871_3	TPGPGVRYPL	TFGWPFKLVP	VD.PREVEED	NNGENNCLLH	PMSQHGMDDK
00BW3876_9	TPGPGTRFPL	TFGWCFKLVP	VD.PREVEEA	NEGENSCLLH	PISQHGMEDE
00BW3886_8	TPGPGVRYPL	TFGWPFKLVP	VD.PREVEEA	NQGENNCLLH	PMSQYGMEDK
00BW3891_6	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PISQHGMEDE
00BW3970_2	TPGPGVRYPL	TFGWCFKLVP	VD.PREIEEA	NKGEDNCLLH	PMSQHGMEDK
00BW5031_1	TPGPGVRYPL	TFGWCFKLVP	VD.PKEVEEA	TEGENTCLLH	PICQHGMEDK
96BW01B21	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	SEGEDNCLLH	PMSQHGMEDK
96BW0407	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSLHGMEDD
96BW0502	TPGPGVKYPL	TFGWCFKLVP	VD.PGEVEEA	NKGEDNCLLH	PMSQHGMEDK
96BW06_J4	TPGPGITYPL	TFGWPFKLVP	VD.PREVEEA	NNGENNCLLH	PMSQHGMDDK
96BW11_06	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NEGENNCLLH	PMAQHGMEDK
96BW1210	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NGGEDNCLLH	PMSQHGMEDK
96BW15B03	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NQGENHCLLH	PMSQHGMDDK
96BW16_26	TPGPGVRFPL	TFGWCFKLVP	VD.PREVEEA	TEGEDNCLLH	PMNQHGMDDP
96BW17A09	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEED	NEGENNCLLH	PMSQHGMEDK
96BWM01_5	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEA	NKGENSCLLH	PVSLHGMEDK
96BWM03_2	TPGPGVRYPL	TFGWCFKLVP	VD.PKEVEEA	SEGENNCLLH	PMNQHGMEDE
98BWM12_2	TPGPGVRYPL	TFGWPFKLVP	VD.PKEVEEA	NKGENNCLLH	PMSLHGIEDE

98BWMC13_4	TPGPGVRYPL	TFGWCYKLVP	VD.PREVEEA	NEGENNCLLH	PMSLHGIEDA
98BWMC14_a	TPGPGTRYPL	TFGWPFKLVP	VD.PREVEEA	NNGENNCLLH	PMSQHGMDDE
98BWM014_1	TPGPGVRYPL	TFGWCYKLVP	VD.PREVEEA	NEGEDNCLLH	PMSQHGIEDP
98BWM018_d	TPGPGVRYPL	TFGWCYKLVP	VD.PREVEEA	NEGEDNCLLH	PMSQHGIMEDA
98BWM036_a	TPGPGTRYPI	TFGWCFKLVP	VD.PREVEEA	NEGENNSLLH	PVSLHGMEDD
98BWM037_d	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	TEGEDNCLLH	PLSQHGIEDA
99BW3932_1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEN	NQRENSCLLH	PMSQHGIMEDP
99BW4642_4	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGIMEDA
99BW4745_8	TPGPGVRYPL	TFGWCLKLVP	VD.PREVEED	NEGENNCLLH	PMSQHGIMEDA
99BW4754_7	TPGPGIRYPL	TFGWCFKLVP	VD.PREVQEA	NEGDDNCLLH	PMSQFGMDDD
99BWMC16_8	TPGPGIRYPL	TFGWCFRLVP	VD.PSEVEEA	NQGENNCLLH	PISQHGIMEDD
A2_CD_97CD	TPGPGARFPL	TFGWCFKLVP	VD.PSEVEEA	TEGENNSLLH	PICQHGIMEDP
A2_CY_94CY	TPGPGIRYPL	TFGWCFKLVP	VE.PSEVEEA	TQGENNSLLH	PICQHGIMDDP
A2D_97KR	TPGPGIRYPL	TFGWCFKLVP	VS.PAEVEEA	TEGETNSLLH	PICQHGIMEDP
A2G_CD_97C	TPGPGVRYPL	TFGWCFKLVP	MD.PAEVEEA	NKEENSLLH	PICQHGIMEDD
A_BY_97BL0	TPGPXIRFPL	TFXXCYKLVP	VD.PAEVEEA	TXGENNSLLH	PICQHGIMDD
A_KE_Q23	TPGPGTRFPL	TFGWCFKLVP	VD.PDEVEKA	TEGENNSLLH	PICQHGIMDD
A_SE_SE659	TPGPGIRFPL	TFGWCFKLVP	VD.PDEVEKD	TEGENNSLLH	PICQHGIMDD
A_SE_SE725	TPGPGVRYPL	TFGWCFKLVP	VD.PDEVEQA	NEGENNSLLH	PMCQHGIMDD
A_SE_SE753	TPGPGIRYPL	TFGWCFKLVP	VD.PDEVKDD	TEGENNSLLH	PMCQHGIMDD
A_SE_SE853	TPGPGVRYPL	TFGWCFKLVP	VE.PEEVEKA	NEGENNSLLH	PICQHGIMDD
A_SE_SE889	TPGPGTRFPL	TFGWCFKLVP	VD.PDEVEKA	TEGENNSLLH	PICQHGIMDD
A_SE_UGSE8	TPGPGIRYPL	TFGWCFKLVP	VD.PDEVEKA	TEGENNSLLH	PMCQHGIMDD
A_UG_92UG0	TPGPGIRYPL	TFGWCFKLVP	VD.EDEVEEA	TGGENNSLLH	PICQHGIMDD
A_UG_U455	TPGPGIRYPL	TFGWCYKLVP	VD.PAEVEEA	TGGENNSLLH	PICQHGIMDD
AC_IN_2130	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	TGGEDNCLLH	PVCQHGIMED
AC_RW_92RW	TPGPGVRYPL	TFGWCYKLVP	VD.PREVEEA	NEGEDNCLLH	PLSQHGIMED
AC_SE_SE94	TPGPGIRYPL	TFGWCFKLVP	VN.PDEVEEA	TKGENNSLLH	PMCQHGIMDD
ACD_SE_SE8	TPGPGTRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGIMED
ACG_BE_VI1	TPGPGTRFPL	TFGWCFKLVP	MD.PTEVEEA	NEGENNCLLH	PISQHGIMED
AD_SE_SE69	TPGPGIRYPL	IFGWCFELVP	VD.PKEVEED	IG.ENSSLLH	PMHQHGIMED
AD_SE_SE71	TPGPGTRFPL	TFGWCFKLVP	VD.PDEVEKA	TEGETNTLLH	PICQHGIMDD
ADHK_NO_97	TPGPGERFPL	TFGWCFKLVP	VD.PQEVEKA	NDGENNCLLH	PMCQHGIMED
ADK_CD_MAL	TPGPGIRFPL	TFGWCFKLVP	MS.PEEVEEA	NEGENNCLLH	PISQHGIMEDA
AG_BE_VI11	IPGPGTRFPL	TFGWCFKLVP	MD.PAGIEKA	NEGENNSLLH	PICQHGIMDD
AG_NC_92NG	TPGPGTRFPL	TFRWCFKLVP	MD.PAEIEEA	NKGENNSLLH	PICQHGIMEDA
AGHU_GA_VI	TPGPGIRYPL	CFGWCFKLVP	VD.PKEVEEA	TEGENNCLLH	PICQHGIMDD
AGU_CD_Z32	TPGPGTRYPL	CFGWCFKLVP	VD.PREVEEA	NTGENNCLLH	PMSQHGIMDD
AJ_BW_BW21	TPGPGTRFPL	TFGWCFKLVP	VD.PKEVEEA	NEGENNCLLH	PLCQHGIMED
B_AU_VH	TPGPGTRYPL	TFGWCFKLVP	VE.PDQVEKA	NEGENISLLH	PMSLHGIMED
B_CN_RL42	TPGPGTRFPL	TFGWCFKLVP	VD.PEQVEEA	NEGENNCLLH	PMSQHGIMDD
B_DE_D31	TPGPGTRFPL	TFGWCFKLVP	VK.PEQVEEA	NEGENNSLLH	PMSLHGIMDD
B_DE_HAN	TPGPGVRYPL	TFGWCFKLVP	VE.PDEEENSSLLH	PASLHGIMED
B_FR_HXB2	TPGPGVRYPL	TFGWCFKLVP	VE.PDKIEEA	NKGENTSLLH	PVSLHGIMDD
B_GA_OYI	TPGPGIRYPL	CFGWCFKLVP	MD.PDQVEEA	NEGENNSLLH	PISLHGIMDD
B_GB_CAM1	TPGPGIRYPL	TFGWCFKLVP	VE.PEQVEEA	NKRENASLLH	PMSQHGIMDD
B_GB_GB8	TPGPGTRFPL	TFGWCFKLVP	VE.PEEVEKA	NEGENNCLLH	PMSQHGIMED
B_GB_MANC	TRGPGIRYPL	AFGWCFKLVP	VD.PEQVEEA	NEGENNSLLH	PMSLHGIMDD
B_KR_WK	TPGPGTRFPL	TFGWCFKLVP	VE.PEKVEEA	TVGKNNCLLH	PMNLHGIMDD
B_NL_3202A	TPGPGIRYPL	TFGWCFKLVP	VE.QEKIEEA	NEGENNSLLH	PMSQHGIMDD
B_TW_TWCYS	TPGPGVRYPL	TFGWCFKLVP	VE.PEQVEKA	NEGENXCLLH	PMSQHGIMDD
B_US_BC	TPGPGIRYPL	TFGWCFKLVP	VD.PEKIEEA	NEGENNSLLH	PMSQHGIMDD
B_US_DH123	TPGPGIRYPL	TFGWCFKLVP	VD.PEKVEEA	NEGENNCLLH	PISLHGIMED
B_US_JRCSP	TAGPGVRFPL	TFGWCFKLVP	VD.PEKVEEA	NEGENNCLLH	PMSQHGIMDD
B_US_MNCG	TPGPGIRYPL	TFGWCFKLVP	VE.PEKIEEA	NKGENNCLLH	PMSQHGIMDD
B_US_P896	TPGPGIRYPL	TFGWCFKLVP	VE.PDEGENN	RE..DNSLLH	PANQHGIMED
B_US_RF	TPGPGTRYPL	TFGWCFKLVP	VE.PDKVEEA	TEGENNSLLH	PICLHGIMDD
B_US_SF2	TPGPGIRYPL	TFGWCFKLVP	VE.PEKVEEA	NEGENNSLLH	PMSLHGIMEDA
B_US_WEAU1	TPGPGTRYPL	CFGWCFKLVP	VE.PEKVEEA	NEGENNSLLH	PMSLHGIMDD
B_US_WR27	TPGPGTRYPL	TFGWCFKLVP	LE.PDQVEEA	NKGENNCLLH	PMSQHGIMDD

B_US_YU2	TPG.GTRWPL	TFGWCFKLVP	VE.PEKIEEA	NAGENNCLLH	PMSQHGMDDP
BF1_BR_93B	TPGPGTRYPL	TLGWCFKLVP	VD.PEEVEKA	NEGENNCLLH	PMSQHGMEDF
C_BR_92BR0	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NTGENNSLLH	PMSLHGMEDS
C_BW_96BW0	TPGPGVRYPL	TFGWCFKLVP	VD.PKEVEEA	NEGENNRLH	PMSLHGMEDA
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NEGEN.CLLH	PIAQHGMEDF
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.PGEVEEA	NGGEDNCLLH	PMSQHGIEDA
C_BW_96BW1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEN	NQGENHCLLH	PMSQHGMNDP
C_ET_ETH22	TPGPGVRYPL	TFGWCFKLVP	VD.PSEVEEI	NEGENNCLLH	PASLHGMEDF
C_IN_93IN1	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PVCQHGMEDF
C_IN_93IN9	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PVCQHGMDDF
C_IN_93IN9	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NEGENNCLLH	PVCQHGMEDF
C_IN_94IN1	TPGPGTRFPL	TFGWCFKLVP	VD.PREVEEA	NEGEDNCLLH	PVCQHGMEDD
C_IN_95IN2	TPGPGVRYPL	TFGWCFKLVP	VD.PREVEEA	NKGEDNCLLH	PVCQHGMEDD
CRF01_AE_C	TPGPGIRYPL	CFGWCYKLVP	VD.PKEVEED	NKDESNCLLH	PMSQHGVDDF
CRF01_AE_C	TPGPGVRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIIDD
CRF01_AE_C	TPGPGTRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIEDF
CRF01_AE_T	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PLSQHGIEDF
CRF01_AE_T	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEED	NKEENNCLLH	PMSQHGIDDF
CRF01_AE_T	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGIEDF
CRF01_AE_T	TPGPGIRFPL	CFGWCYKLVP	VD.PREVEED	NKGENNCLLH	PMSQHGMGDG
CRF01_AE_T	TPGPGIRFPL	CFGWCYKLVP	VD.QREVEED	NKGENNCLLH	PMSQHGIEDF
CRF01_AE_T	TPGPGVRLPL	CFGWCYKLVP	VD.PREVEED	NKGENNSLLH	PMSQHGIEDF
CRF02_AG_F	TPGPGTRYPL	TFGWCFNLEP	ID.PAEIEEA	NKEENNSLLH	PICQHGMEDF
CRF02_AG_F	TPGPGTRYPL	TFGWCFKLEP	MD.PAEVEEA	NKGENNSLLH	PICQHGMEDF
CRF02_AG_G	TPGPGTRFPL	TFGWCFKLVP	MD.PKAVEEA	TEGENNSLLH	PICQHGIEDF
CRF02_AG_N	TPGPGTRFPL	TFGWCFKLVP	MD.PAEVEEA	NEGENNSLLH	PICQHGMEDD
CRF02_AG_S	TPGPGTRFPL	TFGWCFKLVP	MD.PADIEKD	TEGENNSLLH	PICQHGMEDF
CRF02_AG_S	TPGPGIRYPL	TFGWCFKLVP	MD.PAEVEEA	NQGENNSLLH	PICQHGMEDF
CRF03_AB_R	...PGIRFPL	TFGWCFKLVP	VD.PAEVEEA	TEGENNSLLH	PICQHGMDDF
CRF03_AB_R	TPGPGIRFPL	TFGWCFKLVP	VD.PDEVEEA	TEGENNSLLH	PICQHGMDDF
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CRF04_cpx_	TPGPGERFPL	CFGWCYKLVP	VD.PQEVEEA	NEGENNCLLH	PISQHGMEDF
CRF04_cpx_	TPGPGTRFPL	CFGWCYKLVP	VD.PQEVEEI	TAGEDNCLLH	PISQHGMEDF
CRF05_DF_B	TPGPGIRYPL	TLGWCFKLVP	VN.PEEVEKA	NEGEDNCLLH	PMSLHGMEDD
CRF05_DF_B	TPGPGTRYPL	TFGWCFKLVP	VD.PEEVEKA	NEGENKCLLH	PMQHGMDDF
CRF06_cpx_	TPGPGTRFPL	TFGWCFKLVP	VD.PEEVEEL	TKGENNCLLH	PICQHGAEDF
CRF06_cpx_	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEE	TKGENNSLLH	PMCQHGAEDF
CRF06_cpx_	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEED	TKGENNCLLH	PMSQHGMEDF
CRF06_cpx_	TPGPGIRYPL	TFGWCFKLVP	VD.PKEVEEE	TKGENXSLLH	PMCQHGVDDP
CRF11_cpx_	TPGPGVRYPL	CFGWCYKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGMDDF
CRF11_cpx_	TPGPGIRYPL	CFGWCYKLVP	VD.PREVEEA	NEGENNCLLH	PMSQHGIEDF
D_CD_84ZR0	TPGPGIRYPL	TFGWCFELVP	VD.PEVVEKA	TEGEDNCLLH	PICQHGMEDF
D_CD_ELI	TPGPGIRYPL	TFGWCFELVP	VD.PQEVEED	TEGETNSLLH	PICQHGMEDP
D_CD_NDK	TPGPGIRYPL	TFGWCFQLV	VD.PQEVEEA	TEREDNCLLH	PMCQGMEDP
D_UG_94UG1	TPGPGIRYPL	TFGWCFELVP	ME.PKEVEEN	TEGEDNCLLH	PINQHGMEDP
F1_BE_VI85	TPGPGIRYPL	TLGWCFKLVP	VD.PEEVEKA	NEGENNCLLH	PMSQHGMEDF
F1_BR_93BR	TPGPGIRYPL	TMGWCFKLVP	VD.PEEVEKA	NEGENNCLLH	PMSQHGMEDF
F1_FI_FIN9	TPGPGVRYPL	TFGWCFKLVP	VE.PEBVEKA	NEGENNCLLH	PMSQHGMEDF
F1_FR_MP41	TPGPGIRFPL	TFGWCFKLVP	VD.PDEVEKA	NEGENNCLLH	PMSQHGMDDF
F2_CM_MP25	TPGPGPRFPL	TFGWCFKLVP	VD.PEEVEKA	NEGENNCLLH	PMSLHGMEDD
F2KU_BE_VI	TPGPGIRYPL	CFGWCYKLVP	MD.PQEVEEA	NVGENNSLLH	PICQHGIDDT
G_BE_DRCBL	TPGPGTRVPL	TFGWCFKLVP	ME.PSEVEEA	NKGENNSLLH	PICQHGMEDF
G_NG_92NG0	TPGPGTRLPL	TFGWCFKLVP	MD.PAEIEEA	NKGENISLLH	PICQHGMEDF
G_SE_SE616	TPGPGTRFPL	TFGWCFKLVP	MD.PAEVEEA	NKGENNSLLH	PICQHGMEDF
H_BE_VI991	TPGPGERYPL	TFGWCFKLVP	VD.PQDVEKA	NEGENNSLLH	PMCQHGIEDP
H_BE_VI997	TPGPGEGYPL	TFGWCFKLIP	VD.PQEVEEA	NEGENNCLLY	PICQHGMEDF
H_CF_90CF0	TPGPGERFPL	TFGWCFKLVP	VN.PQEVEQA	NEGENNSLLH	PMSLHGMEDD
J_SE_SE702	TPGPGTXYPL	TFGWCFKLVP	VD.PSEVEEA	NEGENNCLLH	PACQHGIEDF
J_SE_SE788	TPGPGIRYPL	TFGWCFKLVP	VD.PSEVEEA	NEGENNCLLH	PICQHGIEDF
K_CD_EQTB1	TPGPGIRYPL	TFGWCFKLVP	VD.PREVEEA	TEGENNCLLH	PVNQHGMEDF

K_CM_MP535	TPGPGIRYPL	TFGWCYKLVP	VD.PAEVEET	TEGEDNCLLH	PINQHGMED
N_CM_YBF30	TPGPGIRYPV	TFGWCFKLVP	LS.AEEVEEA	NEGDNNALLH	PICQHGADDD
O_CM_ANT70	TPGPGTRFPL	TFGWLFKLVP	VSEEEAERLG	NTCERANLLH	PACAHGFEDT
O_CM_MVP51	TPGPGPRFPL	TFGWLFKLVP	VSAEEAERLG	NTNEDASLLH	PACNHGAEDA
O_SN_MP129	TPGPGPRFPL	TFGWLFKLVP	VSEAAEELG	NKCERASLLH	PACNHGFEDN
O_SN_MP130	TPGPGTRFPL	TFGWLFKLVP	VSEAAEELG	NKCDRAKLLH	PVCNHGFEDP
U_CD__83C	TPGPGIRYPL	TFGWPFKLVP	VD.PKEVEEA	NEGENNCLLH	PICQHGMDD

	201		232
00BW0762_1	HREVLWKFD	SSLARRHVAR	E.LHPEYYKD C.
00BW0768_2	EREVLRWKFD	SSLARRHMAR	E.LHPEYYKD C.
00BW0874_2	DREVLKWQFD	SSLVRRHMAR	E.LHPEYYKD C.
00BW1471_2	DREVLKWVFD	SSLARRHMAR	E.LHPEYYKD C.
00BW1616_2	DREVLRWKFD	SSLARRHLAR	E.LHPEYYKD C.
00BW1686_8	DREVLWKFD	SHLAYRHMAR	E.LHPEYYKD C.
00BW1759_3	HGEVLWKFD	SALARRHMAR	E.LHPEYYKD C.
00BW1773_2	HGEVLKWFD	SSLARRHLAR	E.KHPEFYKD C.
00BW1783_5	DKEVLQWFD	SSLARRHMAR	E.LHPEYYKD C.
00BW1795_6	DREVLWKFD	SHLARRHTAR	E.LHPEFYKD CR
00BW1811_3	HGEVLEWFD	SMLARRHMAR	E.LHPEYYKD C.
00BW1859_5	EREVLRWKFD	SQLARRHMAR	E.LHPEYYKD C.
00BW1880_2	HKEVLRWKFD	SSLARRHLAR	E.LHPEYYKD C.
00BW1921_1	DREVLWKFD	SQLAHRHLAR	E.KHPEWYKD C.
00BW2036_1	HKEVLTWFD	SHLARRHMAR	E.LHPEYYKD C.
00BW2063_6	HREVLQWFD	SQLARRHIAR	E.RHPEYYKD C.
00BW2087_2	DREVLKWVFD	SSLARRHLAR	E.KHPEFYKD C.
00BW2127_2	EREVLQWFD	SLSRRHLAR	IXIHAEYYKD C.
00BW2128_3	HGEVLWKFD	SHLAYRHMAR	E.KHPEFYKD C.
00BW2276_7	EREVLKWFD	SSLARRHMAR	E.LHPEYYKA C.
00BW3819_3	EGEVLQWFD	SLLAYRHMAR	E.QHPEYYKD C.
00BW3842_8	DREVPMWKFD	SLLAHRHMAR	E.LHPGYKYD C.
00BW3871_3	DREVLWKFD	SHLVHRHMAR	E.LHPEYYKG C.
00BW3876_9	DREVLRWKFD	S.LARRHIAR	E.LHPEYYKN C.
00BW3886_8	EREVLKWFD	SQLAYRHMAR	E.IHPEYYKD C.
00BW3891_6	DREVLRWKFD	SHLARRHMAR	E.LHPEWYKD C.
00BW3970_2	DREVLKWQFD	ISLARRHMAR	E.LHPEWYKD ..
00BW5031_1	DREVLRWKFD	SELARRHIAR	E.RHPEFYKD C.
96BW01B21	HREVLKWFD	SQLARRHMAR	E.LHPEYYKD C.
96BW0407	DREVLRWKFD	SSLAHRHMAR	E.LHPEYYKD C.
96BW0502	HGEVLKWFD	SQLARRHMAR	E.LYPEYYKD C.
96BW06_J4	EREVLTWFD	SHLVHRPMAR	E.IHPEYYKD C.
96BW11_06	HKEVLKWFD	SQLARRHLAR	E.LHPEFYKD C.
96BW1210	DREVLKWFD	SSLARRHLTR	E.KHPEYYKD C.
96BW15B03	DKEVLWKFD	SHLARRHMAR	E.LHPEYYKD C.
96BW16_26	ERGVLKWFD	SHLARRHMAR	E.LHPEYYKD C.
96BW17A09	DREVLKWVFD	SHLARKHMAR	E.LHPEYYKN C.
96BWM01_5	HREVLKWFD	SSLARRHMAR	E.LHPEFYKD C.
96BWM03_2	HGEVLWKFD	SQLARRHMAR	E.LHPEYYKD C.
98BWMC12_2	EREVLKWQFD	SSLARRHMAR	E.LHPEYYKD C.
98BWMC13_4	GKEVLIWFD	SHLARRHMAR	E.LHPEFYKD C.
98BWMC14_a	DREVLWKFD	SQLARRHIAR	E.IHPEYYKD C.
98BWM014_1	EKEVLKWVFD	SSLARRHVAR	E.LHPEFYKD C.
98BWM018_d	DREVLRWKFD	SSLARRHMAR	E.LHPEYYKD C.
98BWM036_a	DREVLKWEFD	IRLAHTHMAR	Q.LHPEFYKN C.
98BWM037_d	DREVLKWQFD	SSLAHRHVAR	E.LHPEYYKD C.
99BW3932_1	DREVLKWFD	SMLARRHMAR	E.LHPEFYKD C.
99BW4642_4	DREVLWKYD	SQLARRHMAR	E.LHPDYKYD C.
99BW4745_8	DREVLRWKFD	SHLARRHMAR	E.LHPEFYKD C.
99BW4754_7	HKEVLKWFD	SHLARRHMAR	E.LHPEFYKD C.
99BWMC16_8	DREVLKWQFD	SSLARRHMAR	E.LHPEYYKD C.

A2_CD_97CD	EREVLKWKFD	SRLALRHLAR	E.QHPEFYKD	C.
A2_CY_94CY	EREVLRWKFD	RSLARRHRAR	E.LHPEYYKD	C.
A2D__97KR	EREVLKWKFD	SHLALVHKAR	E.LHPEFYKD	C.
A2G_CD_97C	DKQVLGWRFD	SSLARRHIAR	E.KHPEYYKD	C.
A_BY_97BL0	EKEVLMWKFD	SRLALKHRAR	E.LHPEFYKD	C.
A_KE_Q23	EREVLKWKFD	SRLALKHRAR	E.LHPEWYKD	C.
A_SE_SE659	EKEVLKWKFD	SRLALKHLAC	E.KHPEFYKD	C.
A_SE_SE725	EKETLRWRFD	SRLALRHRAQ	E.MHPEFYKD	C.
A_SE_SE753	EREVLKWKFD	SRLALKHRAQ	E.LHPEFYKD	C.
A_SE_SE853	ERETLMWKFD	SKLALKHRAH	E.LHPEYFKN	C.
A_SE_SE889	ERETLMWKFD	SRLALTHRAR	E.LHPEFYKD	C.
A_SE_UGSE8	ERETLMWKFD	PHLAFKHRAR	E.LHPEYYKN	..
A_UG_92UG0	EKETLRWKFD	SSLARVHKAR	E.LHPEFYKD	C.
A_UG_U455	EKEVLMWKFD	STLALKHRAH	E.LHPEFYKD	..
AC_IN_2130	YGEVLQWKFD	SHLAYKHQAR	E.RHPEFYKD	C.
AC_RW_92RW	DREVLKWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
AC_SE_SE94	ERETLVWRFD	SRLALKHLAR	E.KHPEFYKD	C.
ACD_SE_SE8	DKEVLRWKFD	SQLARRHMAR	E.MHPEYYKD	C.
ACG_BE_VI1	DREVLVWRFD	SRLALKHIAK	E.KHPEYFKD	C.
AD_SE_SE69	EREVLMWRFN	SRLAFEHKAH	Q.LHPEYYKD	C.
AD_SE_SE71	EKEVLKWKFD	SRLALKHLAR	E.KHPEFYKD	C.
ADHK_NO_97	EXEVLMWRFN	SRLAFKHRAR	E.LHPEFYKD	C.
ADK_CD_MAL	EREVLKWKFD	SSLALRHRAR	E.QHPEYYKD	C.
AG_BE_VI11	EREVLVWKFD	SMLAFKHRAR	E.LHPEYYKD	C.
AG_NG_92NG	DREVLVWRFD	SSLARRHIAR	E.QHPEYYKD	C.
AGHU_GA_VI	EREVLMWKFD	SSLAREHVAR	K.LYPEFFKD	C.
AGU_CD_Z32	EREVLMWKFD	SSLARKHLAR	E.MHPEFYKD	..
AJ_BW_BW21	DREVLMWKFD	SSLARRHLAR	E.KHPEFYKD	C.
B_AU_VH	EKEVLMWKFD	SRLAVHHMAR	E.LHPEYYKN	..
B_CN_RL42	EREVLMWKFD	SRLAIHHMAR	E.MHPEYHKD	C.
B_DE_D31	EREVLVWRFD	SRLAFKHMAR	E.LHPEYYKN	..
B_DE_HAN	EREVLKWKFD	SHLAFHHKAR	E.LHPEYYKD	C.
B_FR_HXB2	EREVLEWRFD	SRLAFHHVAR	E.LHPEYFKN	C.
B_GA_OYI	EKEVLVWKFD	SRLAFRHHMAR	E.VHPEYYKD	C.
B_GB_CAM1	EKEVLMWKFD	SRLAFHHMAR	E.KHPEFYKD	C.
B_GB_GB8	EKEVLVWKFN	SRLAFHHMAR	E.LHPEFYKD	C.
B_GB_MANC	EKEVLVWKFD	SRLAFHHVPD	E.LHPEYYKD	C.
B_KR_WK	EGEVLVWRFD	SRLAFHHMAR	E.KHPEYYKD	C.
B_NL_3202A	EREVLEWRFD	SRLAFHHMAR	E.LHPEYYKD	C.
B_TW_TWCYS	EKEVLVWRFD	STLAFHHRAR	E.LHPEYYKX	C.
B_US_BC	EREVLEWRFD	SRLAFHHMAR	E.LHPEYYKN	R.
B_US_DH123	EKEVLLWKFD	SRLAYHHMAR	E.LHPEYYKN	C.
B_US_JRCSF	EKEVLVWKFD	SKLALHHVAR	E.LHPEYYKD	C.
B_US_MNCG	EREVLVWKS	SHLAFQHYAR	E.LHPEYYKN	C.
B_US_P896	ERQVLVWRFD	SRLAFHHVAR	E.LHPEYFKN	..
B_US_RF	EKEVLVWKFD	SRLAFHHVAR	E.KHPEYYKD	C.
B_US_SF2	EKEVLVWRFD	SKLAFHHMAR	E.LHPEYYKD	C.
B_US_WEAU1	EKEVLMWKFD	SKLAFHHVAR	E.LHPEYFKD	C.
B_US_WR27	EKEVLVWKFD	SRLAFHHKAR	E.LHPEYYKN	..
B_US_YU2	EREGLEWRFD	SRLAFHHVAR	E.LHPEYYKN	..
BF1_BR_93B	DRETLQWRFD	SRLAFHHMAR	E.LHPEYYKD	C.
C_BR_92BR0	HREVLQWKFD	SLARRHMAR	E.LHPEYYKD	C.
C_BW_96BW0	DGEVLRWKFD	SHLAHRHMAR	E.LHPEYYKD	C.
C_BW_96BW1	HKEVLKWKFD	SQLARRHLAR	E.LHPEFYKD	C.
C_BW_96BW1	DREVLKWKFD	SSLARRHLTR	E.KHPEYYKD	C.
C_BW_96BW1	DKEVLMWKFD	SHLARRHMAR	E.LHPEYYKD	C.
C_ET_ETH22	DREVLKWKFD	SHLARRHMAR	E.LHPEYYKD	C.
C_IN_93IN1	HREVLKWKFD	SQLARRHMAR	E.LHPEFYKD	C.
C_IN_93IN9	HREVLQWKFD	SLAHRHRAR	E.LHPEFYKD	C.
C_IN_93IN9	HREVLQWKFD	SHLAHRHMAR	E.LHPEYYKD	C.

C_IN_94IN1	HREVLWVK..	QLARRHIAR	E.LHPEFYKD	C.
C_IN_95IN2	HNEVLVWKFD	SQLARKHRAR	E.LHPEFYNK	DC
CRF01_AE_C	EREVLWVKFD	SSLARRHIAR	E.LRPEYYKD	C.
CRF01_AE_C	EREVLWVKFD	SSLARRHIAR	E.LHPEYYKD	..
CRF01_AE_C	EREVLWVKFD	SSLARRHIAR	E.LHPEYYKD	C.
CRF01_AE_T	EREVLWVKFD	SALARKHTAR	E.LHPEYYKD	C.
CRF01_AE_T	EREVLWVKFD	STLARKHIAR	E.QHPEFYKD	C.
CRF01_AE_T	EREVLWVKFD	SALARRHIAR	E.LRPEFYKD	C.
CRF01_AE_T	EREVLWVKFD	SALARKHIAR	E.MHPEYYKD	C.
CRF01_AE_T	EREVLWVKFD	SALARKHVAR	E.QHPEYYKD	C.
CRF01_AE_T	EREVLWVKFD	SSLARKHLAR	E.LHPEYYKD	C.
CRF02_AG_F	DREVLVWRFD	SSLARTHVAR	E.LHPEYYKD	C.
CRF02_AG_F	DREVLVWRFD	SSLARRHIAR	E.RHPEFYKD	C.
CRF02_AG_G	DREVLVWRFD	SSLAFTHVAR	E.MHPEFYKD	C.
CRF02_AG_N	DREVLVWRFD	SRLAFRHTAR	E.LHPEYYKD	C.
CRF02_AG_S	DREVLVWRFD	SRLAFTHVAR	E.MHPEFYKD	CX
CRF02_AG_S	DREVLVWRFD	SRLAFRHTAR	E.LHPEYYKD	C.
CRF03_AB_R	EKEVLWVKFD	SRLALTHVAR	E.LHPEFYKD	C.
CRF03_AB_R	EKEVLWVKFD	SRLALTHVAR	E.LHPEFYKD	C.
CRF04_cpx	EREVLWVKFD	SRLAYKHVAR	E.LHPEFYKD	C.
CRF04_cpx	EREVLWVKFD	SRLAFKHVAR	E.LHPEFYKD	C.
CRF04_cpx	EREVLWVKFD	SRLAYRHVAR	E.LHPEFYKD	C.
CRF05_DF_B	DREVLQWKFD	SSLALRHVAR	E.RHPEFYKD	..
CRF05_DF_B	DREVLQWKFD	SSLALKHVAR	E.RRPEFYKD	..
CRF06_cpx	EREVLWVKFD	SSLARRHIAR	E.KHPEFYKD	C.
CRF06_cpx	EGEVLWVKFD	SSLARRHIAR	E.LHPDFYKD	C.
CRF06_cpx	EREVLWVKFD	SSLARRHTAR	E.MHPEFYKD	C.
CRF06_cpx	EXEVLWVKFD	SSLARRHIAX	E.XHPEFXKD	C.
CRF11_cpx	EREVLWVKFD	SSLARKHIAR	E.LHPDFYKD	..
CRF11_cpx	DREVLWVKFD	SSLARRHIAR	E.LHPDFYKD	..
D_CD_84ZR0	EKEVLVWRFN	SRLAFEHKAK	E.KYPEFYKN	C.
D_CD_ELI	ERQVLKWRFN	SRLAFEHKAR	E.MHPEFYKN	..
D_CD_NDK	ERQVLWWRFN	SRLALEHKAR	E.LHPEFYKD	C.
D_UG_94UG1	EREVLVWRFN	SRLAFEHKAK	M.KHPEYYKD	C.
F1_BE_VI85	DREVLWVKFD	SSLALRHVAR	E.RHPEFYKD	..
F1_BR_93BR	DREVLWVKFD	SRLALRHVAR	E.RHPEFYKD	..
F1_FI_FIN9	DREVLWVKFD	SRLALKHVAR	E.RHPEFYKD	..
F1_FR_MP41	DREVLWVKFD	SRLAFRHVAR	E.KHPEFYQN	..
F2_CM_MP25	DREVLWVKFD	SRLALRHVAR	E.RHPEYYKD	..
F2KU_BE_VI	EREVLWVKFD	SRLALKHLAR	E.KHPEYYKD	C.
G_BE_DRCBL	DREVLVWRFD	SSLARRHLAR	E.LHPEYYKD	C.
G_NG_92NG0	DREVLVWRFN	SSLARRHLAR	E.LHPEYYKD	C.
G_SE_SE616	DREVLVWRFD	SSLARRHIAR	E.LHPEYYKD	C.
H_BE_VI991	EREVLWVKFD	SRLALRHVAR	E.LHPEFYKD	C.
H_BE_VI997	EGEVLWVKFD	SRLAFTHVAR	E.KHPEFYKD	C.
H_CF_90CF0	EREVLWVKFD	SRLALTHVAR	V.KHPEY.KD	C.
J_SE_SE702	EREVLWVKFD	SSLARRHIAR	E.LHPEFYKD	C.
J_SE_SE788	EREVLQWKFD	SSLARRHIAR	E.LHPEFYKD	C.
K_CD_EQTB1	HREVLWVKFD	SSLARKHVAR	E.MHPEYYKD	..
K_CM_MP535	HREILWVKFD	SSLARRHVAR	E.LHPDYYKD	..
N_CM_YBF30	HKEVLVWRFD	SSLARRHVAR	E.LHPEFYKN	C.
O_CM_ANT70	HKEILWVKFD	RSLGNTHVAR	ITHPELFQKD	..
O_CM_MVP51	HGEILWVKFD	RSLGLTHIAL	QKHPELFPSN	..
O_SN_MP129	HGQILWVKFD	RSLGSTHVAM	VTNPELFNKO	..
O_SN_MP130	HKEMLWVKFD	RSLGSTHVAM	ITHPELFQKD	..
U_CD_83C	EKEVLWVKFD	SSLARRHIAR	E.LHPEFYKD	C.

Table 14. HIV Pol Sequence Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: 00BW0762_1	Len: 1046	Check: 4376	Weight: 1.00
Name: 00BW0768_2	Len: 1046	Check: 8430	Weight: 1.00
Name: 00BW0874_2	Len: 1046	Check: 8925	Weight: 1.00
Name: 00BW1471_2	Len: 1046	Check: 1324	Weight: 1.00
Name: 00BW1616_2	Len: 1046	Check: 935	Weight: 1.00
Name: 00BW1686_8	Len: 1046	Check: 8131	Weight: 1.00
Name: 00BW1759_3	Len: 1046	Check: 579	Weight: 1.00
Name: 00BW1773_2	Len: 1046	Check: 1975	Weight: 1.00
Name: 00BW1783_5	Len: 1046	Check: 216	Weight: 1.00
Name: 00BW1795_6	Len: 1046	Check: 5932	Weight: 1.00
Name: 00BW1811_3	Len: 1046	Check: 6525	Weight: 1.00
Name: 00BW1859_5	Len: 1046	Check: 2879	Weight: 1.00
Name: 00BW1880_2	Len: 1046	Check: 7093	Weight: 1.00
Name: 00BW1921_1	Len: 1046	Check: 2524	Weight: 1.00
Name: 00BW2036_1	Len: 1046	Check: 8279	Weight: 1.00
Name: 00BW2063_6	Len: 1046	Check: 3935	Weight: 1.00
Name: 00BW2087_2	Len: 1046	Check: 7898	Weight: 1.00
Name: 00BW2127_2	Len: 1046	Check: 728	Weight: 1.00
Name: 00BW2128_3	Len: 1046	Check: 5356	Weight: 1.00
Name: 00BW2276_7	Len: 1046	Check: 9456	Weight: 1.00
Name: 00BW3819_3	Len: 1046	Check: 6369	Weight: 1.00
Name: 00BW3842_8	Len: 1046	Check: 4573	Weight: 1.00
Name: 00BW3871_3	Len: 1046	Check: 6948	Weight: 1.00
Name: 00BW3876_9	Len: 1046	Check: 6609	Weight: 1.00
Name: 00BW3886_8	Len: 1046	Check: 8244	Weight: 1.00
Name: 00BW3891_6	Len: 1046	Check: 5718	Weight: 1.00
Name: 00BW3970_2	Len: 1046	Check: 3940	Weight: 1.00
Name: 00BW5031_1	Len: 1046	Check: 2442	Weight: 1.00
Name: 96BW01B21	Len: 1046	Check: 2358	Weight: 1.00
Name: 96BW0407	Len: 1046	Check: 8537	Weight: 1.00
Name: 96BW0502	Len: 1046	Check: 3948	Weight: 1.00
Name: 96BW06_J4	Len: 1046	Check: 7173	Weight: 1.00
Name: 96BW11_06	Len: 1046	Check: 973	Weight: 1.00
Name: 96BW1210	Len: 1046	Check: 5817	Weight: 1.00
Name: 96BW15B03	Len: 1046	Check: 5157	Weight: 1.00
Name: 96BW16_26	Len: 1046	Check: 3303	Weight: 1.00
Name: 96BW17A09	Len: 1046	Check: 1256	Weight: 1.00
Name: 96BWMO1_5	Len: 1046	Check: 5593	Weight: 1.00
Name: 96BWMO3_2	Len: 1046	Check: 3661	Weight: 1.00
Name: 98BWMC12_2	Len: 1046	Check: 7159	Weight: 1.00
Name: 98BWMC13_4	Len: 1046	Check: 3254	Weight: 1.00
Name: 98BWMC14_a	Len: 1046	Check: 5638	Weight: 1.00
Name: 98BWMO14_1	Len: 1046	Check: 7680	Weight: 1.00
Name: 98BWMO18_d	Len: 1046	Check: 1619	Weight: 1.00
Name: 98BWMO36_a	Len: 1046	Check: 8852	Weight: 1.00
Name: 98BWMO37_d	Len: 1046	Check: 4750	Weight: 1.00
Name: 99BW3932_1	Len: 1046	Check: 5391	Weight: 1.00
Name: 99BW4642_4	Len: 1046	Check: 1514	Weight: 1.00
Name: 99BW4745_8	Len: 1046	Check: 52	Weight: 1.00
Name: 99BW4754_7	Len: 1046	Check: 4905	Weight: 1.00
Name: 99BWMC16_8	Len: 1046	Check: 1544	Weight: 1.00
Name: A2_CD_97CD	Len: 1046	Check: 9703	Weight: 1.00
Name: A2_CY_94CY	Len: 1046	Check: 3235	Weight: 1.00
Name: A2D_97KR	Len: 1046	Check: 3776	Weight: 1.00
Name: A2G_CD_97C	Len: 1046	Check: 2059	Weight: 1.00
Name: A_BY_97BL0	Len: 1046	Check: 2724	Weight: 1.00

Name: A_KE_Q23_A	Len: 1046	Check: 1835	Weight: 1.00
Name: A_SE_SE659	Len: 1046	Check: 647	Weight: 1.00
Name: A_SE_SE725	Len: 1046	Check: 263	Weight: 1.00
Name: A_SE_SE753	Len: 1046	Check: 2271	Weight: 1.00
Name: A_SE_SE853	Len: 1046	Check: 5036	Weight: 1.00
Name: A_SE_SE889	Len: 1046	Check: 8414	Weight: 1.00
Name: A_SE_UGSE8	Len: 1046	Check: 3268	Weight: 1.00
Name: A_UG_92UG0	Len: 1046	Check: 2007	Weight: 1.00
Name: A_UG_U455_	Len: 1046	Check: 2277	Weight: 1.00
Name: AC_IN_2130	Len: 1046	Check: 5353	Weight: 1.00
Name: AC_RW_92RW	Len: 1046	Check: 4695	Weight: 1.00
Name: AC_SE_SE94	Len: 1046	Check: 4206	Weight: 1.00
Name: ACD_SE_SE8	Len: 1046	Check: 7281	Weight: 1.00
Name: ACG_BE_VI1	Len: 1046	Check: 1400	Weight: 1.00
Name: AD_SE_SE69	Len: 1046	Check: 4640	Weight: 1.00
Name: AD_SE_SE71	Len: 1046	Check: 1057	Weight: 1.00
Name: ADHK_NO_97	Len: 1046	Check: 3502	Weight: 1.00
Name: ADK_CD_MAL	Len: 1046	Check: 2578	Weight: 1.00
Name: AG_BE_VI11	Len: 1046	Check: 8416	Weight: 1.00
Name: AG_NG_92NG	Len: 1046	Check: 9397	Weight: 1.00
Name: AGHU_GA_VI	Len: 1046	Check: 9562	Weight: 1.00
Name: AGU_CD_Z32	Len: 1046	Check: 8398	Weight: 1.00
Name: AJ_BW_BW21	Len: 1046	Check: 3451	Weight: 1.00
Name: B_AU_VH_AF	Len: 1046	Check: 2033	Weight: 1.00
Name: B_CN_RL42_	Len: 1046	Check: 1369	Weight: 1.00
Name: B_DE_D31_U	Len: 1046	Check: 4607	Weight: 1.00
Name: B_DE_HAN_U	Len: 1046	Check: 1771	Weight: 1.00
Name: B_FR_HXB2_	Len: 1046	Check: 4569	Weight: 1.00
Name: B_GA_OYI_	Len: 1046	Check: 3682	Weight: 1.00
Name: B_GB_CAM1_	Len: 1046	Check: 3161	Weight: 1.00
Name: B_GB_GB8_A	Len: 1046	Check: 6253	Weight: 1.00
Name: B_GB_MANC_	Len: 1046	Check: 7670	Weight: 1.00
Name: B_KR_WK_AF	Len: 1046	Check: 8737	Weight: 1.00
Name: B_NL_3202A	Len: 1046	Check: 2083	Weight: 1.00
Name: B_TW_TWCYS	Len: 1046	Check: 3056	Weight: 1.00
Name: B_US_BC_L0	Len: 1046	Check: 3160	Weight: 1.00
Name: B_US_DH123	Len: 1046	Check: 1102	Weight: 1.00
Name: B_US_JRCSF	Len: 1046	Check: 5571	Weight: 1.00
Name: B_US_MNCG_	Len: 1046	Check: 3988	Weight: 1.00
Name: B_US_P896_	Len: 1046	Check: 2465	Weight: 1.00
Name: B_US_RF_M1	Len: 1046	Check: 3672	Weight: 1.00
Name: B_US_SF2_K	Len: 1046	Check: 1754	Weight: 1.00
Name: B_US_WEAU1	Len: 1046	Check: 2993	Weight: 1.00
Name: B_US_WR27_	Len: 1046	Check: 4098	Weight: 1.00
Name: B_US_YU2_M	Len: 1046	Check: 5564	Weight: 1.00
Name: BF1_BR_93B	Len: 1046	Check: 4182	Weight: 1.00
Name: C_BR_92BR0	Len: 1046	Check: 5481	Weight: 1.00
Name: C_BW_96BW0	Len: 1046	Check: 6833	Weight: 1.00
Name: C_BW_96BW1	Len: 1046	Check: 2166	Weight: 1.00
Name: C_BW_96BW1	Len: 1046	Check: 5817	Weight: 1.00
Name: C_BW_96BW1	Len: 1046	Check: 5157	Weight: 1.00
Name: C_ET_ETH22	Len: 1046	Check: 3509	Weight: 1.00
Name: C_IN_93IN1	Len: 1046	Check: 5471	Weight: 1.00
Name: C_IN_93IN9	Len: 1046	Check: 4102	Weight: 1.00
Name: C_IN_93IN9	Len: 1046	Check: 3150	Weight: 1.00
Name: C_IN_94IN1	Len: 1046	Check: 5157	Weight: 1.00
Name: C_IN_95IN2	Len: 1046	Check: 4641	Weight: 1.00
Name: CRF01_AE_C	Len: 1046	Check: 87	Weight: 1.00
Name: CRF01_AE_C	Len: 1046	Check: 3758	Weight: 1.00
Name: CRF01_AE_C	Len: 1046	Check: 2775	Weight: 1.00

Name: CRF01_AE_T	Len: 1046	Check: 1864	Weight: 1.00
Name: CRF01_AE_T	Len: 1046	Check: 7414	Weight: 1.00
Name: CRF01_AE_T	Len: 1046	Check: 7837	Weight: 1.00
Name: CRF01_AE_T	Len: 1046	Check: 3529	Weight: 1.00
Name: CRF01_AE_T	Len: 1046	Check: 7503	Weight: 1.00
Name: CRF01_AE_T	Len: 1046	Check: 5730	Weight: 1.00
Name: CRF02_AG_F	Len: 1046	Check: 9432	Weight: 1.00
Name: CRF02_AG_F	Len: 1046	Check: 2064	Weight: 1.00
Name: CRF02_AG_G	Len: 1046	Check: 9849	Weight: 1.00
Name: CRF02_AG_N	Len: 1046	Check: 1793	Weight: 1.00
Name: CRF02_AG_S	Len: 1046	Check: 4817	Weight: 1.00
Name: CRF02_AG_S	Len: 1046	Check: 1764	Weight: 1.00
Name: CRF03_AB_R	Len: 1046	Check: 1695	Weight: 1.00
Name: CRF03_AB_R	Len: 1046	Check: 1425	Weight: 1.00
Name: CRF04_cpx_	Len: 1046	Check: 8496	Weight: 1.00
Name: CRF04_cpx_	Len: 1046	Check: 2074	Weight: 1.00
Name: CRF04_cpx_	Len: 1046	Check: 9245	Weight: 1.00
Name: CRF05_DF_B	Len: 1046	Check: 62	Weight: 1.00
Name: CRF05_DF_B	Len: 1046	Check: 3427	Weight: 1.00
Name: CRF06_cpx_	Len: 1046	Check: 142	Weight: 1.00
Name: CRF06_cpx_	Len: 1046	Check: 6688	Weight: 1.00
Name: CRF06_cpx_	Len: 1046	Check: 8524	Weight: 1.00
Name: CRF06_cpx_	Len: 1046	Check: 4725	Weight: 1.00
Name: CRF11_cpx_	Len: 1046	Check: 2194	Weight: 1.00
Name: CRF11_cpx_	Len: 1046	Check: 8466	Weight: 1.00
Name: D_CD_84ZR0	Len: 1046	Check: 515	Weight: 1.00
Name: D_CD_ELI_K	Len: 1046	Check: 2096	Weight: 1.00
Name: D_CD_NDK_M	Len: 1046	Check: 3376	Weight: 1.00
Name: D_UG_94UG1	Len: 1046	Check: 3505	Weight: 1.00
Name: F1_BE_VI85	Len: 1046	Check: 3993	Weight: 1.00
Name: F1_BR_93BR	Len: 1046	Check: 2251	Weight: 1.00
Name: F1_FI_FIN9	Len: 1046	Check: 9772	Weight: 1.00
Name: F1_FR_MP41	Len: 1046	Check: 1447	Weight: 1.00
Name: F2_CM_MP25	Len: 1046	Check: 2842	Weight: 1.00
Name: F2KU_BE_VI	Len: 1046	Check: 5026	Weight: 1.00
Name: G_BE_DRCBL	Len: 1046	Check: 5377	Weight: 1.00
Name: G_NG_92NG0	Len: 1046	Check: 6000	Weight: 1.00
Name: G_SE_SE616	Len: 1046	Check: 7901	Weight: 1.00
Name: H_BE_VI991	Len: 1046	Check: 9107	Weight: 1.00
Name: H_BE_VI997	Len: 1046	Check: 5776	Weight: 1.00
Name: H_CF_90CF0	Len: 1046	Check: 9201	Weight: 1.00
Name: J_SE_SE702	Len: 1046	Check: 9700	Weight: 1.00
Name: J_SE_SE788	Len: 1046	Check: 8817	Weight: 1.00
Name: K_CD_EQTB1	Len: 1046	Check: 3723	Weight: 1.00
Name: K_CM_MP535	Len: 1046	Check: 3729	Weight: 1.00
Name: N_CM_YBF30	Len: 1046	Check: 3336	Weight: 1.00
Name: O_CM_ANT70	Len: 1046	Check: 9461	Weight: 1.00
Name: O_CM_MVP51	Len: 1046	Check: 2986	Weight: 1.00
Name: O_SN_99SE_	Len: 1046	Check: 377	Weight: 1.00
Name: O_SN_99SE_	Len: 1046	Check: 9312	Weight: 1.00
Name: U_CD_83C	Len: 1046	Check: 1358	Weight: 1.00

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1		50
00BW0762_1	FFRENLAFFQ G.EAREFPPE QT.....RANSPT SR.....E
00BW0768_2	FFRENLAFFQ .GEAGEFPPEQTRANSTT SR.....K
00BW0874_2	FFRENLAFFQ G.EAREFPPE QA.....RAISPT SR.....E
00BW1471_2	FFRENLAFFQ G.EARELPSE Q.....	...ARASPT SR.....E
00BW1616_2	FFRENLAFFQ G.KAGEFPPE QTRANSP...	..SSTSANSPT SR.....E

00BW1686_8	FFRENLAFPQ	G.EAREFPSE	Q.....	...ARAIPT	SR.....E
00BW1759_3	FFRENLAFPQ	.GEAREFPSEQTRANSPT	TR.....E
00BW1773_2	FFRENLAFPQ	G.EAREFPSE	QTRAN.....SPT	SR.....E
00BW1783_5	FFRENLAFFE	GGEAREFPSE	QTSRE.....	..QTRANSPT	SR.....E
00BW1795_6	FFRENLAFPQ	G.EAREFPSE	QT.....RANSPT	SR.....E
00BW1811_3	FFRENLAFPQ	G.EAREFPSE	QARANSPTANSPT	SR.....E
00BW1859_5	FFRENLAFPQ	G.KAREFSPE	QA.....RANSPT	SR.....E
00BW1880_2	FFRENLAFPQ	G.EAREFPPE	QT.....RADSPT	SR.....E
00BW1921_1	FFRENLAFPQ	G.EAREFPSE	Q.....ARANSST	SR.....E
00BW2036_1	FFRENLAFFQ	G.KAREFPSE	QNSP.....	..TTRANSPT	SR.....E
00BW2063_6	FFRENLAFPQ	G.EAREFPSE	QT.....RANSPT	SR.....K
00BW2087_2	FFRENLAFPQ	GGEAREFPSEQTRANSPT	SR.....A
00BW2127_2	FFGENLAFPQ	G.EAREFPPE	QARTNSP...	..QAGAIPT	SR.....E
00BW2128_3	FFRENLAFFQ	.GEAREFPSE	QTRTNSPTSR	..EQTRANSPT	SG.....E
00BW2276_7	FFRETLAQQ	G.KARELPSE	QDRANSPTANSPT	GR.....Q
00BW3819_3	FFRENLAFPQ	G.EAREFPK	QARTNSP...NSPT	SR.....E
00BW3842_8	FFREDLAFPR	R.KAREFPSE	QNRAN.....	..SPTRANSPT	SR.....E
00BW3871_3	FFRENLAFPQ	G.EAREFPSE	Q.....TRANSPT	SR.....K
00BW3876_9	FFRENLAFPQ	G.KAREFPSK	QA.....RANSPT	GR.....E
00BW3886_8	FFRENLAFPQ	G.EAREFPSE	QTRANSPT..SRANSPT	SR.....E
00BW3891_6	FFRENLAFPQ	G.EAREFSSEQ....ARANSPT	SR.....E
00BW3970_2	FFREILAFPE	G.EAREFPSE	Q.....IRANSPT	SR.....E
00BW5031_1	FFRENLAFFQ	G.EARELPPE	Q...TRTNS.	..PTNANSPT	SR.....E
96BW01B21	FFRENLAFPQ	G.KAREFPSE	Q.....TR.AISPT	SR.....E
96BW0407	FFRENLAFPQ	G.EAREFPSE	Q.....TRANSPT	SR.....E
96BW0502	FFRENLAFPQ	G.EAREFPPE	QIRASSPNS.TNSPT	SR.....E
96BW06_J4	FFRENLAFPQ	RGEAREFPSEQARANSPT	SR.....E
96BW11_06	FFRENLAFPQ	G.EAREFPSEQTGANSPT	SR.....E
96BW1210	FFRENLAFPQ	G.EAREFPSE	QTRAIS.....PT	SR.....E
96BW15B03	FFREDLAFQ	G.KAREFPSE	QN.....RANSPT	SR.....E
96BW16_26	FFRENLAFPQ	.GEAREFPSEQTRANSPT	SG.....E
96BW17A09	FFRENLAFPQ	GGEAREFPSE	Q.....ARANSPT	SR.....E
96BWM01_5	FFRENLAFPQ	G.EAREFPSE	QT.....RANSPT	SR.....N
96BWM03_2	FFRENLAFPQ	G.EAREFPPE	QT.....RANSPT	SR.....A
98BWM012_2	FFRETLAFPQ	G.EAREFSSE	QG.....RANSPT	SR.....E
98BWM013_4	FFRENLAFPQ	G.EAREFPSE	QT.....RANSPT	SR.....K
98BWM014_a	FFRENLAFPQ	G.EARELPSE	Q.....TRTISPT	SR.....E
98BWM014_1	FFRENLAFPQ	RGEAREFPSEKTRANSPT	SR.....E
98BWM018_d	FFRENLAFPQ	G.EAGKFHSE	QTSANSPT...	..TSRANSPT	SR.....E
98BWM036_a	FFRENLAFPQ	G.EAREFPPE	QTRANSPT...	..TSRANSPT	GR.....E
98BWM037_d	FFRENLAFPQ	G.EAREFPSE	K.....TRANSPT	GR.....E
99BW3932_1	FFRENLAFFQ	G.EAREFPPE	QDSANSPTSR	ELQDRANSPT	SR.....E
99BW4642_4	FFRENLAFPQ	G.EAREFLPE	QD.....RANSPT	SR.....E
99BW4745_8	FFRENLAFFQ	G.EAREFPSE	QTRANSPT...TRANSPT	SR.....E
99BW4754_7	FFRKNLAFFQ	G.EAREFPSE	QT.....RANSPT	SR.....E
99BWM016_8	FFREDLAFQ	R.EAREFPSE	Q TRANS...	..PTRANSPT	SR.....E
A2_CD_97CD	FFRENLAFFQ	R.EAREFSSEQDRANSPT	N.....
A2_CY_94CY	FFRENLAFFQ	R.EARKFSSEQNRANSPT	SR.....E
A2D_97KR	FFRENLAFPQ	R.EAREFSSEQNRTNSPT	SR.....G
A2G_CD_97C	FFRENLAFFQ	R.EAREFS..	SEQDRANSPT	RR.....E
A_BY_97BL0	FFRKNLAFFQ	R.EARKFSSEQTRAISPT	S.....RK
A_KE_Q23_A	FFRENLAFFQ	G.EAREFSSEQTGTNSST	S.....RD
A_SE_SE659	FFRENLAFFQ	R.EARKFSSEQTRANSPT	S.....RD
A_SE_SE725	FFRENVAFFQ	G.EARKFSSEQTGANSPT	S.....RA
A_SE_SE753	FFRENLAFFQ	G.EAGKFSSEQTGANSPT	S.....RD
A_SE_SE853	FFRENLAFFQ	R.EARKFSSEQTRANSPT	S.....RD
A_SE_SE889	FFRENLAFFQ	G.EARKFSSEQTGANSPT	S.....RD
A_SE_UGSE8	FFRENLAFPQ	G.EAGKFSSEQTGAISPT	S.....RD
A_UG_92UG0	FFRENLAFFQ	R.EARKFSSEQTRTNSPT	SS.....RD
A_UG_U455_	FFRENLAFFQ	G.EAREFSSEQTRANSPT	SR.....N.

AC_IN_2130	FFRENLAFPQ	G.EAREFPSEQTRANSPA	SR.....E
AC_RW_92RW	FFRENLAFPQ	G.EARKFSPE	Q.....	..TGANSPT	SR.....E
AC_SE_SE94	FFRENLAFPQ	G.EARKFSSEQTGANSPT	S.....RD
ACD_SE_SE8	FFREDMAFPQ	G.KAREFPSEQTRTNSPT	S.....RE
ACG_BE_VI1	FFRENLAFPQ	G.EARKFSSEQTRANSPT	SRANSPTSRE
AD_SE_SE69	FFRENLAFPQ	G.KAREFPSEQTRANSPS	SR.....E
AD_SE_SE71	FSRENLAFPQ	G.EARKFSSEQTGTNSST	SR.....N.
ADHK_NO_97	FFRENLAFPQ	R.KARELSSEQTGAISPT	SR.....E
ADK_CD_MAL	FFRENLAFPQ	G.KAREFPSEQTRANSPT	SR.....E
AG_BE_VI11	FFRENLAFPQ	G.EARKFSSEQTGANSPT	S.....RE
AG_NG_92NG	FFRENLAFPQ	G.EAREFS..	SEQARANSPT	RR.....E
AGHU_GA_VI	FFRENLAFPQ	G.EAREFS..	PEQTRANSPT	SR.....E
AGU_CD_232	FFRENLAFPQ	G.EAREFSSEQTRANSPT	RR.....E
AJ_BW_BW21	FFRENLAFPQ	G.KAREFSPEQTRANSPT	SR.....E
B_AU_VH_AF	FFREDLALPQ	G.KARELSSEQTRANSPT	RR.....E
B_CN_RL42	FFREDLAFPQ	G.KARELSSEQTRANSPT	RG.....E
B_DE_D31_U	FFREDLAFLQ	G.KAREFSSAQTRANSPT	RR.....E
B_DE_HAN_U	FFREDLAFPQ	G.EARKFSSEQTRANSPT	RR.....E
B_FR_HXB2	FFREDLAFLQ	G.KAREFSSEQTRANSPT	RR.....E
B_GA_OYI	FFREDLAFPQ	G.KAREFSSEQTRANSPT	SR.....E
B_GB_CAM1	FFRENLAFPQ	G.EAREFSSEQTRANSPT	RR.....E
B_GB_GB8_A	FFREDLAFPQ	G.KAREFSPE	QTRANS....	..PTRADSPT	RR.....E
B_GB_MANC	FFREDLALPQ	G.KAREFSSEQTRANSPT	RG.....E
B_KR_WK_AF	FFREDLAFPQ	G.KAREFPSEQTRAI SPA	RR.....E
B_NL_3202A	FFREDLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
B_TW_TWCYS	FFRENLAFPQ	G.KARKFSSEQTRANSPT	RG.....E
B_US_BC_L0	FFREDLAFPQ	G.KAREFSSEQTRANSST	RR.....E
B_US_DH123	FFRENLAFPQ	G.KAREFSSEQTRAI SPT	RR.....E
B_US_JRCSE	FFREDLAFLQ	G.KAREFPSEQTRANSPT	RR.....E
B_US_MNCG	FFREDLAFLQ	G.KAEFS.SEQNRANSPT	RR.....E
B_US_P896	FFRENLAFPQ	G.KAREFSSEQTRANSPT	RR.....E
B_US_RF_M1	FFRENLAFPQ	G.KARELSSEQTRANSPT	RR.....E
B_US_SF2_K	FFREDLAFLQ	G.KAREFSSEQTRANSPT	RR.....E
B_US_WEAU1	FFREDLVFPK	G.KAREFSSEQTRTNSPT	RR.....E
B_US_WR27	FFREXPAPPH	X.KARXFPSEQTRAI SPT	SR.....E
B_US_YU2_M	FFREDLAFPQ	G.KARKFSSEQTRANSPI	RR.....E
BF1_BR_93B	FFRENLAFPQ	G.KAREFPSEQTRANSPT	SR.....E
C_BR_92BR0	FFRENLAFPQ	.GEARKSSSEQNRANSPT	RR.....E
C_BW_96BW0	FFRENLAFPQ	G.EAREFPSE	Q.....	..TRANSPT	SR.....E
C_BW_96BW1	FFRENLAFPQ	G.EAREFPSEQTGANSPT	SR.....K
C_BW_96BW1	FFRENLAFPQ	G.EAREFPSE	QTRAI S....PT	SR.....E
C_BW_96BW1	FFREDLAFPQ	G.KAREFPSE	QN.....	..RANSPT	SR.....E
C_ET_ETH22	FFRETLAFPQ	G.KAREFPSE	QTRANSPTRE	S.QTRANSPT	TR.....E
C_IN_93IN1	FFRENLAFPQ	G.EAREFPPEQTGANSPT	SR.....E
C_IN_93IN9	FFRENLAFPQ	G.EAREFPPEQTRADSPT	SR.....E
C_IN_93IN9	FFRENLAFPQ	G.EAREFPSE	QTRANSPSS.	..QTRANSPS	SR.....E
C_IN_94IN1	FFRENLAFPQ	G.EAREFPPEQTRANSPT	SR.....E
C_IN_95IN2	FFRENLAFPQ	G.EAREFPPEETRANSST	SR.....E
CRF01_AE_C	FFRENLA SQ	G.EAREFSSEQTRANSPT	SR.....E
CRF01_AE_C	FFRENLAFPQ	G.EARKFPSEQTRANSPT	NG.....E
CRF01_AE_C	FFRENLAFPQ	G.EAREFSSEQTRANSPT	SR.....E
CRF01_AE_T	FFREILAFQ	G.KAGKFSSEQTRANSPA	SR.....K
CRF01_AE_T	FFRENLAFPQ	R.KAGEFSSEQTRANSPT	SR.....
CRF01_AE_T	FFRENLAFPQ	G.KAREFSSEQTGANSSA	SR.....K
CRF01_AE_T	FFRENLAFPQ	G.KAGKFSSEQTRANSPT	SR.....E
CRF01_AE_T	FFRENLAFPQ	G.KAGEFSSEQTRANSPT	SR.....K
CRF01_AE_T	FFRENLAFPQ	G.KAGKFSSEQTRTNSPT	SR.....K
CRF02_AG_F	FFRENLAFPQ	G.EARKFPSSKQTGTNSPT	S.....RE
CRF02_AG_F	FFRENLAFPQ	G.EARKFPSSKQTGTNSPT	S.....RE
CRF02_AG_G	FFRENLAFPQ	R.EARELSSEQTGAISPT	G.....RE

CRF02_AG_N	FFRENLAFAQ	G.EARKFSSE	..QTGTNSST	S.....RE
CRF02_AG_S	FFRENLAFAQ	G.EARKFSSE	..QTGTNSPA	S.....RE
CRF02_AG_S	FFRENLAFAQ	G.EARKLSSE	..QTGTNSPT	S.....RE
CRF03_AB_R	FFRENLAFAQ	R.EARKFSSE	..QTRAIPT	S.....RK
CRF03_AB_R	FFRENLAFAQ	R.EARKFSSE	..QTRAIPT	S.....RK
CRF04_cpx	FFRENVAFAQ	R.EARKFSSE	..QARANSPT	RG.....M
CRF04_cpx	FFRENVAFAQ	R.KAGEFSSE	..QARANSPT	RR.....E
CRF04_cpx	FFRENVAFAQ	G.EARKFSSE	..QDRANSPT	RR.....E
CRF05_DF_B	FFRESLAFAQ	G.EARELPPE	..QTGALSPA	SR.....E
CRF05_DF_B	FFRESLAFAQ	G.KAREFPPE	..QARTLSPT	SR.....E
CRF06_cpx	FFRENLAFAQ	G.EAREFS..	..SEQARANSPT	HR.....E
CRF06_cpx	FFREDLAFAQ	G.EARKFS..	..SEQARANSPT	RG.....E
CRF06_cpx	FFRENLAFAQ	G.EAGELS..	..SEQARANSPT	RR.....E
CRF06_cpx	FFRENLAFAQ	G.EAREFSPE	..TEQARTLSPT	CR.....E
CRF11_cpx	FFRENLAFAQ	R.KARELSPE	..QTRANSPT	SR.....E
CRF11_cpx	FFRENLAFAQ	G.EAREFPTE	..QARANSPT	SR.....E
D_CD_84ZR0	FFRENLAFAQ	G.KAGELSSSE	..QTRANSPT	S.....R
D_CD_ELI_K	FFRENLAFAQ	G.KAGELSPK	..QTRANSPT	SR.....E
D_CD_NDK_M	FFREDLAFAQ	G.KAGEFSSE	..QTRANSPT	SR.....E
D_UG_94UG1	FFRENLAFAQ	W.KAREFPSE	..QTRANSPT	SR.....D
F1_BE_VI85	FFRENLAFAQ	G.EARKFPSE	..QTRANSPT	SR.....E
F1_BR_93BR	FFRENLAFAQ	G.EARKLHPE	..QARAVSPA	SR.....E
F1_FI_FIN9	FFRENLAFAQ	G.EARKFPS.	..ETRANSPA	SR.....E
F1_FR_MP41	FFRENLAFAQ	G.EARKFSSE	..QARANSPT	SG.....E
F2_CM_MP25	FFRENVAFAQ	G.EARKFSSE	..QTRANSPT	SR.....E
F2KU_BE_VI	FFRENLAFAQ	R.EAGKFSSE	..QTRANSPT	SR.....E
G_BE_DRCBL	FFRENLAFAQ	G.EAREFP..	..SEQARANSPT	RR.....E
G_NG_92NG0	FFRENLAFAQ	G.EARKLS..	..PEQDRANSPT	SR.....E
G_SE_SE616	FFRENLAFAQ	G.EAREFS..	..SEQDRTNSPT	CR.....K
H_BE_VI991	FFRENLAFAQ	G.KAREFP..	..PEEARANSPT	SR.....E
H_BE_VI997	FFRENLAFAQ	R.EARKFS..	..PEQARANSPT	SR.....E
H_CF_90CF0	FFRENLAFAQ	R.EARKFS..	..PEQARTNSPT	SR.....E
J_SE_SE702	FFREDLAFAQ	R.EAREFSPE	..QTRANSPT	SR.....E
J_SE_SE788	FFREDLAFAQ	R.EARELSPE	..QTRANSPT	SR.....E
K_CD_EQTB1	FFREVLASQQ	R.EARKFSSE	..QTRANSPT	SR.....E
K_CM_MP535	FFRENLAFAQ	G.EAREFSSE	..QTRANSPT	SR.....E
N_CM_YBF30	FFREELVSLQ	R.ETRKLPPD	..NN.....	..KERAHSPA
O_CM_ANT70	FFRQILASGG	H.EARQLCAE	T.....	..STPISPT
O_CM_MVP51	FFREVLASGG	H.EARQLCAE	T.....	..SVPIST
O_SN_99SE	FFREILASGG	H.EARQLCAE	T.....	..SVPIST
O_SN_99SE	FFREILASGG	H.EARQLCTE	T.....	..SVPIST
U_CD_83C	FFRENLAFAQ	G.EAREFSSE	..QTRANSPT	SR.....E

	51		100
00BW0762_1	LQVR.....GDK.	PHSEAG AERQ..... GTLNFPQITL
00BW0768_2	LQVRG.....DNN.	PCSEAG AERQ..... GTLNCPQITL
00BW0874_2	PQARAIPTS	REPQVRRDN.	SRFEAG VEREG..... .TLNFPQITL
00BW1471_2	LQVR.....GDN.	PRSEAG AERQ..... .TLNLPQITL
00BW1616_2	LQVR.....GNN.	PLSEAG GERQ..... GTLNFPQITL
00BW1686_8	LQVR.....GDN.	PRSEAG AERQ..... GTLNLPQITL
00BW1759_3	LQVRG.....NN.	PRSEAG AERQ..... GNLNFPQITL
00BW1773_2	LQVR.....GDN.	PRSEAG AERQ..... GTLNFPQITL
00BW1783_5	LQVR.....GDN.	PCSEAG DERQ..... GTFNFPQITL
00BW1795_6	LQVR.....GDN.	PLSEAG AERQ..... GTLNFPQITL
00BW1811_3	LQVR.....GDN.	PRFEAC EKRQG..... .NLNFPQITL
00BW1859_5	LQVR.....GDD.	PRSEAG AERQ..... GTLNFPQITL
00BW1880_2	LQVR.....GDN.	PRSEAG AEGQ..... GTLNFPQITL
00BW1921_1	LQVR.....GDN.	PCSEAG AERQ..... .TLNFPQITL
00BW2036_1	LQVR.....GDN.	PRSEAG AERQ..... GTLNFPQITL
00BW2063_6	L...R.....GDN.	PCSEAG DERQ..... GTLNFPQITP

00BW2087_2	NSPTSREL..	...QVRGDN.PSIKAG	PERQ.....	GALNFPQITL
00BW2127_2	LQVR.....GDN.PRSEAG	AERQG.....	.SLNFPQITL
00BW2128_3	LQVR.....GDN.TRSEAG	AKKQ.....	GTLNFPQITL
00BW2276_7	LQVR.....GDN.PRAEAG	AERQG.....	.TLNFPQITL
00BW3819_3	LQVR.....GDN.PRSEAG	DERQG.....	.ALNFPQITL
00BW3842_8	LQVR.....GDN.PRSEAG	AERQGT..LQ	GTLNFPQITL
00BW3871_3	LQVR.....GDN.PRSEAG	ADRQ.....	GTLNFPQITL
00BW3876_9	LQVR.....GDN.PHSEAG	AERQ.....	GTLNFPQITL
00BW3886_8	LQVR.....GDN.PRSEAG	AERQG.....	.SLNFPQITL
00BW3891_6	LQVR.....GDN.PRSEAG	AERQG.....	.TLNFPQITL
00BW3970_2	LQVR.....GDN.PRSETG	AEGQG.....	.TFNFPQITL
00BW5031_1	LQVR.....GDN.PRSEAG	DEREG.....	.TLNFPQITL
96BW01B21	LQVR.....GDN.PRSEAG	AEGQG.....	.ALNLPQITL
96BW0407	LQVR.....GDN.PRSETR	VEGQG.....	.NFNFPQITL
96BW0502	LQVR.....GDN.PRSEAG	AEGQGT..LQ	GTLNCPQITL
96BW06_J4	LQIR.....GDN.PRFEAG	TKRQ.....	GTLNFPQITL
96BW11_06	LRG.....NN.PCSEAG	DERQ.....	GTLNFPQITL
96BW1210	LQVR.....GDN.PCSEAG	AEGQG.....	TTFSFPQITL
96BW15B03	LQVR.....GDN.PRSEAG	AERQ.....	GTLNFPQITL
96BW16_26	LQVW.....GDN.PRSETG	AKGQ.....	GTFNFPQITL
96BW17A09	LQVR.....GDN.PRSEAG	AERQG.....	.TLNFPQITL
96BWM01_5	L..R.....GDN.PCSEAG	DERQGT..LQ	GALNFPQITL
96BWM03_2	LQAR.....TNSP.TSREAG	VEGQG.....	.TLNFPQITL
98BWM012_2	P.....	...QARGDN.TRFEAG	DEGQG.....	.TLNFPQITL
98BWM013_4	P..R.....GDN.PCSEAG	AERQ.....	GTLNLPQITL
98BWM014_a	LQVR.....GDN.PRSEAG	AEGQ.....	GTLNFPQITL
98BWM014_1	LQVREQTR..	...ANSSTS.RELQAG	AKRQ.....	GALNCPQITL
98BWM018_d	LQVR.....GDN.PCSEAG	AERQGS....	.TLNFPQITL
98BWM036_a	LQVR.....GDK.PRSEAG	AEGQG.....	.TLNFPQITL
98BWM037_d	LQVR.....GDN.PRSEAG	GERQG.....	.TLKFPQITL
99BW3932_1	FQVR.....GDN.PCSEAG	AERQG.....	.SLNFPQITL
99BW4642_4	LQIR.....GDD.PRSEAG	AERQ.....	RTLNFPQITL
99BW4745_8	LQVR.....GGN.PHSEAG	AERQG.....	.TLNFPQITL
99BW4754_7	LQVR.....GDN.PHSEAR	VKGQ.....	GTPNFPQITL
99BWM016_8	LQVR.....GDK.SRSEAG	VEKQG.....	.NLNFPQITL
A2_CD_97CD	...GGR....DN.LLAEAG	E..QG...AV	HPCNFPQITL
A2_CY_94CY	LENGGR....DN.LLPEAG	TGDQG...TI	QSCNFPQITL
A2D_97KR	LWNGGG....DN.PLAEAG	AEKQG...TT	HSCNFPQITL
A2G_CD_97C	PRVRR....GDS.LLPEAG	DEG...KGAV	YPCNFPQITL
A_BY_97BL0	LD.GGR....DN.PLPETG	TERQG...TV	SSFNFPQITL
A_KE_Q23_A	LWDGGR....DS.LPSEAG	AERQGT..G.	PTLSFPQITL
A_SE_SE659	PWDRRR....DS.LPSETG	ADP.....	.TFNFPQITL
A_SE_SE725	FWDGGR....DS.LPSEAG	AERQGT..E.	LTFSFPQITL
A_SE_SE753	LWNEGR....DS.LPSEAG	AEG..T..R.	PTFSFPQITL
A_SE_SE853	LWDGGS....DN.LPSEAG	AERQGT..G.	PTLSFPQITL
A_SE_SE889	LWDGGR....DN.LPSEAG	EERQGV..GG	TTLNFPQITF
A_SE_UGSE8	..DGGR....DS.LPSEAG	AKQP.....	.TFNFPQITL
A_UG_92UG0	LWDEGR....DS.LPSEAG	AERQGP..E.	PTFSFPQITL
A_UG_U455_	LWDGK....DD.LPCETG	AERQ...GT	DSFSFPQITL
AC_IN_2130	LQIR.....GDN.PRTEAG	AKRQG.....	.TLNFPQITL
AC_RW_92RW	LWNGG....RDS.LSSETG	AERQG.....	.TFNFPQITL
AC_SE_SE94	LRDGGGR....D..NSEAG	TDRQGT..G.	PAFSFPQITL
ACD_SE_SE8	LRVWRR....DN.PLPEAG	AERQ....GT	VSFSLPQITL
ACG_BE_VI1	LWEGGR....DR.LLPEAG	TEGQG...TI	SSFNFPQITL
AD_SE_SE69	LRVWRG....DS.TFSETG	AER...QGA	VSFSFPQITL
AD_SE_SE71	LWDGGR....DS.LPSEAG	AEKQG...TG	STLNFPQITL
ADHK_NO_97	LWDRGR....DN..LLSEAG	TEGQG...TA	PSLSFPQITL
ADK_CD_MAL	LRVWGG....DK..TLSETG	AERQ...GI	VSFSFPQITL
AG_BE_VI11	LGDGGR....DN.PLSEAG	TECHC...TI	SSLNFPQITL
AG_NG_92NG	LRVRR....GDS.PFPEAG	AEG...KGIT	SIN.LPQITL

AGHU_GA_VI	LRVRR.....	GDS.	PLPEAG	AKG....	KGA	VSFNLPQITL
AGU_CD_Z32	LRDER.....	GDN.	LLSEAG	TEGQG...	TI	PSFSFPQITL
AJ_BW_BW21	LRVWR.....	GDS.	PLPEAG	GEGQ....	GT	VSFNFPQITL
B_AU_VH_AF	LQVWGR.....	DNN.	SLSEAG	ADR....	QGT	VSFNFPQITL
B_CN_RL42	LQVWGR.....	DNN.	SISEAG	ADR....	QGT	ISFSFPQITL
B_DE_D31_U	LQVWGR.....	DSN.	SLSEAG	ADR....	QGT	VSFNFPQITL
B_DE_HAN_U	LQVWG.....	SNS.	SLSEAG	ADR....	QGT	VSLSLPQITL
B_FR_HXB2	LQVWGR.....	DNN.	SPSEAG	ADR....	QGT	VSFNFPQVTL
B_GA_OYI	LRVWGR.....	DNN.	SPSEAG	ADR....	QGT	VSFNLPQITL
B_GB_CAM1	LQVWGR.....	ENN.	SLSEAG	ADR....	QGT	VSFNFPQITL
B_GB_GB8_A	LQVRGR.....	DNN.	SLTETG	ADK....	QGT	VSFNFPQITL
B_GB_MANC	LQVWGR.....	DNN.	SCSEAG	TDR....	QGT	VSLSFPQTTL
B_KR_WK_AF	LQVWGR.....	DNN.	SLSEAG	ANR....	QGT	VSFNFPQITL
B_NL_3202A	LQVWGR.....	DNN.	SLSEAG	AEG....	QGT	VSLSLPQITL
B_TW_TWCYS	LQVWGT.....	DNN.	SLSEAG	ADR....	QGP	VSFNFPQITL
B_US_BC_L0	LQVWGG.....	DNN.	SPSEAG	AGR....	QGN	VSLSFPQITL
B_US_DH123	LQVWGG.....	DSN.	SLSEAG	AEG.....	T	ISLSLPQITL
B_US_JRCFS	LQVWGR.....	DSN.	SLSEAG	AEAGADRQGI		VSFNFPQITL
B_US_MNCG	LQVWGR.....	DNN.	SLSEAG	EEAGDDRQGP		VSFNFPQITL
B_US_P896	LQVWGG.....	DNN.	SLSEAG	ADR....	QGT	VSLSFPQITL
B_US_RF_M1	LQVWGR.....	DN.	SLSEAG	EDR....	QGT	VSFNFPQITL
B_US_SF2_K	LQVWGG.....	ENN.	SLSEAG	ADR....	QGT	VSFNFPQITL
B_US_WEAU1	LQVQGR.....	DNN.	SLSEAG	ANR....	QGA	VSFNFPQITL
B_US_WR27	LQVWXR.....	DNN.	SLSEAG	TDR....	QGT	VSFNFPQITL
B_US_YU2_M	RQVWRR.....	DNN.	SLSEAG	ADR....	QGT	VSFNFPQITL
BF1_BR_93B	LQVWGR.....	GNN.	SLSETG	ADR....	QGD	VSGFGPQITL
C_BR_92BR0	LQVWGR.....	DNN.	SLSEAG	DDRQG....		TALNFPQITL
C_BW_96BW0	LQVR.....	GDN.	PRSETR	AEGQG....		TLNFPQITL
C_BW_96BW1	LRG.....	NN.	PCSEAG	DERQ....		GTLNFPQITL
C_BW_96BW1	LQVR.....	GDN.	PCSEAG	AEGQG....		TTFNFPQITL
C_BW_96BW1	LQVR.....	GDN.	PRSEAG	AERQ....		GTLNFPQITL
C_ET_ETH22	LQVR.....	GSN.	TFSEAG	AERQG....		SLNFPQITL
C_IN_93IN1	LQVR.....	GDN.	PSSKAG	AERQG....		TLNFPQITL
C_IN_93IN9	LQVR.....	GDT.	PSSKAG	AERQG....		TLNFPQITL
C_IN_93IN9	LQVR.....	GDN.	PRSEAG	AKRQG....		TLNFPQITL
C_IN_94IN1	LQVR.....	GDT.	PSSKAG	AEREG....		TLNFPQITL
C_IN_95IN2	LQVR.....	GDN.	PSSEAG	AERQG....		TFNFPQITL
CRF01_AE_C	LGDGGR.....	DN.	LLPEAG	AERQG...	TP	FSFSFPQITF
CRF01_AE_C	LGDGGR.....	DN.	LLPEAG	AERQE...	TA	SSFSFPQITL
CRF01_AE_C	LRDGGR.....	DN.	LLLEAG	AERQG...	TS	SSLSFPQITL
CRF01_AE_T	LGDGGR.....	DN.	LLTEAG	AERQG...	TS	SSFSFPQITL
CRF01_AE_T	MGDGGR.....	DN.	LLTEAG	AERQ...	GS	SSFSFPQITL
CRF01_AE_T	LGDGG.....		G	AERQG...	TS	SSFSFPQITL
CRF01_AE_T	LGDGGR.....	DN.	LLAETG	AERQG...	TP	SSFNFPQITL
CRF01_AE_T	LGDGGR.....	DNG	GRDNLLTEAG	AERQG...	TS		SSFSFPQITL
CRF01_AE_T	LGDGGR.....	DN.	LLPEAG	AERQG...	TP	SSFSFPQITL
CRF02_AG_F	LGDGGR.....	DN.	LPSEAG	SEPG...	TI	SSLSFPQITL
CRF02_AG_F	LWDGGR.....	DN.	LPSEAG	TEPG...	TI	SPSSFPQITL
CRF02_AG_G	LWDKGR.....	NN.	LLSAAG	TEGQG...	TI	SSFNFPQITL
CRF02_AG_N	LWDGGR.....	DT.	SLSTAG	TEGQG...	AI	SSFNFPQITL
CRF02_AG_S	PWDRGR.....	DN.	LLSEAG	TGGQG...	TI	SSLSFPQITL
CRF02_AG_S	LWDGGR.....	DN.	LLPEAG	TGGQG...	TI	PSFNFPQITL
CRF03_AB_R	LWDGGR.....	DN.	PLPETG	TEGQG...	TA	SSFNFPQITL
CRF03_AB_R	LWDGGR.....	DN.	PLPETG	TERQG...	TA	SSFNLPQITL
CRF04_cpx	LREERG.....	DN.	LLSEAG	TEGQ...	GT	ISFNFPQITL
CRF04_cpx	LRDERG.....	DN.	LLSEAG	TEGQ...	GT	ISFNFPQITL
CRF04_cpx	LRDERG.....	DN.	LLSEAG	TEGQ...	GT	ISHNFPQITL
CRF05_DF_B	LQVWGG.....	DS.	LLSEAG	AEG...	RGTV	PSLSFPQITL
CRF05_DF_B	LRVWRG.....	DN.	PLAEAG	AEG...	RGEV	PSLSFPQITF
CRF06_cpx	LRFR.....	GDS.	PLPETG	VEGEGKGAI		SLS.LPQITL

CRF06_cpx_	LRVRR.....	GDS.	PLPGAE	AEG...KGAI	SLN.FPQITL
CRF06_cpx_	LRVRR.....	GDS.	PLPEAG	TEGKG.KGAI	SLS.FPQITL
CRF06_cpx_	LRVRG.....	GNS.	PLPEAG	AEG...EGAI	SLS.FPQITL
CRF11_cpx_	LRVRR.....	GDS.	PLPETG	AEGEGE..GA	ISFNLPQITL
CRF11_cpx_	LRVRG.....	GDN.	PLPETG	AQGE....GT	ISYNFPQITL
D_CD_84ZR0	LRVWGG....	DN..	PLPETG	TEG..QRQGT	VSLSFPPQITL
D_CD_ELI_K	LRVWGR....	DN..	PLSKTG	AE....RQGT	VSNFNPQITL
D_CD_NDK_M	LRVWGG....	DN..	PLSETG	AE....RQGT	VSFNFPQITL
D_UG_94UG1	LRIRGG....	DN..	TSSETG	AER....QGT	VSNLFPQITL
F1_BE_VI85	LRVQRG....	DN..	PLSEAG	AERR...GTV	PSLSFPQITL
F1_BR_93BR	LQVRGG....	DN..	PISEAG	AERR...GTV	PSLSFPQITL
F1_FI_FIN9	PRDQRR....	GN..	SLSEAG	AERR...GTV	PSLSFPQITL
F1_FR_MP41	LRVQRG....	NN..	PLSEAG	AEGRGT.GTV	SSLSLPQITF
F2_CM_MP25	LRVRGG....	DS..	SLPEAG	AERQG...TG	SSLDFFQITL
F2KU_BE_VI	LRVWGG....	DK..	PLSEAG	DERQG...TG	ASFNLPQITL
G_BE_DRCBL	LRVRG.....	GDS.	PLPEAG	AEG...KGTI	S.SIFPQITL
G_NG_92NG0	LRIRR.....	GDS.	PLPEAG	AKG...EGAI	SLN.FPQITL
G_SE_SE616	PRVRR.....	GDS.	PLPEAG	DEG...KGAI	S...LPQITL
H_BE_VI991	LRVRR.....	GDH.	PLSEAG	AE.....RTG	TSFNFPQITL
H_BE_VI997	LRVRG.....	GDD.	LLPEAG	AE.....GQG	TSLCFPQITL
H_CF_90CF0	LRVRR.....	GDD.	PLSEAG	AAE.....GQG	TSLSFPPQITL
J_SE_SE702	PRVRR.....	GD..	PLPETG	AEGQ....GT	VSSNFPQITL
J_SE_SE788	PRARR.....	GD..	PLPETG	AEGQ....GT	VSSNFPQITL
K_CD_EQTB1	LWVRGE....	DN..	PLSETG	NERSG...TG	SSFNFPQITL
K_CM_MP535	LRVRGG....	DN..	PLSEAG	DQRQG...TE	PSFNFPQITL
N_CM_YBF30	LWVSG.....	GEEH	TGEGDAGEPG	EDRE...LSV	PTFNFPQITL	
O_CM_ANT70	GSEGTG....	ESG.	TERG	PER.....A	LSVCLPQIPL
O_CM_MVP51	GSEGTR....	ESE.	SEGG	SGR.....A	VPICLPQIPL
O_SN_99SE_	GNEGTR....	ESG.	TEGG	PER.....T	LSVCLPQIPL
O_SN_99SE_	GNEGTR....	KSG.	TEGG	PER.....T	LSVCLPQIPL
U_CD___83C	LRVRR.....	GDN.	PLAEAG	AEGQG..VPL	PSFNFPQITL

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00BW0762_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW0768_2	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW0874_2	WQRPLVSIKI	EGQIREALLD	TGADDTVLEE	ITLSGRWKPK	MIGGIGGFIK
00BW1471_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW1616_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW1686_8	WQRPLVTIKV	GGQVKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW1759_3	WQRPLVSIKV	GGQVKEALLD	TGADDTVLEE	LALPGRWKPK	MIGGIGGFIK
00BW1773_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW1783_5	WQRPLVTIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW1795_6	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
00BW1811_3	WQRPLVTIKV	GGQTKAALLD	TGADDTVLEE	MNLPGKWKPK	MIGGIGGFIK
00BW1859_5	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW1880_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW1921_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW2036_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWKPK	MIGGIGGFIK
00BW2063_6	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLLGKWKPK	MIGGIGGFIK
00BW2087_2	WQRPLVSIKI	EGQIKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
00BW2127_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW2128_3	WQRPLVSIKI	GDQVKEALLD	TGADDTVLEE	IKLPGKWKPK	MIGGIGGFIK
00BW2276_7	WQRPLVSIKV	GGQIREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW3819_3	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLSGKWKPK	MIGGIGGFIK
00BW3842_8	WQRPLVTIKV	GGQIKEALLD	TGADDTVLEE	MNMPGKWKPK	MIGGIGGFIK
00BW3871_3	WQRPLVTIKV	GGQVKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
00BW3876_9	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW3886_8	WQRPLVSIKV	GGQIKEALLD	IGADDTVLEE	LSLPGKWKPK	MIGGIGGFIK
00BW3891_6	WQRPLVTIKV	GGQIKEALLD	TGADDTVLEE	ISLPGKWKPK	MIGGIGGFIK
00BW3970_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK

00BW5031_1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
96BW01B21	WQRPLVTIRV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
96BW0407	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
96BW0502	WQRPLVSIKV	GGQIKEALLD	TGADNTVLEE	INLPGKWKPK	MIGGIGGFIK
96BW06_J4	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLSGKWKPK	MIGGIGGFIK
96BW11_06	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWRPK	MIGGIGGFIK
96BW1210	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
96BW15B03	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWKPK	MMGGIGGFIK
96BW16_26	WQRPLVSIKV	GGQVKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
96BW17A09	WQRPLVSIKV	GGQIREALLD	TGADDAVLED	INLPGKWKPK	MIGGIGGFIK
96BWM01_5	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	VNLPGKWKPK	MIGGIGGFIK
96BWM03_2	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
98BWMC12_2	WQRPLVSIKI	GGQIREALLD	TGADDTVLEE	LSLPGRWKPK	MIGGIGGFIK
98BWMC13_4	WQRPLVSIKV	GGQVKEALLD	TGADDTVLED	IELPGKWRPK	MIGGIGGFIK
98BWMC14_a	WQRPLVSIKV	GGQTKAALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
98BWM014_1	WQRPLVSIKI	GGQIKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
98BWM018_d	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
98BWM036_a	WQRPLVSIKV	GGQTKAALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
98BWM037_d	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
99BW3932_1	WQRPLVPIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGLIK
99BW4642_4	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	ISLPGKWKPK	MIGGIGGFIK
99BW4745_8	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
99BW4754_7	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
99BWMC16_8	WRRPLVTIKV	GGQIKEALLH	PGADDTVLEE	INLPRKWKPK	MIGGIGGFIK
A2_CD_97CD	WQRPLVTVKI	EGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A2_CY_94CY	WQRPLVTVKI	EGQLKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
A2D_97KR	WQRPLVTVKI	EGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A2G_CD_97C	WQRPLVTVKI	GGQLIEALLD	TGADDTVLED	INLPGRWKPK	MIGGIGGFIK
A_BY_97BL0	WQRPLVTVRI	GGQLKEALLD	TGADXTVLED	INLPGKWKPK	MIXGIXGFIK
A_KE_Q23_A	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE659	WQRPLVTVKV	GGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE725	WQRPLVTVKI	GGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE753	WQRPLVTVKI	EGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_SE853	WQRPLVTVKV	GGQLKEALLD	TGADDTVLED	INLPGKWRPK	MIGGIGGFIK
A_SE_SE889	WQRPLVTVRI	GGMQKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_SE_UGSB8	WQRPIVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_UG_92UG0	WQRPLVTVKI	GGQLKALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
A_UG_U455_	WQRPLVTVKI	GGQLIEALLD	TGADDTVLED	INLPGKWKPK	IIGGIGGFIK
AC_IN_2130	WQRPLVSIRV	GGQTKAALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AC_RW_92RW	WQRPLVTVKI	GGQLREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AC_SE_SE94	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
ACD_SE_SE8	WQRPLVKVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
ACG_BE_VI1	WQRPLVTVRL	GGQLIEALLD	TGADDTVLEQ	INLPGKWKPK	MIGGIGGFIK
AD_SE_SE69	WQRPLVTVKI	GGQLREALLD	TCADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AD_SE_SE71	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
ADHK_NO_97	WQRPVVTVKV	GGQLKEALLD	TGADDTVLED	MNLPKWKPK	MIGGIGGFIK
ADK_CD_MAL	WQRPVVTVRV	GGQLKEALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
AG_BE_VI11	WQRPLVTVRI	GGQLIEALLD	TGADDTVLAE	ISLPGKWKPK	MIGGIGGFIK
AG_NG_92NG	WQRPLVTVRI	GGQLIEALLD	TGADDTVLEQ	INLPGKWKPK	MIGGIGGFIK
AGHU_GA_VI	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLLGKWKPK	MIGGIGGFIK
AGU_CD_Z32	WQRPIVTVKI	GGQPIEALLD	TGADDTVLEE	IKLPGKWKPK	MIGGIGGFIK
AJ_BW_BW21	WQRPLVTIRV	AGQVKEALLD	TGADDTVLEE	MELPGKWKPK	MIGGIGGFIK
B_AU_VH_AF	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MCLPGRWKPK	MIGGIGGFIK
B_CN_RL42_	WQRPLVTIKV	GGQLKEALLD	TGADDTVLED	MNLPGRWKPK	MIGGIGGFIK
B_DE_D31_U	WQRPLVTIKI	GGQLKEALLD	TCADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_DE_HAN_U	WQRPLVTIKI	GGQLKEALLD	TGADDTVVEE	MSLPGRWKPK	MIGGIGGFIK
B_FR_HXB2_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIK
B_GA_OYI_	WQRPIVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_GB_CAM1_	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIK
B_GB_GB8_A	WQRPIVTIKI	GGQLKEALLD	TGADDTVLED	MNLPGRWKPK	MIGGIGGFIK

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B_GB_MANC	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIFK
B_KR_WK_AF	WQRPLVAIKI	GGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIFK
B_NL_3202A	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIFK
B_TW_TWCYS	WQRPLVTIRI	GGQLKEALLD	TGADDTVLEE	MNLPGKWKP	MIGGIGGFIFK
B_US_BC_L0	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIFK
B_US_DH123	WQRPLVKIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
B_US_JRCSE	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	MDLPRGWKP	MIGGIGGFIFK
B_US_MNCG	WORPIVTKI	GGQLKEALLD	TGADDTVLEGE	MNLPRRWKPK	MIGGIGGFIFK
B_US_P896	WQRPLVTIKV	GGQLKEALLD	TGADDTVLED	MSLPGRWKPK	MIGGIGGFIFK
B_US_RF_M1	WQRPIVTVKI	GGQLKEALLD	TGADDTVLEE	MNLPGKWKP	MIGGIGGFIFK
B_US_SF2_K	WQRPLVTIRI	GGQLKEALLD	TGADDTVLEE	MNLPGKWKP	MIGGIGGFIFK
B_US_WBAU1	WQRPLVTIKI	EGQLKEALLD	TGADDTVLED	MNLPGKWKP	MIGGIGGFIFK
B_US_WR27	CORPLVAIKI	GGQIKEALLD	TGADDTVLEE	MSLPGRWKPK	MVGIGGFIFK
B_US_YU2_M	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	MNLPGRWKPK	MIGGIGGFIFK
BF1_BR_93B	WQRPLVTVKI	GGQLKEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIFK
C_BR_92BR0	WQRPLVNIKV	GGQLKEALLD	TGADDTVLEE	IKLPGNWKPK	MIGGIGGFIFK
C_BW_96BW0	WQRPLVSIKV	GGQIREALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	INLPGKWRP	MIGGIGGFIFK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
C_BW_96BW1	WQRPLVSIKV	GGQIKEALLD	TGADDTVLEE	MSLPGKWKP	MMGIGGFIFK
C_ET_ETH22	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
C_IN_93IN1	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	VNLPGKWKP	MIGGIGGFIFK
C_IN_93IN9	WQRPLVSIRV	GGQIKETLLD	TGADDTVLEE	VNLPGKWKP	MIGGIGGFIFK
C_IN_93IN9	WQRPLVSIKV	GGQIREALLD	TGADDTVLEE	VNLPGKWKP	MIGGIGGFIFK
C_IN_94IN1	WQRPLVSIRV	GGQTREALLD	TGADDTVLEE	VNLPGKWKP	MIGGIGGFIFK
C_IN_95IN2	WQRPLVSIRV	GGQIKEALLD	TGADDTVLEE	VSLPGKWRP	MIGGIGGFIFK
CRF01_AE_C	WQRPLVTVKI	EGQLKEALLD	TGADDTVLED	INLPGRWKPK	MIGGIGGFIFK
CRF01_AE_C	WQRPLVTVKV	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF01_AE_C	WQRPIVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF01_AE_T	WQRPLVTVKI	GGBELKEALLD	TGADDTVLED	INLPGKWKP	MIGGICGFIFK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF01_AE_T	WQRPLVTVKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF02_AG_F	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
CRF02_AG_F	WQRPLVTVRI	GGQLIEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
CRF02_AG_G	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF02_AG_N	WQRPLVTVRI	EGQLIEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF02_AG_S	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
CRF02_AG_S	WQRPLFTVRI	EGQLIKALLD	TGANDTVLEK	INLPGKWKP	MIGGIGGFIFK
CRF03_AB_R	WRRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF03_AB_R	WQRPLVTVRI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF04_cpx	WQRPLVTIKL	GGQIREALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
CRF04_cpx	WQPPLVTIKI	GGQIREALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF04_cpx	WQRPLVTIKI	GGQLREALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIFK
CRF05_DF_B	WQRPVVTIRI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF05_DF_B	WQRPVVTIKI	EGQLKEALLD	TGADDTVLEE	MNLPGKWKP	MIGGIGGFIFK
CRF06_cpx	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF06_cpx	WQRPLVTVRI	GGQLIEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF06_cpx	WQRPLVTVGI	EGQLIEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
CRF06_cpx	WQRPLVTVKV	EGQLIEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIFK
CRF11_cpx	WQRPIVKIKV	AGQLKEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIFK
CRF11_cpx	WQRPVVPVKV	AGQLKEALLD	TGADDTVLEE	MSLPGRWKPK	MIGGIGGFIFK
D_CD_84ZR0	WQRPVVTIKI	GGQLKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
D_CD_ELI_K	WQRPLVAIKI	GGQLKEALLD	TGADDTVLEE	MNLPGKWKP	MIGGIGGFIFK
D_CD_NDK_M	WQRPLVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
D_UG_94UG1	WQRPVVTIKI	GGQLKEALLD	TGADDTVLEE	INLPGKWKP	MIGGIGGFIFK
F1_BE_VI85	WQRPLVTIKI	GGQIKEALLD	TGADDTVLED	INLPGKWKP	MIGGIGGFIFK
F1_BR_93BR	WQRPLVTIRV	GGQLKEALLD	TGADDTVLED	VNLPGKWKP	MIGGIGGFIFK

F1_FI_FIN9	WQRPLVTIKI	GGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
F1_FR_MP41	WQRPLVTIRV	GGQLREALLD	TGADDTVLED	IDLPGKWKPK	IIGGIGGFIK
F2_CM_MP25	WQRPVVTIKV	GGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
F2KU_BE_VI	WQRPIVTIKI	GGQLREALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
G_BE_DRCBL	WQRPIVKVRI	GGQLIEALLD	TGADDTVLEE	IDLPGKWKPK	MIGGIGGFIK
G_NG_92NG0	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEG	INLPGKWKPK	MIGGIGGFIK
G_SE_SE616	WQRPLVTVKI	GGQLIEALLD	TGADDTVLEE	INLPGRWKPK	MIGGIGGFIK
H_BE_VI991	WQRPIVTVKI	EGQLKEALLD	TGADDTVLED	INLPGKWKPK	MIGGIGGFIK
H_BE_VI997	WQRPLVTVKI	EGQLREALLD	TGADDTVLEE	INLLGRWKPK	MIGGIGGFIK
H_CF_90CF0	WQRPLVTVKI	EGQLREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
J_SE_SE702	WQRPLVTIRI	GGQLREALLD	TGADDTVLEE	IDLPGKWKPK	MIGGIGGFIK
J_SE_SE788	WQRPLVTIRI	GGQLREALLD	TGADDTVLED	IDLPRKWKPK	MICGIGGFIK
K_CD_EQTB1	WQRPVVTVKV	GGQLREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
K_CM_MP535	WQRPIVTIKV	GGQLREALLD	TGADDTVLEE	INLPGKWKPK	MIGGIGGFIK
N_CM_YBF30	WQRPIVTVKI	GKEVREALLD	TGADDTVIEE	LQLEGKWKPK	MIGGIGGFIK
O_CM_ANT70	WDRPIVTARV	GGHLCVLLD	TGADDTVLENN	IQLEGKWKPK	MIGGIGGFIK
O_CM_MVP51	WDRPIVTAKV	GGHLCVLLD	TGADDTVLENN	IQLEGRWTPK	MIGGIGGFIK
O_SN_99SE_	WDRPVVTARV	GGHLCVLLD	TGADDTVLTN	IQLEGKWTPK	MIGGIGGFIK
O_SN_99SE_	WDRPIVPARV	GGHLCVLLD	TGADDTVLENN	IQLEGKWTPK	MIGGIGGFIK
U_CD_83C	WQRPLVTVKI	GGQLKEALLD	TGADDTVVEE	MTLPGKWKPK	MIGGIGGFIK

	151				200
00BW0762_1	VRQYDQILIE	ICGKRAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW0768_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW0874_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1471_2	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1616_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1686_8	VRQYDQISIE	ICGKRAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1759_3	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1773_2	VRQYDQISIE	ICGKKAIGAV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1783_5	VRQYDQILIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1795_6	VRQYDHIPIE	ICGKRAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1811_3	VRQYDEILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1859_5	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1880_2	VRQYDQILIE	ICGKRAMGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW1921_1	VRQYDQITIE	ICGKKAIGAV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2036_1	VRQYDQIPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2063_6	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2087_2	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2127_2	VRQYDQVIVIE	ICGKKTIGTV	LVGPTPVNIV	GRNMLTQLGC	TLNFPISPIE
00BW2128_3	VRQYDEIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW2276_7	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3819_3	VRQYEQVPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3842_8	VRQYDQIVIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3871_3	VRQYEQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3876_9	VRQYDQILVE	ICGKKAIGTV	SVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3886_8	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3891_6	VRQYDQIAIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW3970_2	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
00BW5031_1	VRQYDQIMIE	ICGQKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW01B21	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW0407	VRQYEQILIE	ICGKKTIGTV	LVGPTPVDII	GRNMLTQLGC	TLNFPISPIE
96BW0502	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW06_J4	VRQYDQIPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW11_06	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW1210	VRQYDQIVIE	ICGKKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW15B03	VRQYDQILIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW16_26	VRQYDQITIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BW17A09	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
96BWM01_5	VRQYDQIPIE	ICGKRAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE

96BWM03_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM012_2	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM013_4	VRQYDRIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM014_a	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM014_1	VGQYDQIPIE	ICGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
98BWM018_d	VKQYEQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLAQLGC	TLNFPISPIE
98BWM036_a	VRQYDQILIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQLGC	TLNFPISPIE
98BWM037_d	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW3932_1	VRQYDQVVE	ICEKKTIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
99BW4642_4	VRQYDQIPIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW4745_8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BW4754_7	VRQYDQIHIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
99BWM016_8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTPLGC	TLNFPISPIE
A2_CD_97CD	VRQYDQIVIE	ICGKKAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2_CY_94CY	VRQYDQIAIE	ICGKKAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2D_97KR	VRQYDQITIE	ICEKKAIGTV	LVGPTPVNII	GRNMLVQLGC	TLNFPISPIE
A2G_CD_97C	VRQYDQILIE	ISGKKAIGTV	LVGPTPINII	GRNMLIQIGC	TLNFPISPIE
A_BY_97BL0	VRQYDQILVE	ICXKKAIXTV	LVGPTPXNII	XRNMLTQLGC	TLNFPISPIE
A_KE_Q23_A	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE659	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE725	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE753	VKQYDQVLE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE853	VKQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_SE889	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_SE_UGSE8	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
A_UG_92UG0	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTLIGC	TLNFPISPIE
A_UG_U455	VRQYDQILIE	ICGKKTIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AC_IN_2130	VRQYDQISIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
AC_RW_92RW	VKQYDQILIE	ICGKKAIGTV	LVGPTSVNII	GRNMLTQIGC	TLNFPISPIE
AC_SE_SE94	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ACD_SE_SE8	VRQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
ACG_BE_VI1	VRQYDQIMIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AD_SE_SE69	VRQYDQILIE	ICGYKAIGTV	LVGPTPVNII	GRNLLTQIGC	ALNFPISPIE
AD_SE_SE71	VKQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ADHK_NO_97	VRQYDXILIE	ICGKKAIGTV	LAGPTPVNII	GRNMLTQIGC	TLNFPISPIE
ADK_CD_MAL	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AG_BE_VI11	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
AG_NG_92NG	VKQYDQILIE	IEGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AGHU_GA_VI	VRQYDQVPIE	ICGKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AGU_CD_Z32	VRQYDQILIE	IGEKKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
AJ_BW_BW21	VRQYNDIHIE	VEGKKAIGTV	LIGPTPINII	GRNMLTQLGC	TLNFPISPIT
B_AU_VH_AF	VRQYDQVLE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_CN_RL42	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIK
B_DE_D31_U	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_DE_HAN_U	VRQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_FR_HXB2	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_GA_OYI	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_CB_CAM1	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_GB_GB8_A	VKQYDQILVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_GB_MANC	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_KR_WK_AF	VRQYDQVAIE	ICGHKAIGTV	LIGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_NL_3202A	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_TW_TWCYS	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPID
B_US_BC_LO	VRQYDQIPIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_DH123	VRQYDQVLE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_JRCSF	VRQYDQIPID	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_MNCG	VRQYDQITIG	ICGHKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
B_US_P896	VRQYEQIDIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_RF_M1	VRQYDQILIE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_SF2_K	VRQYDQIPVE	ICGHKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE

B_US_WEAU1	VRQYDQVP	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_WR27	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
B_US_YU2_M	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
BF1_BR_93B	VRQYDQIP	ICGRKATGT	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
C_BR_92BR0	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_BW_96BW0	VRQYEQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_BW_96BW1	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
C_BW_96BW1	VRQYDQIV	ICGKAIGSV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIK
C_BW_96BW1	VRQYDQIL	ICGKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_ET_ETH22	VRQYDQIII	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGR	TLNFPISPIE
C_IN_93IN1	VRQYDQIP	ICGKAIGTV	LVGPTPINII	GRNMLTQLGC	TLNFPISPIE
C_IN_93IN9	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_IN_93IN9	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNLLTQLGC	TLNFPISPIE
C_IN_94IN1	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
C_IN_95IN2	VRQYEEIP	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF01_AE_C	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_C	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_C	VRQYDQIII	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF01_AE_T	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF02_AG_F	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_F	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_G	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_N	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_S	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF02_AG_S	LRQYDQIL	ICGKKAMGSV	LVGPTPVNII	GKNILTQIGC	TLNFPISPIE
CRF03_AB_R	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF03_AB_R	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF04_cpx	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNMLTQLGC	TLNFPISPIE
CRF04_cpx	VKQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF04_cpx	VRQYDQIT	ICGKKATGT	LVGPTPANII	GRNMLTQLGC	TLNFPISPIE
CRF05_DF_B	VRQYDQIL	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF05_DF_B	VRQYDQIL	ICGHKAVGT	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
CRF06_cpx	VKQYDQIL	ICGKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx	VRQYDQIL	ICGKRAMGT	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx	VRQYDQIL	ICGKKAMGT	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF06_cpx	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
CRF11_cpx	VKQYEEIII	IEGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPID
CRF11_cpx	VKQYEDIT	IEGKAIGTV	LIGPTPVNII	GRNMLTQIGC	TLNFPISPVD
D_CD_84ZR0	VRQYDHIL	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_CD_ELI_K	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_CD_NDK_M	VRQYDQIL	ICGYKAMGT	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
D_UG_94UG1	VRQYDQIP	ICGKAIGTV	LVGPTPVNII	GRNLLTQIGC	TLNFPISPIE
F1_BE_VI85	VKQYDNIL	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPVSP
F1_BR_93BR	VKQYDSIL	ICGHRAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F1_FI_FIN9	VKQYDHIL	ICGKAIGTV	LVGPTPVNIV	GRNMLTQIGC	TLNFPISPIE
F1_FR_MP41	VKQYDQIT	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F2_CM_MP25	VRQYDQV	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
F2KU_BE_VI	VRQYDQV	ICGKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
G_BE_DRCBL	VRQYDQIL	ISGKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
G_NG_92NG0	VRQYDQIL	ISGKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
G_SE_SE616	VRQYDQVP	ISGKAIGTV	LVGPTPINII	GRNMLTQIGC	TLNFPISPIE
H_BE_VI991	VRQYEQVA	IFGKAIGTV	LVGPTPVNII	GRNILTQMG	TLNLPISPIE
H_BE_VI997	VRQYDQVA	ICGKAIGTV	LVGPTPVNII	GRNILTQIGC	TLNFPISPIE
H_CF_90CF0	VRQYEQVA	ICGKAIGTV	LVGPTPVNII	GRNILTQIGC	TLNFPISPIE
J_SE_SE702	VRQYNEVP	IEGKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE

J_SE_SE788	VRQYNEVP	IEGKKAIGTV	LIGPTPVNII	GRNMLTQLGC	TLNFPISPIE
K_CD_EQTB1	VRQYDQVCME	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
K_CM_MP535	VRQYDQVLIE	ICGQKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
N_CM_YBF30	VRQYDNITVD	IQGRKAVGT	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE
O_CM_ANT70	VKEYDNVTVE	IEGREVQGT	LVGPTPVNII	GRNMLTGLGC	TLNFPISPIA
O_CM_MVP51	VKEYNNVTVE	VQKKEVQGT	LVGPTPVNII	GRNMLTGLGC	TLNFPISPIA
O_SN_99SE	VKEYNQVPVE	IEGREVLGT	LVGPTPVNII	GRNMLTGLGC	TLNFPISPIA
O_SN_99SE	VKEYNQVPVE	IEGREVLGT	LVGPTPVNII	GRNMLTGLGC	TLNFPISPIA
U_CD_83C	VRQYDQILIE	ICGKKAIGTV	LVGPTPVNII	GRNMLTQIGC	TLNFPISPIE

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00BW0762_1	TVPVKLKPGM	DGPKVRQWPL	TEEKIKALTA	ICDEMEKEGK	ITKIGPENPY
00BW0768_2	TVPVKLKPGM	NGPKVKQWPL	TEEKIKALTA	ICEEMEREK	ITKIGPENPY
00BW0874_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIQALTA	ICEEMEKEGK	ITKIGPENPY
00BW1471_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALKA	ICEEMEKEGK	ITKIGPENPY
00BW1616_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1686_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1759_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1773_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1783_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1795_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1811_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1859_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1880_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW1921_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALKE	ICEEMEKEGK	ITKIGPENPY
00BW2036_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2063_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTG	ICEEMEKEGK	ITKIGPENPY
00BW2087_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2127_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2128_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW2276_7	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALME	ICEEMEKEGK	ITKIGPENPY
00BW3819_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
00BW3842_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
00BW3871_3	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3876_9	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3886_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3891_6	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW3970_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
00BW5031_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW01B21	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW0407	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW0502	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
96BW06_J4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
96BW11_06	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW1210	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
96BW15B03	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW16_26	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BW17A09	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BWMO1_5	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
96BWMO3_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
98BWMC12_2	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMC13_4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMC14_a	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMO14_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
98BWMO18_d	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMO36_a	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
98BWMO37_d	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
99BW3932_1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY
99BW4642_4	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
99BW4745_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	ITKIGPENPY

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99BW4754_7	TVPXKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ISKIGPENPY
99BWMC16_8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEEBEGK	IEKIGPENPY
A2_CD_97CD	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2_CY_94CY	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2D_97KR	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A2G_CD_97C	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICKEMEKEGK	ISKIGPENPY
A_BY_97BL0	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALXD	ICKEXEKEGK	ISKIXPENPY
A_KE_Q23_A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE659	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE725	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE753	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE853	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_SE_SE889	TVPVTLKPGM	DGPRIKQWPL	TEEKIKALTE	ICREMEKEGK	ISKIGPENPY
A_SE_UGSE8	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_UG_92UG0	TVPVKLKPGM	DGPRIKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
A_UG_U455_	TVPVKLKPEM	DGPKVKQWPL	TEEKIKALTE	ICADMEREGR	ISKIGPENPY
AC_IN_2130	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICNEMEKEGK	ISKIGPENPY
AC_RW_92RW	TVPVALKPGM	DGPKVKQWPL	TEEKIKALRE	ICTEMEKEGK	ISKIGPENPY
AC_SE_SE94	TVPVTLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	LSRIGPENPY
ACD_SE_SE8	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISRIGPENPY
ACG_BE_VI1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTD	ICKEMEKEGK	ISKIGPENPY
AD_SE_SE69	TVPVQLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	IARIGPENPY
AD_SE_SE71	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
ADHK_NO_97	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICLEMEKEGK	ISKIGPENPY
ADK_CD_MAL	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICKDMEKEGK	ILKIGPENPY
AG_BE_VI11	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
AG_NG_92NG	TVPVKLKPGI	DGPKVKQWPL	TEEKIKALTE	ICTDMEKEGK	ISKIGPENPY
AGHU_GA_VI	TVPVKLKPGI	DGPKVKQWPL	TEEKIKALTE	ICNEMEKEGK	ISRIGPENPY
AGU_CD_Z32	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
AJ_BW_BW21	TVPVNLKPGM	DGPRVRQWPL	TEEKIKALTE	IFTEMEKEGK	ISKIGPENPY
B_AU_VH_AF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_CN_RL42_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_DE_D31_U	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_DE_HAN_U	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISKIGPENPY
B_FR_HXB2_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GA_OYI_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKVLI	ICTEMEKEGK	ISKVGPENPY
B_GB_CAM1_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GB_GB8_A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_GB_MANC_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_KR_WK_AF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_NL_3202A	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_TW_TWCYS	TVPVKLKPGM	DGPKVKQWPL	TEEKIKVLI	ICTEMEKEGK	ISKIGPENPY
B_US_BC_L0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_DH123	TVPVKLKPGM	DGPRVKQWPL	SEEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
B_US_JRCSF	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_MNCG_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALIE	ICTEMEKEGK	ISKIGPENPY
B_US_P896_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_RF_M1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_SF2_K	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_WEAU1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
B_US_WR27_	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	VTKIGPENPY
B_US_YU2_M	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALVE	ICTEMEKEGK	ISKIGPENPY
BF1_BR_93B	TVPVKLKPGM	DGPRVKQWPL	TEEKIKALTE	ICTEMEKEGK	ISKIGPENPY
C_BR_92BR0	TVPVKLKPGM	DGPKVKQWLL	TEEKIKALTA	ICDEMEREKG	ITKIGPENPY
C_BW_96BW0	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKECK	ITKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTE	ICEEMEKEGK	VTKIGPENPY
C_BW_96BW1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ITKIGPENPY
C_ET_ETH22	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICEEMEKEGK	ISRIGPENPY
C_IN_93IN1	TVPVKLKPGM	DGPKVKQWPL	TEEKIKALTA	ICDEMEREKG	ITKIGPENPY

C_IN_93IN9	TVPVKLKPGM	DGPKVKQWPL	TEKEIEALTA	ICDEMEKEGK	ITKIGPENPY
C_IN_93IN9	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTA	ICDEMEREGK	ITKIGPENPY
C_IN_94IN1	TVPVKLKPGM	DGPKVKQWPL	TKEKIEALT I	ICNEMEKEGK	ITKIGPENPY
C_IN_95IN2	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTA	ICDEMEKEGK	ITKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPT	. . EEEKIALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_C	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	TCKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF01_AE_T	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
CRF02_AG_F	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
CRF02_AG_F	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTD	ICAEMEKEGK	ISKIGPENPY
CRF02_AG_G	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTD	ICMEMEKEGK	ISKIGPENPY
CRF02_AG_N	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTD	ICTEMEKEGK	ISKIGPENPY
CRF02_AG_S	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTD	ICTEMEKEGK	ISRIGPENPY
CRF02_AG_S	TVLPLKLPGM	DGPKVKQWPL	TEEKLHLTD	ICAEMEKEGK	ISKIGPENPY
CRF03_AB_R	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEKEGK	ISKIGPENPY
CRF03_AB_R	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALID	ICKEMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
CRF04_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALRE	ICTEMEQEGK	ISKVGPENPY
CRF05_DF_B	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISRIGPENPY
CRF05_DF_B	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISRIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICKEMEKEGK	ISKIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKIKQWPL	TEEKI KALTE	ICTEMEKEGK	ISRIGPENPY
CRF06_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
CRF11_cpx_	TVPVQLKAGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
CRF11_cpx_	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
D_CD_84ZR0	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISRIGPENPY
D_CD_ELI_K	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISRIGPENPY
D_CD_NDK_M	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISRIGPENPY
D_UG_94UG1	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALIE	ICSELEKEGK	ISKIGPENPY
F1_BE_VI85	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICLEMEKEGK	ISKIGPENPY
F1_BR_93BR	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICMEMEKEGK	ISKIGPENPY
F1_FI_FIN9	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISRIGPENPY
F1_FR_MP41	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTDMEKEGK	ISKIGPENPY
F2_CM_MP25	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
F2KU_BE_VI	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICLEMEKEGK	ISKIGPENPY
G_BE_DRCBL	TVPVKLKPGM	DGPRVKQWPL	TEEKI KALTE	ICNEMEKEGK	ISKIGPENPY
G_NG_92NG0	TVPVKLKPGM	DGPRVKQWPL	TEEKI KALTE	ICKDMEKEGK	ISKIGPENPY
G_SE_SE616	TVPVKLKPGM	DGPRVKQWPL	TEEKI KALTE	ICKEMEEEGK	ISKIGPENPY
H_BE_VI991	TVPVTLKPGM	DGPKVKQWPL	TEEKI KALTE	ICLEMEKEGK	ISKIGPENPY
H_BE_VI997	TVPVKLKPGM	DGPRVKQWPL	TEEKI KALTE	ICMEMEKEGK	ISKIGPENPY
H_CF_90CF0	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISRIGPENPY
J_SE_SE702	TVPVKLKPGM	DGPKIKQWPL	TEEKI KALTO	ICAELEEKGK	ISRIGPENPY
J_SE_SE788	TVPVKLKPGM	DGPKIKQWPL	TEEKI KALTV	ICAEMEEEEGK	ISRVGPNPYY
K_CD_QOTB1	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALVE	ICTEMEKEGK	ISKIGPENPY
K_CM_MP535	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICTEMEKEGK	ISKIGPENPY
N_CM_YBF30	TVPVKLKPGM	DGPKVKQWPL	TTEKIEALRE	ICTEMEKEGK	ISRIGPENPY
O_CM_ANT70	PVPVKLKPGM	DGPKVKQWPL	SKEKIEALTA	ICQE MEQEGK	ISRIGPENPY
O_CM_MVP51	PVPVKLKPGM	DGPKVKQWPL	SREKIEALTA	ICQE MEQEGK	ISRIGPENPY
O_SN_99SE	PVPVKLKPGM	DGPKIKQWPL	SKEKIEALTA	ICQE MEQEGK	ISRIGPENPY
O_SN_99SE	PVPVKLKPGM	DGPKIKQWPL	SKEKIEALTA	ICQE MEQEGK	ISRIGPENPY
U_CD___83C	TVPVKLKPGM	DGPKVKQWPL	TEEKI KALTE	ICLEMEKEGK	ISKIGPENPY

00BW0762_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW0768_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW0874_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1471_2	NTPIFAIKKK	DSTKWRKLVD	FKELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1616_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1686_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1759_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1773_2	NTPVFAIKKK	DSTKWRKLVD	FGELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1783_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1795_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1811_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1859_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1880_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW1921_1	NTPIFAIKKK	DSTKWRKLVD	FGELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2036_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2063_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2087_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2127_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2128_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW2276_7	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3819_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3842_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3871_3	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3876_9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3886_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3891_6	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW3970_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
00BW5031_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PVGLKKKKSV
96BW01B21	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW0407	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW0502	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW06_J4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW11_06	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW1210	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW15B03	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW16_26	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BW17A09	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGSKKKKSV
96BWM01_5	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
96BWM03_2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM012_2	NTSVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM013_4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM014_a	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM014_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM018_d	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM036_a	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
98BWM037_d	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW3932_1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGXKKKKSV
99BW4642_4	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW4745_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BW4754_7	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
99BWM016_8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2_CD_97CD	NTPVFAIKKK	DSDKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2_CY_94CY	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKAV
A2D_97KR	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A2G_CD_97C	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_BY_97BL0	NTPVFAIKKK	DSTKWRKLVD	FXELNKRTQD	FXEVQLGIPH	PAGLKKKKSV
A_KE_Q23_A	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE659	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKNSV
A_SE_SE725	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE753	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

A_SE_SE853	NTPVFAIKKK	DSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_SE_SE889	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FW.....IPH	PAGKKKK.SV
A_SE_UGSE8	NTPVFAIKKK	NSDRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_UG_92UG0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
A_UG_U455_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	TAGLKKKKSV
AC_IN_2130	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AC_RW_92RW	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AC_SE_SE94	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ACD_SE_SE8	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ACG_BE_VI1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AD_SE_SE69	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AD_SE_SE71	NTPVFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ADHK_NO_97	NTPVFAIKKK	DSTKWXXXXD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
ADK_CD_MAL	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
AG_BE_VI11	NTPVFAIKKK	GSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AG_NG_92NG	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRSV
AGHU_GA_VI	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FCEVQLGIPH	PAGLKKKKSV
AGU_CD_Z32	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVRLGIPH	PARLKKKRSV
AJ_BW_BW21	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_AU_VH_AF	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_CN_RL42_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEAQLGIPH	PAGLKKKKSV
B_DE_D31_U	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_DE_HAN_U	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_FR_HXB2_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GA_OYI_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GB_CAM1_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_GB_GB8_A	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PSGLKKKKSV
B_GB_MANC_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_KR_WK_AF	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_NL_3202A	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSG
B_TW_TWCVS	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_BC_LO	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_DH123	NTPVFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_JRCSE	NTPVFAIKKK	DSTKWRKLVD	FRELNRRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_MNCG_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_P896_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_RF_M1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_SF2_K	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_WEAU1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PSGLKKKKSV
B_US_WR27_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
B_US_YU2_M	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
BF1_BR_93B	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BR_92BR0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRT.D	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW0	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_BW_96BW1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_ET_ETH22	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_93IN1	NTPVFAIKKK	DSIKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_93IN9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
C_IN_93IN9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_94IN1	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
C_IN_95IN2	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKEK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGVPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKGTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	D.STKRKLVG	FRELNKRTQD	FWEVQLGIPR	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

CRF01_AE_T	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF01_AE_T	NTPVFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVQLGIPR	PAGLKKKKSV
CRF02_AG_F	NTPVFGIKKR	DSTKWRKLVD	FRELNKRTQD	SWEVQLGIPH	PAGLKKKKSV
CRF02_AG_F	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQG	FWEVQLRIPH	PAGLKKKKSV
CRF02_AG_G	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF02_AG_N	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF02_AG_S	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
CRF02_AG_S	NTPVFAIKRK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF03_AB_R	NTPVFAIKKK	DSTKWRKLVG	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF03_AB_R	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGLPH	PAGLKKKKSV
CRF04_cpx_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF04_cpx_	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF04_cpx_	NTPIFAIKKK	NSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF05_DF_B	NTPIFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSI
CRF05_DF_B	NTPIFAIKKK	DSTRWRKLVN	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF06_cpx_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKRKS
CRF06_cpx_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF11_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
CRF11_cpx_	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEIQLGIPH	PAGLKKKKSV
D_CD_84ZR0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSI
D_CD_ELI_K	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
D_CD_NDK_M	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
D_UG_94UG1	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_BE_VI85	NTPVFAIKKK	DSSKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_BR_93BR	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_FI_FIN9	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F1_FR_MP41	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
F2_CM_MP25	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRS
F2KU_BE_VI	NTPIFAIKKK	NSNRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
G_BE_DRCBL	NTPIFAIKKK	DSTRWRKLVD	FRELNKRTQD	FWEVPLGIPH	PGGLKQKRS
G_NG_92NG0	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKRS
G_SE_SE616	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_BE_VI991	NTPIFAIKKK	NSTRWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_BE_VI997	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
H_CF_90CF0	STPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
J_SE_SE702	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
J_SE_SE788	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
K_CD_EQTB1	NTPVFAIKKK	DSTKWKLVN	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
K_CM_MP535	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
N_CM_YBF30	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV
O_CM_ANT70	NTPIFAIKKK	DGDKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
O_CM_MVP51	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
O_SN_99SE_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
O_SN_99SE_	NTPIFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PGGLKQKQSV
U_CD_83C	NTPVFAIKKK	DSTKWRKLVD	FRELNKRTQD	FWEVQLGIPH	PAGLKKKKSV

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00BW0762_1	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW0768_2	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW0874_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLSQGWKGS
00BW1471_2	TVLDVGDAYF	SVPLDRDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1616_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1686_8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1759_3	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
00BW1773_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NEAPGIRYQY	NVLPQGWKGS
00BW1783_5	TVLDVGDAYF	SVPLHENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW1795_6	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
00BW1811_3	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

00BW1859_5	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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00BW1921_1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW2036_1	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW2063_6	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW2087_2	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
00BW2127_2	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW2128_3	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW2276_7	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3819_3	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3842_8	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3871_3	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3876_9	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3886_8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
00BW3891_6	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW3970_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
00BW5031_1	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW01B21	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW0407	AVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NSTPGIRYQY	NVLPQGWNGS
96BW0502	TVLDMGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW06_J4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGITYQY	NVLPQGWKGS
96BW11_06	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW1210	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSRN	NETPGIRYQY	NVLPQGWKGS
96BW15B03	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BW16_26	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
96BW17A09	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BWM01_5	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
96BWM03_2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
98BWMC12_2	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
98BWMC13_4	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWMC14_a	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWM014_1	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
98BWM018_d	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NATPGIRHQY	NVLPQGWKGS
98BWM036_a	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
98BWM037_d	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
99BW3932_1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NATPGIRYQY	NVLPQGWKGS
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99BW4745_8	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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99BWMC16_8	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A2_CD_97CD	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A2_CY_94CY	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A2D_97KR	TVLDVRDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A2G_CD_97C	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
A_BY_97BL0	TVLDVGDAYF	SVPLDESFRK	XXAFTIPSVN	NETPXIRYQY	NVLPQGWKGS
A_KE_Q23_A	TVLDVGDAYF	SVPLHEEFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A_SE_SE659	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NATPGIRYQX	NVLPQGWKGS
A_SE_SE725	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
A_SE_SE753	TVLDLGDAYF	SVPLHEGFRK	YTAFTIPSTN	NATPGIRYQY	NVLPQGWKGS
A_SE_SE853	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_SE_SE889	TVLDVGDAYF	SVPLDKNFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
A_SE_UGSE8	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_UG_92UG0	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
A_UG_U455	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
AC_IN_2130	TVLDVGDAYF	SVPLYEEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
AC_RW_92RW	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AC_SE_SE94	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ACD_SE_SE8	TILDVGDAYF	SVPLDESFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ACG_BE_VI1	TVLDVGDAYF	SVPLDKFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
AD_SE_SE69	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

AD_SE_SE71	TVLDVGDAYF	SVPLHEEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
ADHK_NO_97	TVLDVGDAYF	SVPLAEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
ADK_CD_MAL	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AG_BE_VI11	TVLDVGDAYF	SVPLDESFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AG_NG_92NG	TVLDVGDAYF	SIPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AGHU_GA_VI	TVLDVGDAYF	SVPLYEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AGU_CD_Z32	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
AJ_BW_BW21	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_AU_VH_AF	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_CN_RL42	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_DE_D31_U	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
B_DE_HAN_U	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_FR_HXB2	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_GA_OYI	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_GB_CAM1	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
B_GB_GB8_A	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_GB_MANC	TVLDVGDAYF	SVPLYEDFRK	YTVFTIPSIN	NEAPGVRYQY	NVLPQGWKGS
B_KR_WK_AF	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
B_NL_3202A	TALDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
B_TW_TWCYS	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_BC_LO	TVLDVGDRYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_DH123	TVLDVGDAYF	SIPLDENFRK	YTAFTIPSVN	NAAPGIRYQY	NVLPQGWKGS
B_US_JRCSE	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_MNCG	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_P896	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_RF_M1	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPRIRYQY	NVLPQGWKGS
B_US_SF2_K	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_WEAU1	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
B_US_WR27	TVLDVGDAYF	SVXLDXEXRK	YTAFTIPSHX	NETPGIRYQY	NVLPQGWKGS
B_US_YU2_M	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGTRYQY	NVLPQGWKGS
BF1_BR_93B	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGLRYQY	NVLPQGWKGS
C_BR_92BR0	TVLDVGDAYF	SVPLDEGFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
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CRF02_AG_F	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
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CRF02_AG_S	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
CRF02_AG_S	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
CRF03_AB_R	TVLDVGDAYF	SVPLDQDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF03_AB_R	TVLDVGDAYF	SVPLDQDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF04_cpx	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS

CRF04_cpx_	TVLDVGDAYF	SVPLDPAFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
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CRF05_DF_B	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSIN	NETPGFRYQY	NVLPQGWKGS
CRF06_cpx_	TVLDVGDAYF	SIPLDEKFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
CRF06_cpx_	TVLDVGDAYF	SIPLDKDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
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D_CD_84ZR0	TVLDVGDAYF	SIPLCEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
D_CD_ELI_K	TVLDVGDAYF	SVPLDEDFRK	YTAFTISSIN	NETPGIRYQY	NVLPQGWKGS
D_CD_NDK_M	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
D_UG_94UG1	TVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
F1_BE_VI85	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
F1_BR_93BR	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSTN	NETPGVRYQY	NVLPQGWKGS
F1_FI_FIN9	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
F1_FR_MP41	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSLN	NETPGIRYQY	NVLPQGWKGS
F2_CM_MP25	TVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
F2KU_BE_VI	TVLDVGDAYF	SVPLDPEFRK	YTAFTIPSVN	NETPGVRYQY	NVLPQGWKGS
G_BE_DRCBL	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSTN	NETPGIRYQY	... PQGWKGS
G_NG_92NG0	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
G_SE_SE616	TVLDVGDAYF	SVPLDEDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
H_BE_VI991	SVLDVGDAYF	SVPLHEDFRK	YTAFTIPSTN	NETPGIRYQY	NVLPQGWKGS
H_BE_VI997	SVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
H_CF_90CF0	SVLDVGDAYF	SVPLDKEFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
J_SE_SE702	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
J_SE_SE788	TVLDVGDAYF	SVPLYEDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
K_CD_EQTB1	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
K_CM_MP535	TVLDVGDAYF	SVPLDKDFRK	YTAFTIPSIN	NETPGVRYQY	NVLPQGWKGS
N_CM_YBF30	TVLDVGDAYF	SCPLDKDFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS
O_CM_ANT70	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
O_CM_MVP51	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGVRYQY	NVLPQGWKGS
O_SN_99SE	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
O_SN_99SE	TVLDVGDAYF	SCPLDPDFRK	YTAFTIPSVN	NETPGIRYQY	NVLPQGWKGS
U_CD_83C	TVLDVGDAYF	SVPLDENFRK	YTAFTIPSIN	NETPGIRYQY	NVLPQGWKGS

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400

00BW0762_1	PAIFQSSMTR	ILEPFRTQNP	EIVIIQYMDD	LYVGSdleig	QHRVKIEELR
00BW0768_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSNLEIG	QHRAKIEELK
00BW0874_2	PAIFQSSMTR	ILEPFRAQNP	ELVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1471_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIQYMDN	LYVRSdleig	QHRAKIEELR
00BW1616_2	PAIFQSSMTK	ILEPFRAKNP	EIVIIQYMDD	LYVGSdleig	QHREKIEELR
00BW1686_8	PAIFQSTMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1759_3	PAIFQSSMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1773_2	PSTFQSSMTK	ILEPFRTQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1783_5	PAIFQSSMTK	ILGPFRTQNP	DIVIIQYMDD	LYVGSdleig	QHRAKIEGLR
00BW1795_6	PAIFQSSMTR	ILEPFRTQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1811_3	PAIFQSSMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW1859_5	PAIFQSSMTR	ILEPFRTQNP	EIVIIQYMDD	LYVESdleig	QHRAKIEELK
00BW1880_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSdlKIG	QHRAKIEELR
00BW1921_1	PAIFQSSMTK	ILEPFRAQNP	DIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW2036_1	PAIFQSSMTK	ILEPFRAKNP	ELVIIQYMDD	LYVGSdleig	QHRARIEELR
00BW2063_6	PAIFQSSMTK	ILEPFRAKNP	DIVIIQYMDD	LYVGSdlDIG	QRREKIEDLR
00BW2087_2	PAIFQCSMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW2127_2	PAIFQSSMTK	ILEPFRAQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW2128_3	PSIFQSSMTK	ILKPFRAQNP	EIVIIQYMDD	LYVGSdleig	QHRAKIOELR
00BW2276_7	PAIFQSSMTR	ILEPFRAQNP	DIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW3819_3	PAIFQCSMTK	ILEPFRAKNP	EIVIIQYMDD	LYVGSdleig	QHRAKIEELR
00BW3842_8	PAIFQSSMTK	ILEPFRAKNP	DIVIIQYMDD	LYVGSdleig	QHRAKIEELR

00BW3871_3	PAIFQSSMTR	ILEPFRTONP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
00BW3876_9	PAVFQSSMTK	ILEPFRVQNP	EIVVYQYMD	LYVGSDEIG	QHRAKIEELR
00BW3886_8	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
00BW3891_6	PAIFQSSMTR	ILEPFRAQNP	GIVIIYQYMD	LYVGSNLEIG	QHRAKIEELR
00BW3970_2	PAIFQSSMTX	ILEPFRARNP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
00BW5031_1	PAIFQSSMTK	ILEPFRAKNP	EIVIIYQYMD	LYVGSDEIV	QHRAKVEELR
96BW01B21	PAIFQSSMTK	ILEPFRALNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW0407	PAIFQSSMTK	ILEPFRTKNP	DILIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW0502	PAIFQSSMTK	ILEPFRQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW06_J4	PAIFQSSMTR	ILEPFRTONP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW11_06	PSIFQSSMTK	ILEPFRAKNP	ELVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW1210	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHTAKIEELR
96BW15B03	PSIFQSSMTK	ILEPFRARNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW16_26	PAIFQSSMTK	ILEPFRAQNP	GIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BW17A09	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BWMO1_5	PAIFQSSMTK	ILEPFRAKNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
96BWMO3_2	PAIFQASMIK	ILEPFRAQNP	EMVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMC12_2	PAIFQSSMTR	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMC13_4	PAIFQCSMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMC14_a	PAIFQSSMTK	ILEPFRARNP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMO14_1	PAIFQCSMTK	ILEPFRAKNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMO18_d	PAIFQSSMTK	ILEPFRTONP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMO36_a	PAIFQSSMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
98BWMO37_d	PAIFQCSMTR	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
99BW3932_1	PAIFQSSMTK	ILKPFREQNP	EMVIIYQYMD	LYVGSDEIG	QHTAKIEELR
99BW4642_4	PAIFQSSMTR	ILEPFRQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
99BW4745_8	PAIFQSSMTK	ILEPFRAKNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
99BW4754_7	PAIFQSSMTK	ILEPFRAQNP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
99BWMC16_8	PAIFQSSMTK	ILEPFRTKNP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
A2_CD_97CD	PAIFQSSMTK	ILDPFRARNP	EMVIIYQYMD	LYVGSDEID	QHRAKIEELR
A2_CY_94CY	PAIFQSSMTK	ILEPFRSKNP	ELIIYQYMD	LYVGSDEIS	QHRVKIEELR
A2D_97KR	PAIFQSSMTK	ILEPFRKQNP	EIVIIYQYMD	LYVGSDEIG	QHRTKIEELR
A2G_CD_97C	PAIFQSSMTK	ILEPFRADNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
A_BY_97BL0	PSIFQSSMTK	ILEPFRKQNP	EIVIIYQYMD	LYVGSDEIG	QHRTKIEELR
A_KE_Q23_A	PAIFQSSMTK	ILEPFRSKNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
A_SE_SE659	PAIFQSSMTK	ILEPFRSKNP	DIIIIYQYMD	LYVGSDEIG	QHRAKIEELR
A_SE_SE725	PAIFQSSMTK	ILEPFRKQNP	EIIIIYQYMD	LYVGSDEIG	QHRTKIEELR
A_SE_SE753	PAIFQSSMTK	ILEPFRERNP	EVIIYQYMD	LYVGSDEIG	QHRTKIEELR
A_SE_SE853	PSIFQSSMTK	ILEPFRSKNP	EIIIIYQYMD	LYVGSDEIG	QHRTKIEELR
A_SE_SE889	PAIFQSSMIK	ILEPFRVQNP	EIIIIYQYMD	LYVGSDEIG	QHRAKIEELR
A_SE_UGSE8	PAIFQSSMTK	ILEPFRSKNP	EIIIIYQYMD	LYVGSDEIE	QHRTKIEELR
A_UG_92UG0	PAIFQASMTK	ILEPFRSKNP	DIVIIYQYMD	LYVGSDEIG	QHRTKIEELR
A_UG_U455_	PSIFQSSMTK	ILEPFRSQHP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AC_IN_2130	PAIFQASMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AC_RW_92RW	PAIFQNSMTK	ILEPFRAQNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AC_SE_SE94	PAIFQSSMTK	ILAPFRSQNP	EIIIIYQYMD	LYVGSDEIG	QHRTKIEELR
ACD_SE_SE8	PAIFQSSMTK	ILEPFRSKNP	DMIIYQYMD	LYVGSDEIG	QHRTKIEELR
ACG_BE_VI1	PAIFQASMTK	ILDPFRREN	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AD_SE_SE69	PAIFQSSMTK	ILEPFRKQNP	EMVIIYQYMD	LYVGSDEIG	QHRKIEELR
AD_SE_SE71	PAIFQSSMTK	ILEPFRSKNP	ELIIYQYMD	LYVGSDEIG	QHRKIEELR
ADHK_NO_97	PAIFQCSMTK	ILEPFRAKNP	EIVIIYQYMD	LYVGSDEIG	QHRTKIEELR
ADK_CD_MAL	PAIFQSSMTK	ILEPFRTKNP	EIVIIYQYMD	LYVGSDEIG	QHRTKIEELR
AG_BE_VI11	PAIFQASMTK	ILEPFRTENP	KIVIIYQYMD	LYVGSDEIG	QHRAKIDELR
AG_NG_92NG	PAIFQSSMTK	ILEPFRTENP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AGHU_GA_VI	PAIFQSSMTK	ILEPFRKQNP	EMVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AGU_CD_Z32	PAIFQSSMTK	ILEPFRTKNP	EIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
AJ_BW_BW21	PAIFQYMTK	ILEPFRANP	EIVIIYQYMD	LYVGSDEIG	QHRTKIEELR
B_AU_VH_AF	PAIFQSSMTK	ILEPFRKQNP	DVVIYQYMD	LYVGSDEIG	QHRTKIEELR
B_CN_RL42_	PAIFQCSMTK	ILEPFRKQNP	DIVIIYQYMD	LYVGSDEIG	QHRAKIEELR
B_DE_D31_U	PAIFQSSMTK	ILEPFRKQNP	DIVIIYQYMD	LYVGSDEIG	QHRTKIEELR

[illegible]

D_CD_ELI_K	PAIFQSSMTK	ILEPFRKQNP	EMVIYQYMD	LYVGSLEIG	QHRTKIEKL
D_CD_NDK_M	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSLEIG	QHRTKIEBL
D_UG_94UG1	PAIFQSSMTK	ILEPFRKQNP	EMIIYQYMD	LYVGSLEIG	QHRKIEBL
F1_BE_VI85	PAIFQCSMTK	ILEPFRMKNP	DIVYQYMD	LYVGSLEIG	QHRTKIEBL
F1_BR_93BR	PAIFQYSMTK	ILDPFRKQNP	DIVYQYMD	LYVGSLEIG	QHRTKIEBL
F1_FI_FIN9	PAIFQCSMTK	ILEPFRTRNP	DIVYQYMD	LYVGSLEIG	QHRTKIEBL
F1_FR_MP41	PAIFQSSMTK	ILEPFRKQNP	DIVYQYMD	LYVGSLEIG	QHRMKIEBL
F2_CM_MP25	PAIFQSSMTK	ILEPFRKENP	EIVYQYMD	LYVGSLEIG	QHRKIEBL
F2KU_BE_VI	PAIFQYSMTK	ILEPFRTRNP	EMVIYQYMD	LYVGSLEIG	QHRTKIEBL
G_BE_DRCBL	PAIFQSSMTK	ILEPFRTRNP	EIVYQYMD	LYVGSLEIG	QHRKIEBL
G_NG_92NG0	PAIFQSSMTK	ILEPSRTKNP	EMVIYQYMD	LYVGSLEIG	QHRKIEBL
G_SE_SE616	PAIFQSSMTK	ILEPFRANNP	EMVIYQYMD	LYVGSLEIG	QHRKIEBL
H_BE_VI991	PAIFQSSMTK	ILEPFRKQNP	EIVYQYMD	LYVGSLEIG	QHRKIEBL
H_BE_VI997	PAIFQSSMTK	ILEPFRKQNP	EIIIYQYMD	LYVGSLEIG	QHRKIEBL
H_CF_90CF0	PAIFQSSMTK	ILAPFRBQNP	EMVIYQYMD	LYVGSLEIG	QHRKIEBL
J_SE_SE702	PAIFQCSMTK	ILKPFRRNP	EIVYQYMD	LYVGSLEIG	QHRKIEBL
J_SE_SE788	PAIFQCSMTK	ILKPFRRNP	EIVYQYMD	LYVGSLEIG	QHRKIEBL
K_CD_EQTB1	PAIFQCSMTK	ILEPFRKQNP	DMVLYQYMD	LYVGSLEIG	QHRKIEBL
K_CM_MP535	PAIFQHSMTK	ILEPFRKQNP	EMVIYQYMD	LYVGSLEIG	QPRTKIEBL
N_CM_YBF30	PAIFQSTMTK	ILEPFRKQNP	EIIIYQYMD	LYVGSLEIG	QHRKIEBL
O_CM_ANT70	PAIFQSSMTK	ILDPFRDNP	ELEICQYMD	LYVGSLEIG	QHRKIEBL
O_CM_MVP51	PAIFQSSMTK	ILDPFRKQNP	EVEIYQYMD	LYVGSLEIG	QHRKIEBL
O_SN_99SE	PAIFQSSMTK	ILDPFRKQNP	ELEICQYMD	LYVGSLEIG	QHRKIEBL
O_SN_99SE	PAIFQSSMTK	ILDPFRKQNP	ELEICQYMD	LYVGSLEIG	QHRKIEBL
U_CD_83C	PAIFQSSMTK	ILEPFRKENP	EIVYQYMD	LYVGSLEIG	QHRKIEBL

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00BW0762_1	RHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
00BW0768_2	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKNSWTVND
00BW0874_2	AHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1471_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1616_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1686_8	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1759_3	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PTKESWTVND
00BW1773_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1783_5	NHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1795_6	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1811_3	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PRKD.STVND
00BW1859_5	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW1880_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
00BW1921_1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW2036_1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW2063_6	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW2087_2	GHLLQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2127_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2128_3	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW2276_7	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3819_3	GHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
00BW3842_8	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW3871_3	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW3876_9	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW3886_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW3891_6	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW3970_2	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
00BW5031_1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW01B21	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
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96BW0502	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW06_J4	NHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW11_06	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND

96BW1210	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW15B03	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
96BW16_26	THLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BW17A09	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
96BWMO1_5	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DQWTVQPIQL	PEKESWTVND
96BWMO3_2	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	AEKDSWTVND
98BWMC12_2	IHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTIQPIQL	PEKDSWTVND
98BWMC13_4	RHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
98BWMC14_a	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PTKDSWTVND
98BWMO14_1	GHLLQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
98BWMO18_d	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
98BWMO36_a	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
98BWMO37_d	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW3932_1	DHLLGWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
99BW4642_4	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW4745_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
99BW4754_7	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKESWTVND
99BWMC16_8	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PTKDSWTVND
A2_CD_97CD	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDSWTVND
A2_CY_94CY	AHLLKWGFYT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDSWTVND
A2D_97KR	NHLLKWGFYT	PDKKHQKEPP	FLWMEYELHP	DKWTVQPIKL	PEKDSWTVND
A2G_CD_97C	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
A_BY_97BL0	AHLLSWGFTT	PDKKHQKEPP	FLWXXYEXHP	DKWTVQPIML	PDKDSWTVND
A_KE_Q23_A	AHLLSWGLIT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
A_SE_SE659	SHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKESWTVND
A_SE_SE725	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
A_SE_SE753	EHLLSWGFTT	PDKKHQKEPP	FLWMGYEVHP	DKWTVQPIVL	PEKESWTVND
A_SE_SE853	AHLLSWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
A_SE_SE889	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKENWTVND
A_SE_UGSE8	AHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
A_UG_92UG0	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
A_UG_U455	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_IN_2130	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_RW_92RW	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AC_SE_SE94	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
ACD_SE_SE8	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
ACG_BE_VI1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AD_SE_SE69	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKESWTVND
AD_SE_SE71	EHLLKWGFYT	PDQKHQKEPP	FLWMGYELHP	DRWTVQPIKL	PEKESWTVND
ADHK_NO_97	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
ADK_CD_MAL	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
AG_BE_VI11	EHLLRWGLTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
AG_NG_92NG	NHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKESWTVND
AGHU_GA_VI	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTVKL	PEKDSWTVND
AGU_CD_Z32	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
AJ_BW_BW21	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEAWTVND
B_AU_VH_AF	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_CN_RL42	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHL	DKWTVQPIML	PEKDSWTVND
B_DE_D31_U	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_DE_HAN_U	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_FR_HXB2	QHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_GA_OYI	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_GB_CAM1	QHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_GB_GB8_A	QHLLRWGFST	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_GB_MANC	QYLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_KR_WK_AF	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_NL_3202A	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_TW_TWCYS	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_BC_L0	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_DH123	QHLLRWGLFT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND

B_US_JRCSE	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_MNCG	RHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_P896	QHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_RF_M1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
B_US_SF2_K	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
B_US_WEAU1	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKESWTVND
B_US_WR27	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
B_US_YU2_M	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
BF1_BR_93B	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
C_BR_92BR0	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_BW_96BW0	EHLLKWGLTT	PYKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
C_BW_96BW1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
C_BW_96BW1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKESWTVND
C_BW_96BW1	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKESWTVND
C_ET_ETH22	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN9	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_93IN9	QHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_94IN1	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
C_IN_95IN2	KHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF01_AE_C	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_C	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIVL	PEKDSWTVND
CRF01_AE_C	AHLLSWGFTT	PDKKHQKESP	FLWMGYELHP	DRWTVQPIQL	PDKESWTVDD
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDQKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PDKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF01_AE_T	AHLLSWGFTT	PGKKHQKEPP	FLWMGYELHP	DRWTVQPIEL	PEKDSWTVND
CRF02_AG_F	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF02_AG_F	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF02_AG_G	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIML	PEKDSWTVND
CRF02_AG_N	GHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIEL	PEKDSWTVND
CRF02_AG_S	EHLLRWGFTT	PDEKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF02_AG_S	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF03_AB_R	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF03_AB_R	DHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIVL	PEKDSWTVND
CRF04_cpx	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQP	AEKDSWTVND
CRF04_cpx	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
CRF04_cpx	EHLLRWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPIQL	VEKESWTVND
CRF05_DF_B	EHLLAWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF05_DF_B	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDSWTVND
CRF06_cpx	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
CRF06_cpx	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKESWSIND
CRF06_cpx	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF06_cpx	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
CRF11_cpx	KHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKECWTVND
CRF11_cpx	KHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKESWTVND
D_CD_84ZR0	EHLLRWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSITL	PEKESWTVND
D_CD_ELI_K	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIKL	PEKESWTVND
D_CD_NDK_M	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPINL	PEKESWTVND
D_UG_94UG1	GHLLKWGFTT	PDKKYQKEPP	FLWMGYELHP	DKWTVQPIHL	PEKESWTVND
F1_BE_VI85	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDSWTVND
F1_BR_93BR	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVND
F1_FI_FIN9	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKDSWTVDD
F1_FR_MP41	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKDSWTVND
F2_CM_MP25	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQAIQL	PDKSSWTVND
F2KU_BE_VI	EHLLRWGFTT	PDEKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEDWTVND
G_BE_DRCBL	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKENWTVND
G_NG_92NG0	EHLLKWGLTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND

G_SE_SE616	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PKESWTVND
H_BE_VI991	AHLLRWGFTT	PDQKHQKEPP	FLWMGYELHP	DKWTVQPVKL	PEKDSWTVND
H_BE_VI997	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPVKL	PEKDSWTVND
H_CF_90CF0	AHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQTVKL	PEKDSWTVND
J_SE_SE702	EHLLKWGFYT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
J_SE_SE788	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PEKEDWTVND
K_CD_EQTB1	EHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PKDSWTVND
K_CM_MP535	EHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PKDSWTVND
N_CM_YBF30	DHLLKWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIKL	PEKDVWTVND
O_CM_ANT70	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQSIQL	PNKDVWTVND
O_CM_MVP51	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PDKEVWTVND
O_SN_99SE	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKEEWTVND
O_SN_99SE	EHLYQWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKEEWTVND
U_CD_83C	AHLLRWGFTT	PDKKHQKEPP	FLWMGYELHP	DKWTVQPIQL	PNKDDWTVND

451

500

00BW0762_1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW0768_2	IQKLVGKLNW	ASQIYPGIKV	RQLCRLLRGA	KVLTDIVPLT	EEAELELAEN
00BW0874_2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW1471_2	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1616_2	IQKLVGKLNW	ASQIYPGVKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW1686_8	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW1759_3	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1773_2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1783_5	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1795_6	IQKLVGKLNW	ASQIYPGIKV	TQLCKLLRGA	KALTDIVPLT	DEAELELAEN
00BW1811_3	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGT	KALTDIVPLT	DEAELELAEN
00BW1859_5	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW1880_2	IQKLVGKLNW	ASQIYKGIKV	KQLCKLLRGA	KALTDIVPLP	EEAELELAEN
00BW1921_1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW2036_1	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW2063_6	IQKLVGKLNW	ASQIYPGIKV	TQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW2087_2	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW2127_2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW2128_3	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIIPLT	EEAELELAEN
00BW2276_7	IQKLVGKLNW	VSQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3819_3	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
00BW3842_8	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIIPLT	EEAELELAEN
00BW3871_3	LQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
00BW3876_9	IQKLVGKLNW	ASQIYPGIKV	RHLCKLLRGA	KALTEIVPLT	EEAELELAEN
00BW3886_8	IQKLVGKLNW	ASQIYTGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
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96BW01B21	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW0407	IQKLVGKLNW	ASQIYPGIRV	RHLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW0502	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW06_J4	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLN	EEAELELAEN
96BW11_06	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BW1210	IQKLVGKLNW	ASQIYPGIKV	RQLCKILRGV	KALTDIVTLT	EEAELELAEN
96BW15B03	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAED
96BW16_26	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIIPLT	EEAELELAEN
96BW17A09	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
96BWM01_5	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	DEAELELAEN
96BWM03_2	VQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC12_2	IQRLVGKLNW	ASQIYSGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC13_4	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWMC14_a	IQKLVGKLNW	ASQNYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
98BWM014_1	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWM018_d	IQKLVGKLNW	ASQIYPGIKV	RQLCKLIRGT	KKLTDIVPLT	EEAELELAEN

98BWM036_a	IQKLVGKLNW	ASQIYPGIKV	KNLCKLLRGA	KALTDIVPLT	EEAELELAEN
98BWM037_d	IQELVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
99BW3932_1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
99BW4642_4	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
99BW4745_8	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
99BW4754_7	IQKLVGKLNW	ASQIYPGIQV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
99BWMC16_8	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
A2_CD_97CD	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
A2_CY_94CY	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	KEAELELEEN
A2D_97KR	IQKLVGKLNW	ASQIYAEIKV	KQLCKLLRGA	KALTDIVPLT	KEAELELEEN
A2G_CD_97C	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEIVSLT	AEAELELAEN
A_BY_97BL0	IQKLXGKLNW	ASQIYPEIKV	RQLCKLLXGA	KALTDIVTLT	EEAELELAEN
A_KE_Q23_A	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDVVTLT	EEAELELAEN
A_SE_SE659	IQKLVGKLNW	ASQIYPGIKV	KQLCRLRGA	KALTDIVELT	EEAELELAEN
A_SE_SE725	IQKLVGKLNW	ASQIYAGIKV	KQLCRLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE753	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE853	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_SE889	IQKLVGKLNW	ASQIYVGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_SE_UGSE8	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
A_UG_92UG0	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVTLT	EEAELELAEN
A_UG_U455	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
AC_IN_2130	IQKLVGKLNW	ASQIYPGIKV	RQLCRLRGA	KALTDIVPLT	EEAELELAEN
AC_RW_92RW	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
AC_SE_SE94	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KSLTDVVTLT	EEAELELAEN
ACD_SE_SE8	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDVVTLT	EEAELELAEN
ACG_BE_VI1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AD_SE_SE69	IQKLVGKLNW	ASQIYPGIKV	RQLCKCIRGA	KALTEVVPLT	EEAELELAEN
AD_SE_SE71	IQKLVGKLNW	ASQIYAGIKV	KQLCKCLRGA	KALTEIVPLT	EEAELELAEN
ADHK_NO_97	IQKLVGKLNW	ASQIYPGIKV	RQLCRLRGT	KALTDIVPLT	AEAELELAEN
ADK_CD_MAL	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
AG_BE_VI11	IQKLVGKLNW	ASQIYAGIRV	KQLCKLLRGA	KALTDIVTLT	EEAELELAEN
AG_NG_92NG	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AGHU_GA_VI	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
AGU_CD_Z32	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
AJ_BW_BW21	IQKLVGKLNW	ASQIYPGIQV	RHLCRLRGA	KALTDIVPLT	AEAELELAEN
B_AU_VH_AF	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_CN_RL42	IQKLVGKLNW	ASQIYAGIKV	KELCKLLRGT	KALTEVIPLT	EEAELELAEN
B_DE_D31_U	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEVIPLT	KEAELELAEN
B_DE_HAN_U	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGP	KALTEVIPLT	KEAELELAEN
B_FR_HXB2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_GA_OYI	IQKLVGKLNW	ASQIYAGIKV	KNLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_GB_CAM1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_GB_GB8_A	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTEVITLT	EEAELELAEN
B_GB_MANC	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTEVIPLT	KEAELELAEN
B_KR_WK_AF	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_NL_3202A	IQKLVGKLNW	ASQIYAGIKV	RHLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_TW_TWCYS	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVVPLT	KEAELELAEN
B_US_BC_L0	IQKLVGKLNW	ASQIYSGIKV	KQLCKLLRGT	KALTEVVTLT	EEAELELAEN
B_US_DH123	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTEVIPLT	EEAELELAEN
B_US_JRCSF	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	KEAELELAEN
B_US_MNCG	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_US_P896	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
B_US_RF_M1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVQLT	KEAELELAEN
B_US_SF2_K	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
B_US_WEAU1	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEIIPIT	EEAELELAEN
B_US_WR27	IQKLVGKLNW	XSQIYAGIKV	XQLCKLLRGT	KALTEVVPLT	EEAELELAGN
B_US_YU2_M	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
BF1_BR_93B	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGT	KALTEVVPLT	AEAELELAEN
C_BR_92BR0	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_BW_96BW0	IQKLVGKLNW	ASQIYPGIRV	KHLCKLLRGA	KALTDIVPLT	EEAELELAEN

C_BW_96BW1	IQKLVGKLNW	ASQIYPGVKV	RQLCKLLRGA	KALTDIVPPT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGIKV	RQLCKILRGV	KALTDIVTLT	EEAELELAEN
C_BW_96BW1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAED
C_ET_ETH22	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
C_IN_93IN1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_93IN9	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_93IN9	IQKLVGKLNW	ASQIYPGIKV	KQLCRLLRGA	KVLTDIVPLT	EEAELELAEN
C_IN_94IN1	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	EEAELELAEN
C_IN_95IN2	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTEVVPLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTDIVTLT	EEAELELAEN
CRF01_AE_C	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKPLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF01_AE_T	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_F	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_F	IQKLVGKLNW	ASQIFAGIKV	KQLCRLLRGA	KALTDIVPLT	EEAELELAEN
CRF02_AG_G	IQKLVGKLNW	ASQIYAGIKV	KELCKLLRGA	KALTDIVTLT	EEAELELAEN
CRF02_AG_N	IQKLVGKLNW	ASQIYAGIKI	KQLCRLLRGA	KALTDIVALT	EEAELELAEN
CRF02_AG_S	IQKLVGKLNW	QVRIYAGIKV	KQLCKLLRGA	KTLTDIVTLT	EEAELELAEN
CRF02_AG_S	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	EEAELELAEN
CRF03_AB_R	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEVIPLT	AEAELELAEN
CRF03_AB_R	IQKLVGKLNW	ASQIYAGIKV	RQLCKLLRGA	KALTEIIPLT	AEAELELAEN
CRF04_cpx	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
CRF04_cpx	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	TEAELELAEN
CRF04_cpx	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
CRF05_DF_B	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
CRF05_DF_B	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
CRF06_cpx	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx	IQKLVGKLNW	ASQIYSGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx	IQKLVGKLNW	ASQIYPGIKV	KHLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF06_cpx	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
CRF11_cpx	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
CRF11_cpx	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGA	KALTDIVPLT	AEAELELAEN
D_CD_84ZRO	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTEVIPLT	EEAELELAEN
D_CD_ELI_K	IQNLVERLNW	ASQIYPGIKV	RQLCKLLRGT	KALTEVIPLT	EEAELELAEN
D_CD_NDK_M	IQKLVGKLNW	ASQIYAGIKV	KQLCKLLRGT	KALTEVVPLT	EEAELELAEN
D_UG_94UG1	IQKLVGKLNW	ASQIYPGIKV	RQLCKCLRGA	KALTEVIPLT	AEAELELAEN
F1_BE_VI85	IQKLVGKLNW	ASQIYPGIKV	RPLCKLLRGA	KALTDIVPLT	AEAELELAEN
F1_BR_93BR	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVPLT	TEAELELAEN
F1_FI_FIN9	IQKLVGKLNW	ASXIYPGIKV	RQLCKLLRGA	KALTDIVPLT	AEAELELAEN
F1_FR_MP41	IQKLVGKLNW	ASQIYPGIKI	KQLCKLLRGA	KALTDIVPLT	EEAELELAEN
F2_CM_MP25	IQKLVGKLNW	ASQIYPGIRV	KHLCKLLRGT	KALTDIVPLT	AEAELELAEN
F2KU_BE_VI	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KTLTDIVPLT	AEAELELAEN
G_BE_DRCBL	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGA	KALTDIVSMT	AEAELELAEN
G_NG_92NG0	IQKLVGKLNW	ASQIYPGIKV	KHLCKLLRGA	KALTDIVPLT	AEAELELAEN
G_SE_SE616	IQKLVGKLNW	ASQIYPGIKV	THLCKLLRGA	KALTDIVSLT	AEAELELAEN
H_BE_VI991	IQKLVGKLNW	ASQIYPGIKV	KQLCXLLRGA	KALTEIVPLT	KEAELELAEN
H_BE_VI997	IQKLVGKLNW	ASQIYPGIKV	RQLCKLLRGA	KALTDIVPLT	KEAELELAEN
H_CF_90CF0	IQKLVGKLNW	ASQIYPNIKV	KQLCKLLRGA	KALTDIIPLT	KEAELELAEN
J_SE_SE702	IQKLVGKLNW	ASQIYPGIKI	KELCKLLRGA	KALTDIVPLT	REAELELAEN
J_SE_SE788	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLKGA	KALTDIVPLT	REAELELAEN
K_CD_EQTB1	IQKLVGKLNW	ASQIFPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
K_CM_MP535	IQKLVGKLNW	ASQIYPGIKV	KQLCKLLRGT	KALTDIVPLT	AEAELELAEN
N_CM_YBF30	IQKLVGKLNW	ASQIYPGIRV	KQLCKLLRGT	KALTEVVNFT	EEAELELAEN
O_CM_ANT70	IQKLVGKLNW	ASQIYQGIRV	RELCKLLRGT	KSLTEVVPLS	REAELELAEN
O_CM_MVP51	IQKLVGKLNW	ASQIYQGIRV	KELCKLLRGT	KSLTEVVPLS	KEAELELAEN

O_SN_99SE	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGA	KSLTEIVPLS	KEAELELEEN
O_SN_99SE	IQKLVGKLNW	ASQIYQGIRV	KELCKLIRGT	KSLTEVVPLS	KEAELELEEN
U_CD_83C	IQKLVGKLNW	ASQIYPGIQV	RQLCKLLRGT	KALTDIVPMT	KEAELELAEN

501

550

00BW0762_1	R.EILKEPVH	GVYYDPSKDL	IADIQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW0768_2	R.EILREPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
00BW0874_2	R.EILREPVH	GVYYDPSKDL	VAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
00BW1471_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1616_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1686_8	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1759_3	R.EILKEPVH	GVYYDPSKEL	IAELQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW1773_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1783_5	R.EILKEPVH	GVYYDPSKDL	KA EIQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW1795_6	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1811_3	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1859_5	R.EILKEPVH	EVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW1880_2	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGD	QWTYQIYQEP	LKNLKTGKYA
00BW1921_1	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGD	QWSYQIYQEP	FKNLKTGKYA
00BW2036_1	R.EILRGPVH	GVYYDPSKDL	VAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW2063_6	R.EILREPVH	GVYYDPSKDL	VAEIQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW2087_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW2127_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW2128_3	R.EILKEPVH	GVYYDSSKEL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW2276_7	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW3819_3	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW3842_8	R.EILREPVH	GVYYDPSKDL	VAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
00BW3871_3	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW3876_9	RXEILKEPVH	GVYYDPSKDL	IAEIQKQGY	QWTYQIYQEP	YKNLKTGKYA
00BW3886_8	R.EILKGPVH	GVYYDPSKDL	IAEIQKQGG	QWTYQIYQEP	FKNLKTGKYA
00BW3891_6	R.EILKEPVH	GVYYDPSKDL	IAEIQKQNG	QWTYQIYQEP	FKNLKTGKYA
00BW3970_2	R.EILREPVH	GVYYDPSKDL	IAEIQKQGN	QWTYQIYQEP	FKNLKTGKYA
00BW5031_1	R.EILREPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
96BW01B21	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW0407	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW0502	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW06_J4	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
96BW11_06	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
96BW1210	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW15B03	R.EILREPVH	GVYYDPSKDL	VAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW16_26	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BW17A09	R.EILKEPVH	GAYYDPSKDL	IAEIQKQNG	QWTYQIYQEP	FKNLKTGKYA
96BWM01_5	R.EILREPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
96BWM03_2	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGD	QWTYQIYQEP	HKNLKTGKYA
98BWMC12_2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGY	QWTYQIYQEP	FKNLKTGKYA
98BWMC13_4	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGL	QWTYQIYQEP	FKNLKTGKYA
98BWMC14_a	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGN	QWTYQIYQEP	FKNLKTGKYA
98BWM014_1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
98BWM018_d	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
98BWM036_a	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
98BWM037_d	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
99BW3932_1	R.ELLKEPVH	GVYYDPSKDL	ITEIQKQGH	QWTYQIYQEP	FKNLKTGKYA
99BW4642_4	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGC	QWTYQIYQEP	FKNLKTGKYA
99BW4745_8	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGN	QWTYQIYQEP	FKNLKTGKYA
99BW4754_7	R.EILKEPVH	GVYYDPSKDL	IAEIQKQNG	QWTYQIYQEP	FKNLKTGKYA
99BWMC16_8	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGN	QWTYQIYQEP	FKNLKTGKYA
A2_CD_97CD	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGG	QWSYQIYQEP	FKNLKTGKYA
A2_CY_94CY	R.EILKTPVH	GVYYDPSKDL	IAEIQKQGD	QWTYQIYQEP	FKNLKTGKYA
A2D_97KR	R.EILKDPVH	GVYYDPSKDL	IAEVQKQGP	QWTYQIYQEP	FKNLKTGKYA
A2G_CD_97C	R.EILKEPVH	GAYYBPSKEL	IAEVQKQGL	QWTYQIYQEP	YKNLKTGKYA

A_BY_97BL0	R.EILKXPVH	XVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
A_KE_Q23_A	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIFQEP	FKNLKTGKYA
A_SE_SE659	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE725	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGLD	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE753	R.EILKDPVH	GAYYDPSKDL	IVEIQKQGQD	QWTYQIYQET	FKNLKTGKYA
A_SE_SE853	R.EILKAPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
A_SE_SE889	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
A_SE_UGSE8	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
A_UG_92UG0	R.EILKDPVH	GAYYDPSKDL	IAEIQKQGQD	QWIYQIYQEP	FKNLKTGKYA
A_UG_U455_	R.EILKDPVH	GVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
AC_IN_2130	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
AC_RW_92RW	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
AC_SE_SE94	R.EILRDPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
ACD_SE_SE8	R.EILKDPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
ACG_BE_VI1	R.EILKEPVH	GVYYDPAKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
AD_SE_SE69	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEQ	YKNLKTGKYA
AD_SE_SE71	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWSYQIYQEQ	YKNLKTGKYA
ADHK_NO_97	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGRG	QWTYQIYQEP	YKNLKTGKYA
ADK_CD_MAL	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEQ	YKNLKTGKYA
AG_BE_VI11	R.EILKEPVH	GVYYDPGKEL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
AG_NG_92NG	R.EILKEPVH	GVYYDPSKEL	IAELQKQGCD	QWTYQIYQEP	YKNLKTGKYA
AGHU_GA_VI	R.EILKEPVH	GVYYDPSKDL	VAEVQKQGPD	QWTYQIYQEP	FKILKTGKYA
AGU_CD_Z32	R.EILKEPVH	GVYYDSKSEL	IAEVQKQGLN	QWTYQIYQEP	FKNLKTGKYA
AJ_BW_BW21	R.EILKEPVH	GVYYDSAKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
B_AU_VH_AF	R.EILKEPVH	GVYYDPSKDL	IAEVQKQEQG	QWTYQIYQEP	FKNLKTGKYA
B_CN_RL42_	R.EILKESVH	GVYYDPSKDL	IAEIQKQGLG	QWTYQIYQEP	YKNLKTGKYA
B_DE_D31_U	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_DE_HAN_U	R.EILKEPVH	GVYCDPSKDL	VAEIQKQGEQ	QWTYQIYQEP	FKNLKTGKYA
B_FR_HXB2_	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_GA_OYI_	R.EILKEPVH	GVYYDPSKDL	VAELQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_GB_CAM1_	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_GB_GB8_A	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGLG	QWTYQIYQEP	FKNLKTGKYA
B_GB_MANC_	R.EILKVPVH	GVYYDPSKDL	TAEIQKQGQD	QWTYQIYQEP	FRSLKTGKYA
B_KR_WK_AF	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_NL_3202A	R.EILKEPVH	GVYYDPSKEL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_TW_TWCYS	R.EILKQPVH	GAYYDPSKDL	VAEIQKQGQD	QWTYQIYQET	FKNLKTGKYA
B_US_BC_L0	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTAKYA
B_US_DH123	R.EILKEPVH	GVYYDPSKDI	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_US_JRCSF	R.EILKEPVH	GVYYDPSKDL	IVEIQKQGQD	QWTYQIFQEP	FKNLKTGKYA
B_US_MNCG_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_US_P896_	R.EILKEPVH	GVYYDPTKDL	IAELQKQGQD	QWTYQIYQEP	YKNLKTGKYA
B_US_RF_M1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_US_SF2_K	R.EILKEPVH	EVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_US_WEAU1	R.EILKEPVH	GVYYDPSKDL	IAELQKQGQD	QWTYQIYQEP	FKNLKTGKYA
B_US_WR27_	R.EILKEPVH	GVYYDPSKDL	VAELQKQGQD	QWTYQIYQEP	FIXLXTGKYA
B_US_YU2_M	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
BF1_BR_93B	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	YKNLKTGKYA
C_BR_92BR0	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW0	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGHG	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
C_BW_96BW1	R.EILREPVH	GVYYDPSKDL	VAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
C_BT_BTH22	R.EILKEPVH	GVFYDPSKDL	IAEIQKQGND	QWTFQFYQEP	FKNLKTGKFA
C_IN_93IN1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
C_IN_93IN9	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQVYQEP	FKNLKTGKYA
C_IN_93IN9	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
C_IN_94IN1	R.EILKEPIH	GVYYDPSKDL	IAEIQKQGQD	QWTYQVYQEP	FKNLKTGKYA
C_IN_95IN2	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKNPVH	GVYYDPSKEL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_C	R.EILKTPVH	GVYYDPSKDL	VAEIQKQGQD	QWTYQIYQEP	FKNLKTGKYA

CRF01_AE_C	R.EILKNPVH	GVYYDPSKDL	VAEIQKQGHN	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILRTPVH	GVYYDPSKDL	VAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILRIPVH	GVYYDPSKDL	VAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYS
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	AAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF01_AE_T	R.EILKTPVH	GVYYDPSKDL	VAEVQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_F	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_F	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_G	R.EILKEPVH	GVYYDPTKDL	IAEIQKQGGD	QWTFQIYQEP	FKNLKTGKYQ
CRF02_AG_N	R.EILKEPVH	GVYYDPTKDL	VAELQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_S	R.EILKEPVH	GVYYDPTKDL	VAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF02_AG_S	R.EILKEPVH	GVYYDPTKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
CRF03_AB_R	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGGG	QWTYQIYQEP	FKNLKTGKYA
CRF03_AB_R	R.EILKVPVH	GVYYDPSKDL	VAEIQKQGGG	QWTYQIYQEP	FKNLKTGKYA
CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGGG	QWTYQIYQEP	HKNLKTGKYA
CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAKIQKQGGG	QWTYQIYQEP	YKNLKTGKYA
CRF04_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGLG	QXTYQIYQEP	YKNLKTGKYA
CRF05_DF_B	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLG	QWTYQIYQEP	FKNLKTGKYA
CRF05_DF_B	R.EILKEPVH	GVYYDPAKDL	IAEIQKQGGG	QWTYQIYQEP	FKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGGY	QWTYQIYQEP	HKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGGG	QWTYQIYQEP	HKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GVYYDPLKDL	IAELQKQGGG	QWTYQIYQEP	HKNLKTGKYA
CRF06_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGG	QWTYQIYQDT	HKNLKTGKYA
CRF11_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
CRF11_cpx_	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
D_CD_84ZR0	R.EILKEPMH	GVYYDPSKDL	IAELQKQGGG	QWTYQIYQEP	FKNLKTGKYA
D_CD_ELI_K	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	FKNLKTGKYA
D_CD_NDK_M	R.EILKEPVH	GVYYDPSKDL	IAELQKQGGG	QWTYQIYQEP	FKNLKTGKYA
D_UG_94UG1	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGGD	QWTYQIYQEQ	YKNLKTGKYA
F1_BE_VI85	R.EILREPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQNP	FKNLKTGKYA
F1_BR_93BR	R.EILKEPVH	GAYYDPSKDL	IAEIQKQGGG	QWTYQIYQEP	FKNLKTGKYA
F1_FI_FIN9	R.EILKEPVH	GVYYDPSKDL	IPKLQKQGGG	QWTYQIYREP	FKNLKTGKYA
F1_FR_MP41	R.EILKEPVH	GVYYDPSKDL	IAELQKQGGG	QWTYQIYQEP	FKNLKTGKYA
F2_CM_MP25	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	HKNLKTGKYA
F2KU_BE_VI	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGGG	QWTYQIYQEP	YKNLKTGKYA
G_BE_DRCBL	R.EILKEPVH	GVYYDPSKDL	IAEVQKQGLG	QWTYQVYQEP	YKNLKTGKYA
G_NG_92NG0	R.EILKEPVH	GVYHDPSKEL	IAEVQKQGGD	QWTYQIYQEP	YKNLKTGKYA
G_SE_SE616	R.EILREPVH	GVYYDPSKEL	IAEVQKQGLD	QWTYQIYQEP	YKNLKTGKYA
H_BE_VI991	R.EILKEPVH	GAYYDPSKEL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
H_BE_VI997	R.EILREPVH	GVYYDPSKDL	IAEIQKQGGD	QWTYQIYQEP	FKNLKTGKYA
H_CF_90CF0	R.EILREPIH	GVYYDPSKDL	IAEIRKQGGG	QWTYQIYQEP	FKNLKTGKYA
J_SE_SE702	K.EILKEPVH	GVYYDPAREL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
J_SE_SE788	K.EILKEPVH	GVYYDSAKEL	IAEVQKQGLD	QWTYQIYQEP	FKNLKTGKYA
K_CD_EQTB1	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGHG	QWTYQIYQEP	YKNLKTGKYA
K_CM_MP535	R.EILKEPVH	GVYYDPSKDL	IAEIQKQGND	QWTYQIYQEP	HKNLKTGKYA
N_CM_YBF30	R.EILKEPLH	GVYYDPGKEL	VAEIQKQGGG	QWTYQIYQEL	HKNLKTGKYA
O_CM_ANT70	R.ERLQPVH	GVYYQPDKDL	WVNIQKQGGG	QWTYQIYQEE	HKNLKTGKYT
O_CM_MVP51	R.EKLKEPVH	GVYYQPDKDL	WVSIQKHGEG	QWTYQVYQDE	HKNLKTGKYA
O_SN_99SE_	R.EKLKEPVH	GVYYQPDKDL	WVNIQKQGGG	QWTYQIYQDE	HKNLKTGKYT
O_SN_99SE_	R.EKLKEPVH	GVYYQPDKDL	WVNIQKQGGG	QWTYQIYQDE	HKNLKTGKYT
U_CD_83C	R.EILKEPVH	GVYYDPSKDL	VAEIQKQGGD	QWSYQIYQEP	FKNLKTGKYA

551

600

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 A2_CY_94CY KRRSTHTNDV KQLTEAVQKI TMESIVIWG. KIPKFRLPIQ KETWETWWAE
 A2D_97KR KRRSTHTNDV KQLTEAVQKI VMESIVIWG. KIPKFRLPIQ KETWETWWTE
 A2G_CD_97C KRGSAHTNDV KQLTEVVQKI ATESIVIWG. KTPKFRLPIQ KETWETWWTE
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 A_KE_Q23_A RKRSAHTNDV RQLAEVVQKV VMESIVIWG. KTPKFRLPIQ KETWDTWWMD
 A_SE_SE659 RKRSAHTNDV RQLAEVVQKV VMESIVIWG. KTPKFRLPIQ KETWETWWMD
 A_SE_SE725 RKRSAHTNDV RQLAEVVQKV VMESIVIWG. KTPKFRLPIQ KETWETWWMD
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 A_SE_SE853 RKRSAHTNDV RQLAEVVQKV VMESIVIWG. KTPKFRLPIQ KETWETWWME
 A_SE_SE889 RKRSAHTNDV RQLVEVVQKV VMESIVIWG. KTPKFRLPIQ KETWETWWMD
 A_SE_UGSE8 RKRSAHTNDV RQLAEVVQKV VMESIVIWG. KTPKFRLPIQ KDTWDTWWMD
 A_UG_92UG0 RKRSAHTNDV RQLAEVVQKV VMESIVIWG. KTPKFRLPIQ KETWETWWMD
 A_UG_U455_ RKRSAHTNDV KQLTEVVQKV STESIVIWG. KIPKFRLPIQ KETWEAWWME
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AC_RW_92RW	KRRTAHTNDV	KQLTEAVQKI	AMESIWIWG.	KTPKFRLPIQ	KETWETWWTD
AC_SE_SE94	KKRSAHTNDV	RQLAEVVQKV	VMESIIIWG.	KTPKFRLPIQ	KETWETWWMD
ACD_SE_SE8	KKRSAHTNDV	KQLAEVVQKV	VMESIWIWG.	KAPKFRLPIQ	KETWETWWMD
ACG_BE_VI1	KRSAAHTNDV	KQLTEAVQKI	AQESIWIWG.	KTPKFRLPIQ	RETWEAWWME
AD_SE_SE69	KVRGHTNDI	KQLTAAVQKI	AQECIWIWG.	KTPKFRLPIQ	KETWETWWTE
AD_SE_SE71	KLRGHTNDI	KQLTAAVQKI	AQECIWIWG.	KTPKFRLPIQ	KETWETWWTE
ADHK_NO_97	RMKSAHTNDV	KQLTEAVQKI	SIESIWIWG.	KTPKFRLPIQ	KETWETWWTE
ADK_CD_MAL	RIKSAHTNDV	KQLTEAVQKI	AQESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
AG_BE_VI11	KRKSHTNDV	KQLVEVVQKV	ATESVWIWG.	KTPKFRLPIQ	RETWEAWWRE
AG_NG_92NG	KRGSHTNDV	KQLTEAVQKI	ATESIWIWG.	KVPKFRLPIR	KETWEVWWTE
AGHU_GA_VI	KKRSAHTNDV	KQLTEAVQKI	ATESIWIWG.	KIPKFRLPIQ	KETWETWWTD
AGU_CD_Z32	RRRTAHTNDV	RQLAEVVQKI	ASESIWIWG.	KTPKFRLPIQ	KETWETWWAD
AJ_BW_BW21	KRRAAHTNDV	KQLAEVVQKI	ALESIWIWG.	KTPKFRLPIQ	KETWETWWTE
B_AU_VH_AF	RMKGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWEAWWME
B_CN_RL42	RMKGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_DE_D31_U	RMKGAHTNDV	KQLTEAVQKI	TTESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_DE_HAN_U	RMKGAHTNDI	KQLTEAVQKI	ATEGIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_FR_HXB2	RMKGAHTNDV	KQLTEAVQKI	TTESIWIWG.	KTPKFRLPIQ	KETWETWWTE
B_GA_OYI	RMKGAHTNDV	KQLTEAVQKI	TOESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_GB_CAM1	KMRGHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWDAAWID
B_GB_GB8_A	KMRGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWEAWWME
B_GB_MANC	KMRGHTNDV	KQLTEAVQKV	TTESIIIWG.	KIPKFRLPIQ	KETWDAAWTE
B_KR_WK_AF	RMKGAHTNDV	KQLTEAVQKV	AIESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_NL_3202A	RMKGAHTNDV	KQLTEAVQKI	TTESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_TW_TWCYS	RTRGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_US_BC_L0	RTRGAHTNDV	KQLTEAVQKI	TTECIIIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_DH123	RTRGAHTNDV	KQLTEVVQKV	TTECIWIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_JRCSE	RTRGAHTNDV	KQLTEAVQKI	ANESIWIWG.	KIPKFRLPIQ	KETWETWWTE
B_US_MNCG	RMKGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_P896	RMKGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWEAWWTD
B_US_RF_M1	RMKGAHTNDV	KQLTEAVQKV	ATESIWIWG.	KTPKFRLPIQ	KETWEAWWTE
B_US_SF2_K	RMKGAHTNDV	KQLTEAVQKV	STESIWIWG.	KIPKFRLPIQ	KETWEAWWME
B_US_WEAU1	RVRGAHTNDV	KQLTEAVQKI	TTESIWIWG.	KTPKFRLPIQ	KETWETWWTE
B_US_WR27	RTRGAHTNDV	XQLXEAQKVX	ATXSIVIWG.	KTPKXILPIQ	KETWESRWTE
B_US_YU2_M	RTRGAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWETWWTE
BF1_BR_93B	RMKGAHTNDV	KQLTEAVQKI	TTESIWIWG.	KIPKFRLPIQ	KETWEAWWIE
C_BR_92BR0	KMRTAHTNDV	RQLTEAVQKI	ALESIIIWG.	KTPKFRLPIQ	KETWEAWWTD
C_BW_96BW0	KMRTAHTNDV	KQLTEVVQKI	TMESIWIWG.	KTPKFRLPIQ	KDTWETWWTD
C_BW_96BW1	KMRTAHTNDV	KQLTEAVQKI	SMESIWIWG.	KIPKFRLPIQ	KEAWWAWWTD
C_BW_96BW1	KLRTAHTNDV	RQLTEAVQKI	AQECIWIWG.	KTPKFRLPIQ	KETWEAWWTD
C_BW_96BW1	KMRTAHTNDV	KQLTEAVQKI	AMESIWIWG.	KTPKFRLPIQ	KETWETWWTD
C_ET_ETH22	KRGTAHTNDV	KQLTAVVQKI	ALESIWIWG.	KTPKFRLPIQ	KETWEAWWTD
C_IN_93IN1	KRRTAHTNDV	KQLTEAVQKI	AMESIWIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_93IN9	KMRTAHTNDV	KQLTEAVQKI	AMESIWIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_93IN9	KMRTAHTNDV	KQLAEAVQKI	AMESIWIWG.	KTPKFRLPIQ	KETWEAWWTD
C_IN_94IN1	KMRTAHTNDV	KQLTEAVQKI	AMESIWIWG.	KTPKFRLPIQ	KETWETWWTD
C_IN_95IN2	KMRTAHTNDV	KQLTEAVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWETWWTD
CRF01_AE_C	RKRSHTNDV	RQLAEVVQKV	ATESIWIWG.	KTPKFRLPIQ	RETWETWWAE
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CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIWIWG.	KTPKFRLPIQ	RETWETWWME
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CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIWIWG.	KTPKFRLPIQ	RETWETWWME
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CRF01_AE_T	RRGSAHTNDV	RQLTEVVQKV	ATESIWIWG.	KTPKFRLPIQ	RETWETWWME
CRF01_AE_T	RKRSHTNDV	RQLTEVVQKI	ATESIWIWG.	KTPKFRLPIQ	KETWETWWME
CRF02_AG_F	KRRSHTNDV	RQLAEVVQKV	VTESIWIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_F	KRRSHTNDV	KQLTEVVQKV	ATESIWIWG.	KTPKFSLPIQ	RETWEAWWME
CRF02_AG_G	ERVAPYDLIS	TELTEVVQKV	TTESIIIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_N	KKRSAHTNDV	KQLTEVVQKV	AMESIWIWG.	KTPKFRLPIQ	RETWETWWME

CRF02_AG_S	KKRSAHTNDV	KQLTEVVQKV	ATESIVIWG.	KTPKFRLPIQ	RETWEAWWME
CRF02_AG_S	KKRSAHTNDV	KQLTEVVQKV	ATESIVVWG.	KTPKFRLPIQ	RETWEAWWME
CRF03_AB_R	RLRSAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF03_AB_R	RLRSAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWAE
CRF04_cpx_	RTRSAHTNDV	RQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWTE
CRF04_cpx_	KTRSAHTNDV	RQLTEVVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWTE
CRF04_cpx_	KTRSAHTNDV	RQLTEAVQKI	AMECIVIWG.	KTPKFRLPIQ	KETWDTWWME
CRF05_DF_B	RARGVHTNDV	KQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWEIWWTE
CRF05_DF_B	RTRNAHTNDV	KQLAEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RIKSAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	KIKSTHTNDV	KQLTEAVQKI	ARESIVIWG.	KTPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RMRSAHTNDI	KQLTEAVQKI	ALEAIVIWG.	KIPKFRLPIQ	KETWETWWTE
CRF06_cpx_	RTKSAHTNDV	RQLTEAVQKI	ALESIVIWG.	KTPKFRLPIH	KETWETWWTE
CRF11_cpx_	KRRAAHTNDV	RQLTEVIQKI	CLEAIVIWG.	KTPKFRLPIQ	RETWETWWTD
CRF11_cpx_	KRRTAHTNDV	RQLAEVVQKI	ALEGIVIWG.	KIPKFRLPIQ	KETWETWWTD
D_CD_84ZR0	RMGAHTNDV	KQLTEAVQKI	AIESIVIWG.	KTPKFRLPIQ	KETWETWWID
D_CD_ELI_K	RMGAHTNDV	KQLAEAVQRI	STESIVIWG.	RTPKFRLPIQ	KETWETWWAE
D_CD_NDK_M	RTRGAHTNDV	KQLTEAVQKI	ATESIVIWG.	KTPKFRLPIQ	KETWETWWIE
D_UG_94UG1	KMRGTHTNDV	KQLTEAVQKI	AQECIVIWG.	KTPKFRLPIQ	KETWETWWTE
F1_BE_VI85	KVRSNAHTNDV	KQLTEAVQKI	ALESIVIWGK	RSPKFRLPIL	KETWDTWWTD
F1_BR_93BR	KMRSNAHTNDV	KQLTEAVQKI	SLESIVIWG.	KTPKFRLPIL	KETWDTWWTE
F1_FI_FIN9	KMRSNAHTNDV	KQLTEAVQKI	ALESIVIWG.	KTPKFRLPIL	KETWDTWWTE
F1_FR_MP41	KTRSAHTNDI	KELTDAVQKV	ARECIVIWG.	KSPKFRLPIQ	KETWEAWWTD
F2_CM_MP25	RRKSAHTNDV	KQLTEVVQKV	ATEGIVIWG.	KVPKFRLPIQ	KETWEIWWTE
F2KU_BE_VI	RMRSAHTNDV	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWETWWTE
G_BE_DRCL	KGSAHTNDV	KQLTEVVQKI	ATEGIIIWG.	KIPKFRLPIK	KETWEVWWTE
G_NG_92NG0	KRGSNAHTNDV	KQLTEVVQKI	ATEGIVIWG.	KIPKFRLPIR	KETWEVWWTE
G_SE_SE616	KRGSNAHTNDV	KQLTEVVQKI	ATESIVIWG.	KTPKFRLPIR	KETWEIWWTD
H_BE_VI991	KMRSNAHTNDV	KQLTEVVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
H_BE_VI997	KMRNAHTSDV	KQLTEAVQKI	ATESIVIWG.	KIPKFRLPIQ	KETWETWWTE
H_CF_90CF0	KMRTAHTNDI	KQLTEAVQKI	STESIVIWG.	KIPKFRLPIQ	KETWETWWTE
J_SE_SE702	KRRSAHTNDV	KQLSQVVQKI	ALEAIVIWG.	KTPKFRLPIQ	KETWETWWTD
J_SE_SE788	KRRSAHTNDV	KQLAEVVQKI	ALEAIVIWG.	KTPKFRLPIQ	RETWETWWTD
K_CD_EQTB1	RIRSAHTNDV	KQLTEVVQKV	AMESIVIWG.	KTPKFRLPIQ	KETWGTWWTE
K_CM_MP535	RMRSAHTNDV	KQLTEAVQKI	ATEGIVIWG.	KTPKFRLPIQ	KETWETWWTE
N_CM_YBF30	KMRSNAHTNDI	KQLVEVVQKV	ATESIVIWG.	KTPKFRLPVQ	KEVWEAWWTD
O_CM_ANT70	RQKASHTNDI	RQLAEVIQKV	SQESIIIWG.	KLPKFRLPVT	RETWETWWAD
O_CM_MVP51	RQKASHTNDI	RQLAEVVQKV	SQEAIVIWG.	KLPKFRLPVT	RETWETWWAE
O_SN_99SE_	RQKASHTNDI	RQLAEVLQRV	SQEAIIIWG.	KLPKFRLPIT	RETWETWWAD
O_SN_99SE_	RQKASHTNDI	RQLAEVLQKV	SQEAIIIWG.	KLPKFRLPIT	RETWETWWAD
U_CD_83C	KRRSAHTNDV	KQLTEAVQKI	SMESIVIWG.	KIPKFRLPIQ	KETWESWWTD

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00BW0762_1	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPL	VGVETFYVDG	AANRDTKIGK
00BW0768_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	LGAETFYVDG	AANRETKKGGK
00BW0874_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGGK
00BW1471_2	YWQATWIPEW	EFVNAPPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGGK
00BW1616_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGIETFYVDG	AANRETKLGGK
00BW1686_8	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKAGK
00BW1759_3	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRDTKGGK
00BW1773_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKIGK
00BW1783_5	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKMGR
00BW1795_6	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPV	AGVETFYVDG	AANRETKMGK
00BW1811_3	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
00BW1859_5	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AAHRETKVEK
00BW1880_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPM	MGVETFYVDG	AANRETKIGK
00BW1921_1	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGGK
00BW2036_1	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGGK
00BW2063_6	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	LCVETFYVDG	AANRETKMGK
00BW2087_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK

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00BW2127_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGVETFYVDG	AVNRETKVGK
00BW2128_3	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGK
00BW2276_7	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
00BW3819_3	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGVETFYVDG	AANRDTKVVGK
00BW3842_8	YWQATWIPDW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANRDTKIGK
00BW3871_3	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKAGK
00BW3876_9	YWQATWIPDW	EFVNTPLVK	LWYQLEKEPI	VRAETFYVDG	AANRETKIGK
00BW3886_8	YWQATWIPEW	EFVNTPLVK	LRYQLEKEPI	AGVETFYVDG	AANRETKVGK
00BW3891_6	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AEVETFYVDG	AANRETKRGK
00BW3970_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPM	AGVETFYVDG	AANRETKIGR
00BW5031_1	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPV	AGVETFYVDG	AANRETKIGK
96BW01B21	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKIGK
96BW0407	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGG
96BW0502	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	PGVETFYVDG	AANRETKLGG
96BW06_J4	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	MGAETFYVDG	AANRETKAGK
96BW11_06	Y.QATWIPEW	EFVNTPLVK	LWYQLETEPM	AGAETFYVDG	AANRETKIGK
96BW1210	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKMGK
96BW15B03	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKIGK
96BW16_26	YWQATWIPKW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
96BW17A09	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
96BWM01_5	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	LGAETFYVDG	AANRETKMGK
96BWM03_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKGP	AGAETFYVDG	ASNRETKLGG
98BWMC12_2	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETLYVDG	AANRETKLGG
98BWMC13_4	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	LGVETFYVDG	AANRETKLGG
98BWMC14_a	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGVETFYVDG	AANRETKAGK
98BWM014_1	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	PGAETFYVDG	AANRETKTGK
98BWM018_d	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	GGAETFYVDG	AANRETKMGK
98BWM036_a	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AASRETKKGK
98BWM037_d	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGVETFYVDG	AASRDTKIGK
99BW3932_1	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	GGVETFYVDG	AANRETKVGK
99BW4642_4	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGK
99BW4745_8	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGVETFYVDG	ATNRETKRGN
99BW4754_7	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGvetFYVDG	AANRDTKLGG
99BWMC16_8	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGK
A2_CD_97CD	WWQATWIPEW	EFVNTPLVK	LWYQLETEPI	AGAETFYVDG	AANRETKLGG
A2_CY_94CY	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGG
A2D_97KR	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	TGAETFYVDG	AANRETKLGG
A2G_CD_97C	YWQATWIPDW	EFVNTPLVK	LWYRLETEPI	PGAETYYVEG	AANRETKLGG
A_BY_97BL0	XWQATXIPE.	EFVNTPLVK	LWYQLEKEPI	VRAETFYVDR	AANRETKIGK
A_KE_Q23_A	YWQATWILEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
A_SE_SE659	YWQATWIPEW	EFVNTPLVL	WWYLLLEEDPI	VGADSEFFVEG	AAKEKTLXGT
A_SE_SE725	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
A_SE_SE753	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
A_SE_SE853	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
A_SE_SE889	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
A_SE_UGSE8	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGG
A_UG_92UG0	YWQAT.IPEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
A_UG_U455_	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
AC_IN_2130	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPM	AGAETFYVDG	AANRETKIGK
AC_RW_92RW	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	LGAETFYVDG	AANRETKIGK
AC_SE_SE94	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGG
ACD_SE_SE8	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGG
ACG_BE_VI1	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
AD_SE_SE69	YWQATWIPEW	EFVNTPLVK	LWYQLEKDP	VGAETFYVDG	AANRETKLGG
AD_SE_SE71	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGG
ADHK_NO_97	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGK
ADK_CD_MAL	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGK
AG_BE_VI11	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	AGAETFYVDG	AANRETKLGG
AG_NG_92NG	YWQATWIPDW	EFVNTPLVK	LWYRLETEPI	PGAETYYVDG	AANKETKLGG
AGHU_GA_VI	HWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKQGG

AGU_CD_232	YWQATWIPEW	EFVNTPLLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKQGK
AJ_BW_BW21	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	ASNRETKLGG
B_AU_VH_AF	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_CN_RL42	YWQATWIPEW	EFINTSPLVK	LWYQLEKEPI	EEAETFYVDG	AANRETKLGG
B_DE_D31_U	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKLGG
B_DE_HAN_U	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_FR_HXB2	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_GA_OYI	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
B_GB_CAM1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETRLGG
B_GB_GB8_A	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGG
B_GB_MANC	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_KR_WK_AF	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_NL_3202A	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_TW_TWCYS	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGG
B_US_BC_LO	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	EGAETFYVDG	AANRETKLGG
B_US_DH123	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AASRETRLGG
B_US_JRCSE	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_US_MNCG	YT.ATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKKGG
B_US_P896	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRDTKSGK
B_US_RF_M1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGG
B_US_SF2_K	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
B_US_WEAU1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANKETKLGG
B_US_WR27	YWQATWIPEW	EXVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AASRETKLGG
B_US_YU2_M	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGG
BF1_BR_93B	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKLGG
C_BR_92BR0	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKMGG
C_BW_96BW0	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKLGG
C_BW_96BW1	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPM	AGAETFYVDG	AANRETKIGK
C_BW_96BW1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKMGG
C_BW_96BW1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKIGK
C_ET_ETH22	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKIGK
C_IN_93IN1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKLGG
C_IN_93IN9	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	AGVETFYVDG	AANRETKKGG
C_IN_93IN9	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	AGVETFYVDG	AANRETKIGK
C_IN_94IN1	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AANRDTKIGK
C_IN_95IN2	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	AGAETFYVDG	AANRETKIGK
CRF01_AE_C	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	AGAETLYVDG	AASRENKLGG
CRF01_AE_C	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	MGAETFYVDG	AASRETKQGG
CRF01_AE_C	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	AGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	IGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF01_AE_T	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AASRETKLGG
CRF02_AG_F	YWQATWIPDW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANKETKLGG
CRF02_AG_G	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKLGG
CRF02_AG_N	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKIGK
CRF02_AG_S	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	VGAETFYVDG	AANRETKIGK
CRF02_AG_S	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKDPI	IGAETFYVDG	AANRETKLGG
CRF03_AB_R	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKSGK
CRF03_AB_R	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKSGK
CRF04_cpx	YWQATWIPEW	EFVNTPLPLVK	LWYQLETDPI	AGAETFYVDG	AANRETKQGG
CRF04_cpx	YWQATWIPEW	EFVNTPLPLVK	LY.QLEPDPI	AGAETFYVDG	AASRETRRGG
CRF04_cpx	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	AGAETFYVDG	AASRETNQGG
CRF05_DF_B	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	LGAETFYVDG	AANRETKLGG
CRF05_DF_B	YWQATWIPEW	EFVNTPLPLVK	LWYQLEKEPI	MGAETFYVDG	AANRETKLGG
CRF06_cpx	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKQGG
CRF06_cpx	YWQATWIPEW	EFVNTPLPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKKGG

CRF06_cpx_	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	AANKETKKGK
CRF06_cpx_	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	IGAETFYVDG	AANRETKIGK
CRF11_cpx_	YWQATWIPEW	EFVNTPLVK	LWYQLEQGP	LGAETFYVDG	AANRETKIGK
CRF11_cpx_	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
D_CD_84ZRO	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANKETKLKG
D_CD_ELI_K	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
D_CD_NDK_M	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	IGAETFYVDG	AANRETKLGK
D_UG_94UG1	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	VGAETFYVDG	AANRETKIGK
F1_BE_VI85	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	AGADTFYVDG	ASNRETKKGK
F1_BR_93BR	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	ASNRETKKGK
F1_FI_FIN9	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	AGAETFYVDG	ASNRETKKGK
F1_FR_MP41	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	IGAETFYVDG	ASNRETKKGK
F2_CM_MP25	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	IGAETFYVDG	AANRETKLGK
F2KU_BE_VI	YWQATWIPEW	EFVNTPLVK	LWYQLETDPI	AGAETFYVDG	AANRETKKGR
G_BE_DRCBL	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	PGVETYYVDG	AANRETKLGK
G_NG_92NG0	YWQAAWIPEW	EFVNTPLVK	LWYQLETEPI	PGAETYYVDG	AANRETKLGK
G_SE_SE616	YWQATWIPEW	EFVNTPLVK	LWYRLETEPI	PGAETYYVDG	AANRETKLGK
H_BE_VI991	HWQATWIPEW	EFVNTPLVK	LWYQLETEPI	EGAETYYVDG	AANRETKMGK
H_BE_VI997	HWQATWIPEW	EFVNTPLVK	LWYQLEAEPI	AGAETYYVDG	AANRETKIGK
H_CF_90CF0	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	AGAETYYIDG	AANRETKLGK
J_SE_SE702	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	MGAETFYVDG	ASNRETKVGK
J_SE_SE788	YWQATWIPEW	EFVNTPLVK	LWYQLEKEPI	MGAETFYVDG	ASNRETKTGK
K_CD_EQTB1	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	AANRETKQGG
K_CM_MP535	YWQATWIPEW	EFVNTPLVK	LWYQLETEPI	VGAETFYVDG	AAHRETKKGR
N_CM_YBF30	HWQATWIPEW	EFVNTPLVK	LWYQLETEPI	SGAETFYVDG	AANRETKLGK
O_CM_ANT70	YWQATWIPEW	EFVSTPLIK	LWYRLESEPI	MGAETYYVDG	AANRETKLGK
O_CM_MVP51	YWQATWIPEW	EFVSTPLIK	LWYQLETEPI	VGAETFYVDG	AANRNTKLKG
O_SN_99SE	YWQATWIPEW	EFVSTPLIK	LWYQLESEPI	MGAETYYVDG	AANRDTKLKG
O_SN_99SE	YWQATWIPEW	EFVSTAPLIK	LWYQLESEPI	IGAETYYVDG	AANRDTKLKG
U_CD_83C	YWQATWIPEW	EFVNTPLVK	LWYQLEKDPI	MGAETFYVDG	AANRETKKGK

651

700

00BW0762_1	AGYVTDKGRQ	KVITLTETTN	OKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
00BW0768_2	AGYVTDGRGRQ	KIVPLTETTN	OKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
00BW0874_2	AGYVTDGRGRQ	KIVSLTETTN	OKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
00BW1471_2	AGYVTDKGRQ	KVVSLTETTN	OKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
00BW1616_2	AGYVTDGRGRQ	KIVSLAETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1686_8	AGYVTDGRGRQ	KVISLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1759_3	AGYVTDGRGRQ	KIVSLTETTN	ORTELQAIQL	ALQDSGLEVN	IVTDSQYALG
00BW1773_2	AGYVTDGRGRQ	KIVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1783_5	AGYVTDGRGRQ	KVISLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1795_6	AGYVTDGRGRQ	KIISLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1811_3	AGYVTDKGRQ	KTVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1859_5	AGYVTDGRGRQ	KIVNLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1880_2	AGYVTDGRGRQ	KVVTLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW1921_1	AGYVTDKGRQ	KVITLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2036_1	AGYVTDGRGRQ	KIISLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2063_6	AGYVTDGRGRQ	KVVSLTGTTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2087_2	AGYVTDKGRQ	KIVCLNETTN	OKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
00BW2127_2	AGYVTDGRGRQ	KVISINETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2128_3	AGYVTDKGRQ	KVVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW2276_7	AGYVTDGRGRQ	KIVSLSETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3819_3	AGYVTDGRGRQ	KIVSINGTTN	OKTELRAIYL	ALQDSGSEVN	IVTDSQYALG
00BW3842_8	AGYVTDGRGRQ	KVVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3871_3	AGYVTDGRGRQ	KVISLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3876_9	AGYVTDGRGRQ	KIVSLTETTN	OKSELQAIHL	ALQDSGSEVN	IVTDSQYALG
00BW3886_8	AGYVTDGRGRQ	KVITLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3891_6	AGYVTDGRGRQ	KIVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
00BW3970_2	AGYVTDGRGRQ	KIITLNETTN	OKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
00BW5031_1	AGYVTDGRGRQ	KIVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG

96BW01B21	AGYVTDGRGQ	RIISLTEATN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW0407	AGYVTNKGRO	KIVPLTETTN	QKAELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW0502	AGYVTDGRGQ	KIVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW06_J4	AGYVTDGRGQ	KVISLTETTN	OKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
96BW11_06	AGYVTDKGRQ	KVVTLTETTN	QKAELQAIQL	ALQDSGPEVN	IVTDSQYALG
96BW1210	AGYVTDGRGQ	KIVSLNETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW15B03	AGYVTDGRGQ	KIVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
96BW16_26	AGCVTDGRGQ	KIVSLTETTN	QKAELQAIQL	ALQDSGAEVN	IVTDSQYALG
96BW17A09	AGYVTDKGRQ	KVVSLETTN	OKTELQAIKL	ALQDSGSEVN	IVTDSQYALG
96BWM01_5	AGYVTDGRGQ	KVVPLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALK
96BWM03_2	AGYVTDGRGQ	KVVSLETTN	OKTELQAIQL	ALQDSGTEVN	IVTDSQYALG
98BWMC12_2	AGYVTDKGRQ	KVVSLETTN	OKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
98BWMC13_4	AGYITDRGRO	KVVSLETTN	OKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
98BWMC14_a	AGYVTDGRGQ	KVISLTETAN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
98BWM014_1	AGYVTDKGRQ	KIVSLNETTN	QKAELQAIQL	ALQDSGLEVN	IVTDSQYALG
98BWM018_d	AGYVTDKGRQ	KIVALTETTN	QKAELQAIQL	ALQDSGSEVN	IVTDSQYALG
98BWM036_a	AGYVTDGRGQ	KCVTLTETTN	OKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
98BWM037_d	AGYVTDGRGQ	KIITLTETTN	OKTELQAIQL	ALQDSGPEVN	IVTDSQYALG
99BW3932_1	AGYVTDKGRQ	KVITINETTN	OKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
99BW4642_4	AGYVTDGRGQ	RIVNLTETTN	OKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
99BW4745_8	AGYVTDGRGQ	KIVSLTETTN	QKAELQAIQL	ALQDSGSEVN	IVTDSQYALG
99BW4754_7	AGYVTDGRGQ	KVVSLETTN	OKTELQAIHL	ALQDSGPEVN	IVTDSQYALG
99BWMC16_8	AGYVTDGRGQ	KVVTLTETTN	OKTELQAIQL	ALQDSSEVN	IVTDSQYALG
A2_CD_97CD	AGYVTDGRGQ	KIVPLTETTN	OKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
A2_CY_94CY	AGYVTDGRGQ	KIVSLTETTN	OKTELHAIYL	ALQDSGLEVN	IVTDSQYALG
A2D_97KR	AGYVTDKGRQ	KIVSLTDTTN	OKTELHAIYL	ALQDSGLEVN	IVTDSQYALG
A2G_CD_97C	AGYVTDKGRQ	KIINLTETTN	OKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
A_BY_97BLO	AGYVTDGRGQ	KVVSLETTN	OKTELHAIHL	ALQDSGSEVD	IVTDSQYALG
A_KE_Q23_A	AGYVTDKGRQ	KVVSLETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE659	GWFAEGGRQ	VVVPLAKTTH	QTTELPAHP	SLQDSGSVVI	IVNDSQSAGG
A_SE_SE725	AGYVTDGRGQ	KVVSLETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE753	AGYVTNRGRQ	KVVSLETTN	OKTELHAILL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE853	AGYVTDGRGQ	KVVSLETTN	OKTEVHAIHL	ALQDSGSEVN	IVTDSQYALG
A_SE_SE889	AGYVTDGRGQ	KVVTLAETTN	OKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
A_SE_UGSE8	AGYVTDGRGQ	KVVSLETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_UG_92UG0	AGYVTDGRGQ	KVVSLETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
A_UG_U455_	AGYVTDGRGQ	KVVSLETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AC_IN_2130	AGYATDRGRO	KIVTLTETTN	OKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
AC_RW_92RW	AGYVTDGRGQ	KIVSLTETTN	OKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
AC_SE_SE94	AGYVTDGRGQ	KVVSLETTN	OKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
ACD_SE_SE8	AGYVTDGRGQ	KVVSLETTN	OKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
ACG_BE_VI1	AGYVTDGRGQ	KAITLTETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AD_SE_SE69	AGYVTDGRGQ	KVVPLTETTN	OKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
AD_SE_SE71	AGYITDRGRO	KVVSLETTN	OKTELQAINL	ALQDSGPEVN	IVTDSQYALG
ADHK_NO_97	AGYVTDGRGQ	KVVFLTETTN	OKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
ADK_CD_MAL	AGYVTDGRGQ	KVVSLETTN	OKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
AG_BE_VI11	AGYVTDGRGQ	KAVSLTETTN	OKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
AG_NG_92NG	AGYVTDGRGQ	KIITIQTETTN	OKTELHAIQL	ALQDSGSEVN	IVTDSQYALG
AGHU_GA_VI	AGYVTDGRGQ	KIVSLTETTN	OKTELQAIHL	ALQDSGPEVN	IVTDSQYALG
AGU_CD_Z32	AGYITDKGRQ	KVITLTETTN	OKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
AJ_BW_BW21	AGYVTDGRGQ	KIVSLTETTN	OKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
B_AU_VH_AF	AGYVTDGRGQ	KVVPLSDTTN	OKTELQAIQL	ALQDSGLEVN	IVTDSQYALG
B_CN_RL42_	AGYVTNKGRO	KVVTLDTTN	OKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
B_DE_D31_U	AGYVTDGRGQ	KVVSLETTN	OKTELQAIHL	ALQDSGLEVN	IVSDSQYALG
B_DE_HAN_U	AGYVTDGRGQ	KVVSLETTN	OKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_FR_HXB2_	AGYVTNRGRQ	KVVTLDTTN	OKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_GA_OYI_	AGYVTDGRGQ	KVVSLETTN	OKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_GB_CAM1_	AGYVTDGRGQ	KVVPLDTTN	OKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_GB_GB8_A	AGYVTDGRGQ	KVVPLDTTN	OKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_GB_MANC_	AGYVTDGRGQ	KVISLDTTN	OKTELQAIHL	ALQDSGLEVN	IVSDSQYALG

B_KR_WK_AF	AGYVTDGRGQ	KVVPLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_NL_3202A	AGYVTDGRGQ	KVVSLNDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
B_TW_TWCYS	AGYVTDKGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_BC_L0	AGYVTNKGRQ	KVVTLTDTTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_DH123	AGYVTNRGRQ	KVVSLTDTTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
B_US_JRCSF	AGYVTSRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_MNCG	AGYVTNRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_P896	AGYVTDGRGQ	KVVSLADTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_RF_M1	AGYVTDGRGQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_SF2_K	AGYVTDGRGQ	KVVSIADTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_WEAU1	AGYVTNRGRQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_WR27	AGYVTDGRGQ	KVVSLNDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
B_US_YU2_M	AGYVTNKGRQ	KVVSLTDTTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
BF1_BR_93B	AGYVTDGRGQ	KVVPLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
C_BR_92BR0	AGYVTDGRGQ	KIVSITETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW0	AGYVTDKGRQ	KIVPLTETTN	QRAELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDKGRQ	EVVTLTETTN	QKAEALQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDGRGQ	KIVSLNETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_BW_96BW1	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_ET_ETH22	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN1	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN9	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
C_IN_93IN9	AGYVTDGRGQ	KIVPLTETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
C_IN_94IN1	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
C_IN_95IN2	AGYVTDKGRN	KIVSLTETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSDVN	IVTDSQHALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_C	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVISLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF01_AE_T	AGYVTDGRGQ	KVVSLTETTN	QKSELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_F	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_F	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_G	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_N	AGYVTDGRGQ	KVVSLTETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_S	AGYVTDGRGQ	KVVSLAETTN	QKTELHAIHL	ALQDSGSEVN	IVTDSQYALG
CRF02_AG_S	AGYVTDGRGQ	NVVSLTETTN	QKTELHAILL	ALQESGSEVN	IVTDSQYALG
CRF03_AB_R	AGYVTDGRGQ	KVVSLTDTTN	QKTELQAIHL	ALQDSGLEVN	IVTDSQYALG
CRF03_AB_R	AGYVTDGRGQ	KVVSLTDTTN	QKTELHAIHL	ALQDSGLEVN	IVTDSQYALG
CRF04_cpx	AGYVTDGRGQ	KVVSLSETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
CRF04_cpx	AGYVTDGRGQ	KVVSLSETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYALG
CRF04_cpx	AGYVTDGRGQ	KVITLPETTN	QKTELQAIYL	ALQDSGSEVN	IVTDSQYAMG
CRF05_DF_B	AGYITDKGRQ	KAVSLTETTN	QKAEALQAIHL	ALQDSGLEVN	IVTDSQYALG
CRF05_DF_B	AGYVTDKGRQ	KAVSLTETTN	QKTELHAIYL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx	AGYVTDGRGQ	KVVTLTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx	AGYVTDGRGQ	KVVSLAETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx	AGYVTDKGRQ	RVISLTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF06_cpx	AGYVTDGRGQ	KVVSLTETTN	QKTELQAINL	ALQDSGSEVN	IVTDSQYALG
CRF11_cpx	AGYVTDKGRQ	KVITLTETTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
CRF11_cpx	AGYVTNKGRQ	KVITPIETTN	QKTELEAIHL	ALQDSGLEVN	IVTDSQYALG
D_CD_842R0	AGYVTDGRGQ	KVVPFTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_CD_ELI_K	AGYVTDGRGQ	KVVPLTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_CD_NDK_M	AGYVTDGRGQ	KVVPFTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
D_UG_94UG1	AGYVTDGRGQ	KVVSLTDTTN	QKTELQAINL	ALQDSGLEVN	IVTDSQYALG
F1_BE_VI85	AGYVTDKGRQ	KVVSLTETTN	QKAEALQAIYL	ALQDSGSEVN	IVTDSQYALG
F1_BR_93BR	AGYVTDGRGQ	KAVSLTETTN	QKAEALQAIQL	ALQDSGSEVN	IVTDSQYALG
F1_FI_FIN9	AGYVTDGRGQ	KVVSLTETTN	QKAEALQAIHL	ALQDSGSEVN	IVTDSQYALG

F1_FR_MP41	AGYVTDGRGQ	KAVILTETTN	QKAELQAIHL	ALQDSGSEVN	IVTDSQYVLG
F2_CM_MP25	AGYITDRGRQ	KVVSLTETTN	QKTELQAIQL	ALQDSGSEVN	IVTDSQYALG
F2KU_BE_VI	AGYVTDKGRQ	KVVSLTETTN	QKTELQTIYL	ALQDSGSEVN	IVTDSQYAIG
G_BE_DRCBL	AGYVTDKGRQ	IIITLTETTN	QKAELHAIQL	ALQDSQSEVN	IVTDSQYALG
G_NG_92NG0	AGHVTDKGKQ	KIITLTETTN	QKAELHAIQL	ALQDSRPEVN	IVTDSQYALG
G_SE_SE616	AGYVTDKGKQ	KIITLTETTN	QKAELQAIQL	ALQDSRSEVN	IVTDSQYALG
H_BE_VI991	AGYVTDGRGQ	KIVSLTETTN	QKTELQAIYL	ALQESGPEVN	IVTDSQYALG
H_BE_VI997	AGYVTDKGKQ	KVVALTETTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
H_CF_90CF0	AGYVTDGRGQ	KVVSLTETTN	QKTELQAIYL	ALQDSGLEVN	IVTDSQYALG
J_SE_SE702	AGYVTDKGRQ	KVITLTDTTN	QKTELQAIYL	ALQDSGIEVN	IVTDSQYALG
J_SE_SE788	AGYVTDKGRQ	KVVTLTDTTN	QKTELHAIYL	ALRDSGLEVN	IVTDSQYALG
K_CD_EQTB1	AGYVTDKGRQ	KVISITETTN	QKTELQAIHL	ALQDSGSEVN	IVTDSQYALG
K_CM_MP535	AGYVTDGRGQ	KVVSITETTN	QKAELQAIHL	ALQDSGSEVN	IVTDSQYALG
N_CM_YBF30	ACFVTDGRGQ	KVVSITADTTN	QKAELQAILM	ALQESGRDVN	IVTDSQYAMG
O_CM_ANT70	AGYVTEQKGQ	KIIKLDETNN	QKAELMAILL	ALQDSKETVN	IVTDSQYALG
O_CM_MVP51	AGYVTEQKGQ	NIIKLEETTN	QKAELMAVLI	ALQDSKEQVN	IVTDSQYVLG
O_SN_99SE	AGYVTEKGRQ	KIIKLEETTN	QRAELMAVLL	ALQDSKETVN	IVQDSQYVLG
O_SN_99SE	AGYVTEKGRQ	KIVKLEETTN	QKAELMAVLL	ALQDSKETVN	IVTDSQYVLG
U_CD_83C	AGYVTDGRGQ	KVISLTETTN	QKAELQALYL	ALQDSGLEAN	IVTDSQYALG

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750

00BW0762_1	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQIDKLVSS
00BW0768_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW0874_2	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1471_2	IIQAQPDSE	SELVNQIIEQ	LIKKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1616_2	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1686_8	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSN
00BW1759_3	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1773_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW1783_5	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSN
00BW1795_6	IIQAQPDKSE	SELVSIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW1811_3	IIQAQPDKSE	SELVNQIIEQ	LIRKERVYLS	WVPAHKGIGG	NERVDKLVSS
00BW1859_5	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGE	NEQVDKLVSS
00BW1880_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
00BW1921_1	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW2036_1	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSR
00BW2063_6	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW2087_2	IIQAQPDKSE	SELVNQIIEQ	LINKEKIYLS	WVPAHKGIGG	NEQVDKLVSN
00BW2127_2	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW2128_3	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
00BW2276_7	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW3819_3	IIQAQPDKSE	SEIVNQIIEQ	LIQKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3842_8	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3871_3	IIQAQPDKSE	SELVNQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3876_9	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3886_8	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW3891_6	IIQSQPGKSE	SELVNQKIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSK
00BW3970_2	IIQAQPDSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
00BW5031_1	IIQAQPDKSE	SELVNQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQIDKLVSS
96BW01B21	IIQAQPDKSE	SELVNQMIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW0407	IIQAQPDKSE	SELVTQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQVDKLVSS
96BW0502	IIQAQPDKSE	SELVNQIIEQ	LIQKEWVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW06_J4	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSN
96BW11_06	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW1210	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
96BW15B03	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQIDKLVSK
96BW16_26	IIQAQPDKSE	SELVNQIIEQ	LINKERIYLS	WVPAHKGIGG	NEQVDKLVSS
96BW17A09	IIQAQPDSE	SELVNQIIEQ	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
96BWM01_5	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
96BWM03_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS

98BWMC12_2	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMC13_4	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMC14_a	IIQAQPDKSE	SELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMO14_1	IIQAQPDKSE	SELVNQIIEQ	LINKEKIYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMO18_d	IIQAQPDKSE	SEIVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSR
98BWMO36_a	IIQAQPDKSE	SELVNQIIEQ	LINKEKIYLS	WVPAHKGIGG	NEQVDKLVSS
98BWMO37_d	IIQAQPDNSE	SELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSK
99BW3932_1	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
99BW4642_4	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
99BW4745_8	IIQAQPDKSE	SELVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSK
99BW4754_7	IIQAQPDKSE	SELVNQIIEQ	LIKKKKVYLS	WVPAHKGIGG	NEQVDKLVSS
99BWMC16_8	IIQAQPDKSE	SELVNQIIEG	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
A2_CD_97CD	IIQAQPDSSSE	SELVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSC
A2_CY_94CY	IIQAQPERSE	SEIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
A2D_97KR	IIQAQPDNRSE	SEIVNLIIEK	LIEKERVYLS	WVPAHKGIGE	NEQVDKLVSS
A2G_CD_97C	IIQAQPDSSSE	AEIVNQIIEQ	LIRKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_BY_97BL0	IISAQPDNRSE	SEIVNKIIEK	LIKKEXVYLS	.VPAHKRIX	NEQVDKLVSN
A_KE_Q23_A	IIQAQPDKSE	SEIVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE659	IIQAQPDNRSE	SELVNQIIEK	LVGKDKVYLA	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE725	IIQAQPDSSSE	SEIVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE753	IIQAQPDNRSE	SELVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE853	IIQAQPDSSSE	SELVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_SE_SE889	IIQAQPDNRSE	SELVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSA
A_SE_UGSE8	IIQAQPDKSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_UG_92UG0	IIQAQPDNRSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
A_UG_U455_	IIQAQPDNRSE	SEIVNQIIEK	LIEKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_IN_2130	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSN
AC_RW_92RW	IIQAQPDSSSE	SEAVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
AC_SE_SE94	IIQAQPDNRSE	SEIVNQIIEK	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ACD_SE_SE8	IIQAQPDNRSE	SELVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ACG_BE_VI1	IIQAQPDKSE	SELVNQIIEQ	LIRKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
AD_SE_SE69	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLS	WVPAHKGIGG	NEQVDKLVSN
AD_SE_SE71	IIQAQPDNRSE	SELVNQIIEK	LIGKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
ADHK_NO_97	IIQAQPDKSE	SDLVNQIIEQ	LIQKDKVYLT	WVPAHKGIGG	NEQVDKLVSS
ADK_CD_MAL	IIQAQPDKSE	SEIVNQIIEQ	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
AG_BE_VI11	IIQAQPDNRSE	SELVNQIIEK	LIEKDKVYVS	WVPAHKGIGG	NEQVDKLVSS
AG_NG_92NG	IIQAQPDNRSE	SELVNQIIEQ	LIKKERKVYLT	WVPAHKGIGG	NEQVDKLVSS
AGHU_GA_VI	IIQAQPDKSE	SELVNQIIEK	LIQKNKVYLS	WVPAHKGIGG	NEQVDKLVSA
AGU_CD_232	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLS	WVPAHKGIGG	NEQVDKLVSS
AJ_BW_BW21	IIQAQPDKSE	SELVSQIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
B_AU_VH_AF	IIQAQPDKSE	SELVNQIIEQ	LIKKERKIYLA	WVPAHKGIGG	NEQVDKLVSA
B_CN_RL42	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_DE_D31_U	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLT	WVPAHKGIGG	NEQVDKLVSA
B_DE_HAN_U	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_FR_HXB2_	IIQAQPDQSE	SELVNQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GA_OYI_	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GB_CAM1_	IIQAQPDKSE	SELVSQIIEE	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_GB_GB8_A	IIQAQPDNRSE	SEVVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSS
B_GB_MANC_	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_KR_WK_AF	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_NL_3202A	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_TW_TWCYS	IIQAQPDKSE	SELVSQIIEE	LIKKERKVYLT	WVPAHKGIGG	NEQVDKLVSA
B_US_BC_LO	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_DH123	IIQAQPDKSE	SELVNQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVST
B_US_JRCSE	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_MNCG_	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_P896_	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_RF_M1	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDRLVST
B_US_SF2_K	IIQAQPDKSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSA
B_US_WEAU1	IIQAQPDQSE	SELVSQIIEQ	LIKKERKVYLA	WVPAHKGIGG	NEQVDKLVSS

B_US_WR27_	IIQAQPDKSE	SELVSIIEQ	LIXKXXVYLA	WVPAHKGIGG	NEQVDKLVSS
B_US_YU2_M	IIQAQPDSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
BF1_BR_93B	IIQAQPDKSE	LEIVNQIIEQ	LIKKEKIYLA	WVPAHKGIGG	NEQVDKLVSS
C_BR_92BR0	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW0	IIQAQPDKSE	SELVTQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SELVNQIIEQ	LICKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_BW_96BW1	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
C_ET_ETH22	IIQAQPDKSE	SEIVNQIIEQ	LISKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN1	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN9	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_93IN9	IIQAQPDKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_94IN1	IIQAQPDKSE	SELVNQIIEQ	LINKERVYLS	WVPAHKGIGG	NEQVDKLVSS
C_IN_95IN2	IIQAQPNKSE	SELVNQIIEQ	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDSE	SEIVNQIIEK	LIEKERVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDSE	SDIVNQIIEK	LIEKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_C	IIQAQPDSE	SEIVNQIIEK	LIEKEKVYLS	RVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDSE	SEVVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	DEQVDKLVSS
CRF01_AE_T	IIQAQPDSE	SEVVSQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDSE	SEVVSQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF01_AE_T	IIQAQPDSE	SEVVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
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CRF01_AE_T	IIQAQPDSE	SEVVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF02_AG_F	IIQAQPDSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF02_AG_F	IIQAQPDSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
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CRF02_AG_S	IIQAQPDSE	SELVTQIIEE	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF02_AG_S	IIQAQPDSE	SELVNQIIEK	LIEKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF03_AB_R	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSA
CRF03_AB_R	IIQAQPDKSE	SELVSIIEQ	LIKKEKFYLA	WVPAHKGIGG	NEQVDKLVSA
CRF04_cpx_	IIQAQPDSE	SDLVNQIIEQ	LIRKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
CRF04_cpx_	IIQAQPDSE	SDLVNQIIEE	LIQKDKVYLS	WVPAHKGIGG	NEQVDKLVSS
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CRF05_DF_B	IIQAQPDKSE	SELVNQIIEQ	LIEKKKVYLS	WVPAHKGIGG	NEQVDKLVSA
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CRF11_cpx_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLT	WVPAHKGIGG	NEQVDKLVSS
CRF11_cpx_	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
D_CD_84ZR0	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
D_CD_ELI_K	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
D_CD_NDK_M	IIQAQPDKSE	SELVSIIEQ	LIKKEKVYLA	WVPAHKGIGG	NEQVDKLVSS
D_UG_94UG1	IIQAQPDKSE	SEVVSQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
F1_BE_VI85	IIQAQPDKSE	SEIVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVSA
F1_BR_93BR	IIQAQPDKSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSA
F1_FI_FIN9	IIQAQPDKSE	SELVNQIIEQ	LIQKEKIYLS	WVPAHKGIGG	NEQVDKLVSA
F1_FR_MP41	IIQAQPDKSE	SEIVNQIIEK	LIQKERVYLS	WVPAHKGIGG	NEQVDRLVSA
F2_CM_MP25	IIQAHPDKSE	SEIVNQIIEQ	LIQKERVYLS	WVPAHKGIGG	NEQVDKLVST
F2KU_BE_VI	IIQAQPDKSE	SELVNQIIEQ	LIQKQIYLS	WVPAHKGIGG	NEQVDKLVSS
G_BE_DRCBL	IIQAQPDSE	SEIVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
G_NG_92NG0	IIQAQPDSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
G_SE_SE616	IIQAQPDSE	AELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
H_BE_VI991	IIQAQPDKSE	SELVNQIIEE	LIKKEKFYLS	WVPAHKGIGG	NEQVDKLVSS
H_BE_VI997	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
H_CF_90CF0	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
J_SE_SE702	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS
J_SE_SE788	IIQAQPDKSE	SELVNQIIEE	LIKKEKVYLS	WVPAHKGIGG	NEQVDKLVSS

K_CD_EQTB1	IIQAQPDKSE	SELVNQIIEQ	LIKKDRVYLS	WVPAHKGIGG	NEQVDKLVSS
K_CM_MP535	IIQAQPDKSE	SDLVNQIIEQ	LIKKERIYLS	WVPAHKGIGG	NEQVDKLVSA
N_CM_YBF30	IIHSQPDKSE	SELVSIIEE	LIKKERVYLS	WVPAHKGIGG	NEQVDKLVSS
O_CM_ANT70	VISSQPTQSE	SPIVQIIEE	LTKKEQVYLT	WVPAHKGIGG	NEKIDKLVSK
O_CM_MVP51	IISSQPTQSD	SPIVQIIEE	LTKKERVYLT	WVPAHKGIGG	NEKIDKLVSK
O_SN_99SE	IISSQPTQSE	SSLVQIIEE	LTKKEQVYLT	WVPAHKGIGG	NEKIDKLVSK
O_SN_99SE	IISSQPTQSE	SPLVQIIEE	LTQKEQVFLT	WVPAHKGIGG	NEKIDKLVSK
U_CD_83C	IIQAQPDSSSE	SELVNQIIEQ	LIKKEKVYLS	WVPAHKGIGG	NEQADKLVSA

751

800

00BW0762_1	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW0768_2	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW0874_2	GIRKALFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW1471_2	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1616_2	GIRKVLFLDG	IDKAQEEHEK	YHSSWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1686_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVAK	EIVASCDKCQ
00BW1759_3	GIRKVLFLDG	IDKAQGGSEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW1773_2	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPVAK	EIVASCDKCQ
00BW1783_5	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1795_6	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1811_3	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVAK	EIVASCDKCQ
00BW1859_5	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW1880_2	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVAK	EIVASCDKCQ
00BW1921_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVAK	EIVASCDKCQ
00BW2036_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW2063_6	GIRKVLFLDG	IDKAQEDHER	YHSNWRMTAS	EFNLPPIVAK	EIVASCDKCQ
00BW2087_2	GVRRLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
00BW2127_2	GIRKVLFLNG	IDKAQEEHEK	YHSNWRAMAN	EFNLPPVAK	EIVASCDKCQ
00BW2128_3	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW2276_7	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
00BW3819_3	GIRKVLFLDG	IDKAQEDHEK	YHNNWRAMVS	EFNLPPIVAK	EIVASCDKCQ
00BW3842_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3871_3	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3876_9	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3886_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW3891_6	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVAK	EIVASCDKCQ
00BW3970_2	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
00BW5031_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRSMAS	DFNLPPIVAK	EIVASCDKCQ
96BW01B21	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW0407	GIRKVLFLDG	IDKAQEEHEK	YHCNWRAMAS	DFNLPPVAK	EIVASCDKCQ
96BW0502	GIRKMLFLDG	IDKAQEEHEK	YHNNWRAMAD	EFNLPPIVAK	EIVASCDKCQ
96BW06_J4	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW11_06	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW1210	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
96BW15B03	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BW16_26	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
96BW17A09	GIRKVLFLDG	IDKAQEDHEK	YHGNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
96BWMO1_5	GIRKVLFLDG	IDKAQEEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
96BWMO3_2	GIRKILFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMC12_2	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMC13_4	GIRKVLFLDG	IDKAQDDHER	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
98BWMC14_a	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMO14_1	GIRKVLFLDG	IDKAQEEHEK	YHSNWRARAS	EFNLPPIVAK	EIVASCDKCQ
98BWMO18_d	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMO36_a	GIRKVLFLDG	IDKAQEEHEK	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
98BWMO37_d	GIRKVLFLDG	IDKAQEDHEK	YHSNWRAMAN	EFNLPPIVAK	EIVASCDKCQ
99BW3932_1	GIRKVLFLDG	IDKAREEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
99BW4642_4	GIRKVLFLDG	IDKAQDEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
99BW4745_8	GIRKVLFLDG	IDKAQEEHEK	YHSNWRAMAS	EFNLPPVAK	EIVASCDKCQ
99BW4754_7	GIRKILFLDE	IDKAQDEHEK	YHSNWRAMAS	EFNLPPVAK	EIVACCDKCQ

99BWMC16_8	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
A2_CD_97CD	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAH	DFNLPPIVAK	EIVASCDKGG
A2_CY_94CY	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAH	DFNLPPVIAK	EIVASCDKCQ
A2D_97KR	GIRKVLFLDG	IDKAEHEHER	YRSNWRAMAH	DFNLPPVIAK	EIVACCDKCQ
A2G_CD_97C	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKGG
A_BY_97BL0	XIRXVLFLEX	IDKAEHEHEK	YHSN.KAMAS	DFNLPPIVAX	EIVASXDKCQ
A_KE_Q23_A	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_SE659	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPVIAK	EIVASCDKCQ
A_SE_SE725	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
A_SE_SE753	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_SE853	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCNKCQ
A_SE_SE889	GVRRLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_SE_UGSE8	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
A_UG_92UG0	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
A_UG_U455	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCNKCQ
AC_IN_2130	GIRRVFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCNQCQ
AC_RW_92RW	GIRRVFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AC_SE_SE94	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
ACD_SE_SE8	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
ACG_BE_VI1	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
AD_SE_SE69	GIRKILFLDG	IDKAEHEHEK	YHNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
AD_SE_SE71	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
ADHK_NO_97	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
ADK_CD_MAL	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AG_BE_VI11	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AG_NG_92NG	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AGHU_GA_VI	GIRKVLFLDG	IDKAEHEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
AGU_CD_Z32	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
AJ_BW_BW21	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
B_AU_VH_AF	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_CN_RL42	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_DE_D31_U	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_DE_HAN_U	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_FR_HXB2	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_GA_OYI	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_GB_CAM1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_GB_GB8_A	GIRKILFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_GB_MANC	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_KR_WK_AF	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_NL_3202A	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAG	DFNLPPVIAK	EIVACCDKCQ
B_TW_TWCYS	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_BC_L0	GVRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_DH123	GIRRVFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_JRCSF	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_MNCG	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_P896	GIRKVLFLDG	IDKAEHEHEK	YHTNWRAMAS	DFNLPPVIAK	EIVASCNKCQ
B_US_RF_M1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_SF2_K	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_WEAU1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
B_US_WR27	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAG	DFNLPPVIAK	EIVACCDKCQ
B_US_YU2_M	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
BF1_BR_93B	GIRKVLFLDG	IDKAEHEHEK	YHNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_BR_92BR0	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_BW_96BW0	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_BW_96BW1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_BW_96BW1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_BW_96BW1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_ET_ETH22	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_IN_93IN1	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ
C_IN_93IN9	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVIAK	EIVASCDKCQ

C_IN_93IN9	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCGQCQ
C_IN_94IN1	GIRRVLFLLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDQCQ
C_IN_95IN2	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDQCQ
CRF01_AE_C	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_C	GIRKVLFLDG	IDKAEEDHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF01_AE_C	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	INKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPVVAKE	EIVANCDKCQ
CRF01_AE_T	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVTNCDCQ
CRF01_AE_T	GIRKVLFLDG	IDKAEHEHER	YHSNWRMTAS	DFNLPPIVAK	EIVANCDKCQ
CRF02_AG_F	GIRKVLFLDG	IDKAEHEHGR	YHSNWRAMAS	DFNLPPIIAK	EIVACCDQCQ
CRF02_AG_F	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVACCDKCQ
CRF02_AG_G	GFRKILFLDG	LDKAEHEHEK	FHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF02_AG_N	GIRKVLFLDG	IDKAEHEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF02_AG_S	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
CRF02_AG_S	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
CRF03_AB_R	GIREVLFLDG	IDKAEHEHEK	YHGNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
CRF03_AB_R	GIRKVLFLDG	IDKAEHAHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
CRF04_cpx	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPSVVAKE	EIVASCNKCQ
CRF04_cpx	GIRKVLFLDG	IDKAEEDHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCNKCQ
CRF04_cpx	GIRKVLFLDG	IDKAEHEHEK	YHNNWKAMAS	DFNLPPVVAKE	EIVASCNKCQ
CRF05_DF_B	GIRKVLFLDG	IDKAEDEHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
CRF05_DF_B	GIRKILFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
CRF06_cpx	GIRKVLFLDG	IDKAEEDHER	YHSNWRAMAN	DFNLPPIVAK	EIVASCDKCQ
CRF06_cpx	GIRKVLFLDG	IDKAEEDHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
CRF06_cpx	GIRKVLFLDG	IDKAEEDHER	YHSNWRAMAS	DFNLPPILAK	EIVACCDKCQ
CRF06_cpx	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAN	DFNLPPIVAK	EIVASCDKCQ
CRF11_cpx	GIRKVLFLDG	IDKAEEDHDR	YHSNWRMTAS	DFNLPPIVAK	EIVASCDKCQ
CRF11_cpx	GIRKVLFLDG	IDKAPEGHER	YHSNWRAMAS	DFNLPPVIAK	EIVANCDKCQ
D_CD_84ZR0	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
D_CD_ELI_K	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
D_CD_NDK_M	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
D_UG_94UG1	GIRKILFLDG	IDKAEHEHEK	YHNNWRAMAS	EFNLPPVVAKE	EIVASCDKCQ
F1_BE_VI85	GVRKILFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
F1_BR_93BR	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNIPAVVAK	EIVASCDKCQ
F1_FI_FIN9	GIRKILFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
F1_FR_MP41	GIRKILFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
F2_CM_MP25	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
F2KU_BE_VI	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
G_BE_DRCBL	GIRKVLFLDG	IDKAEHEHER	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
G_NG_92NG0	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
G_SE_SE616	GIRKVLFLDG	IDKAEHEHER	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
H_BE_VI991	GIRKVLFLDG	IDKAQVQHEK	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
H_BE_VI997	GIRKVLFLDG	IDKAEBAHER	YHNNWRAMAS	EFNLPPIVAK	EIVASCDKCQ
H_CF_90CF0	GVRKVLFLDG	IDKAEHEHER	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
J_SE_SE702	GIRKVLFLDG	IDKAEHEHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
J_SE_SE788	GIRKVLFLDG	IDKAEEDHEK	YHSNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
K_CD_EQTB1	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPVVAKE	EIVASCDKCQ
K_CM_MP535	GIRKVLFLDG	IDKAEHEHEK	YHNNWRAMAS	DFNLPPIVAK	EIVASCDKCQ
N_CM_YBF30	GIRKILFLDG	IEKAQEDHDR	YHSNWKAMAS	DFNLPPIVAK	EIVASCDKCQ
O_CM_ANT70	DIRRVLFLEG	IDQAQEDHEK	YHSNWKALAS	DFGLPPVVAKE	EIIASCPKCH
O_CM_MVP51	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPIVAK	EIIASCPKCH
O_SN_99SE	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPVVAKE	EIIANCPQCH
O_SN_99SE	DIRRVLFLEG	IDQAQEDHEK	YHSNWRALAS	DFGLPPVVAKE	EIIANCPKCH
U_CD_83C	GIRKVLFLDG	IDKAEHEHER	YHSNWRAMAS	DFNLPPIVAK	EIVASCDKCQ

801

00BW0762_1

LKGEAIHGQV DCSPGIWQLD CTHLEGKTIL VAVHVASGYM EAEVIPAETG

850

00BW0768_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
00BW0874_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1471_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1616_2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1686_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1759_3	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPTETG
00BW1773_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW1783_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1795_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIVL	VAVHVASGYL	EAEVIPTETG
00BW1811_3	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW1859_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
00BW1880_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVTPETG
00BW1921_1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2036_1	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAAHVASGYI	EAEVIPAETG
00BW2063_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYV	EAEVIPAETG
00BW2087_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2127_2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2128_3	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW2276_7	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
00BW3819_3	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAIHVASGYM	EAEVTPAETG
00BW3842_8	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW3871_3	LKGEATHRQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW3876_9	QKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW3886_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKITL	VAVHVASGYI	EAEVIPAETG
00BW3891_6	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
00BW3970_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
00BW5031_1	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW01B21	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
96BW0407	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW0502	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
96BW06_J4	SKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BW11_06	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BW1210	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW15B03	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW16_26	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
96BW17A09	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
96BWM01_5	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
96BWM03_2	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYM	EAEVIPAETG
98BWMC12_2	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVITAETG
98BWMC13_4	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWMC14_a	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVISAETG
98BWM014_1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWM018_d	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
98BWM036_a	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
98BWM037_d	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYV	EAEVIPAETG
99BW3932_1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
99BW4642_4	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
99BW4745_8	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
99BW4754_7	QKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
99BWMC16_8	LKGEAIHGQV	DCSPGVWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A2_CD_97CD	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIV	VAVHVASGYI	EAEVIPAETG
A2_CY_94CY	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPTETG
A2D_97KR	VKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
A2G_CD_97C	LKGEAMHGQV	DCSPGVWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
A_BY_97BL0	LKXEXMHXQV	DCSPXIWQLD	CTHLXXKVIL	XAVXVASGYI	EAEVIPAETG
A_KE_Q23_A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIV	VAVHVASGYI	EAEVIPAETG
A_SE_SE659	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE725	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE753	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_SE853	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG

A_SE_SE889	LKGEAMHGQV	DCSPGMWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_SE_UGSE8	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_UG_92UG0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
A_UG_U455_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
AC_IN_2130	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AC_RW_92RW	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AC_SE_SE94	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ACD_SE_SE8	IKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ACG_BE_VI1	LKGEAMHGQV	DCSPGIWQID	CTHLEGKVII	VAVHVASGYM	EAEVIPAETG
AD_SE_SE69	LKGEALHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
AD_SE_SE71	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
ADHK_NO_97	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
ADK_CD_MAL	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
AG_BE_VI11	LKGEAIHGQV	DCSPGIWQLD	CTHLEGKIII	VAVHVASGYI	EAEVIPAETG
AG_NG_92NG	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYI	EAEVIPAETG
AGHU_GA_VI	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AGU_CD_Z32	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
AJ_BW_BW21	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVII	VAVHVASGYM	EAEVIPAETG
B_AU_VH_AF	QKGEAMHGQV	DCSPGLWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_CN_RL42	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_DE_D31_U	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_DE_HAN_U	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_FR_HXB2_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_GA_OYI_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_GB_CAM1_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_GB_GB8_A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_GB_MANC_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_KR_WK_AF	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_NL_3202A	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_TW_TWCYS	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_BC_L0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_DH123	VKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_JRCSE	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_MNCG_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_P896_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
B_US_RF_M1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_SF2_K	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_WEAU1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_WR27_	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
B_US_YU2_M	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
BF1_BR_93B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVAGGYI	EAEVIPAETG
C_BR_92BR0	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW0	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_BW_96BW1	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_ET_ETH22	LKGEATHGQV	NCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN9	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_93IN9	QKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
C_IN_94IN1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
C_IN_95IN2	LKGEATHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYM	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG

CRF01_AE_T	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIVL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_F	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_F	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_G	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_N	MKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF02_AG_S	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF03_AB_R	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF04_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIVM	VAVHVASGYI	EAEVIPAETG
CRF04_cpx	LKGEAMHGQX	DCSPGIWQLD	CTHLEGKIIL	VPVHVASGYI	EAEVIPAETG
CRF04_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF05_DF_B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIVL	VAVHVASGYI	EAEVIPAETG
CRF05_DF_B	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIVL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF06_cpx	LKGEPMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
CRF11_cpx	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIM	VAVHVASGYI	EAEVIPAETG
CRF11_cpx	LKGEAMHGQV	DCSPRIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
D_CD_84ZR0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_CD_ELI_K	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_CD_NDK_M	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
D_UG_94UG1	VKGEALHGQV	DCSPGIWQLD	CTHLEGKGIL	VAVHVASGYI	EAEVIPAETG
F1_BE_VI85	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASEYI	EAEVIPAETG
F1_BR_93BR	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYL	EAEVIPAETG
F1_FI_FIN9	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F1_FR_MP41	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F2_CM_MP25	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
F2KU_BE_VI	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_BE_DRCLB	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_UG_92NG0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
G_SE_SE616	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
H_BE_VI991	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
H_BE_VI997	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
H_CF_90CF0	LKGEAMHGQV	DCSPGIWQLD	CTHLEGQVIL	VAVHVASGYI	EAEVIPAETG
J_SE_SB702	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
J_SE_SB788	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYI	EAEVIPAETG
K_CD_BQTB1	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
K_CM_MP535	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKIIL	VAVHVASGYI	EAEVIPAETG
N_CM_YBF30	LKGEAMHGQV	NCSPGVWQLD	CTHLEGKIIL	VAVHVASGYL	EAEVIPAETG
O_CM_ANT70	IKGEAMHGQV	DCSPEVWQID	CTHMEGKIIL	VAVHVASGFI	EAEVIPAETG
O_CM_MVP51	IKGEATHGQV	DYSPEIWQMD	CTHLEGKIIL	VAVHVASDFI	EAEVIPAETG
O_SN_99SE	IKGEAMHGQV	DCSPEVWQMD	CTHLEGKIIL	VAVHVASGFI	EAEVIPAETG
O_SN_99SE	IKGEAMHGQV	DYSPEVWQMD	CTHLEGKIIL	VAVHVASGFI	EAEVIPAETG
U_CD_83C	LKGEAMHGQV	DCSPGIWQLD	CTHLEGKVIL	VAVHVASGYL	EAEVIPAETG

851

900

00BW0762_1	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW0768_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW0874_2	QDTAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAD	IQQEFGIPYN
00BW1471_2	QEAAYFILKL	AGRWPVQIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1616_2	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1686_8	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1759_3	QETAYLILKL	AGRWPVKIIH	TDNGSNFTST	TVKAACWWAG	IQQEFGIPYN
00BW1773_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	VQQEFGIPYN
00BW1783_5	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	TVKAACWWAG	IQQEFGIPYN
00BW1795_6	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1811_3	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSN	AMKAACWWAG	IQQEFGIPYN
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00BW1880_2	QETAYYILKL	AGRWPVKIIH	TDNGRNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW1921_1	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
00BW2036_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2063_6	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2087_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2127_2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW2128_3	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYS
00BW2276_7	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	TVKAACWWAG	IQQEFGIPYN
00BW3819_3	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
00BW3842_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
00BW3871_3	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	VVKAACWWAG	IQQEFGIPYN
00BW3876_9	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSS	AVKAACWWAG	TQQEFGIPYN
00BW3886_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
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00BW3970_2	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
00BW5031_1	QETVYFILKL	AGRWPVKAIH	TDNGSNFTSA	AVKAACWWAG	INQEFGIPYN
96BW01B21	QETAYYILKL	AGRWPVKVIH	TDNGTNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW0407	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
96BW0502	QETAYFILKL	AGRWPVRVIH	TDNGTNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW06_J4	QDTAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW11_06	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW1210	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	TQQEFGIPYN
96BW15B03	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BW16_26	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAG	IQQEFGIPYN
96BW17A09	QETADFILKL	AGRWPVQIIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
96BWM01_5	QETAYFLLKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
96BWM03_2	QDTAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AMKAACWWAG	IQQEFGIPYN
98BWMC12_2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSG	AVKAACWWAG	IQQEFGIPYN
98BWMC13_4	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWMC14_a	QETAYYILKL	AARWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM014_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM018_d	QETAYYILKL	AGRWSVKTIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM036_a	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
98BWM037_d	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BW3932_1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
99BW4642_4	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
99BW4745_8	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BW4754_7	QETAYYILKL	AGRWPVKTIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
99BWMC16_8	QDTAYYMLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	VQQEFGIPYN
A2_CD_97CD	QETAYFLLKL	AGRWPVKVIH	TDNGPNFTSA	AVKAACWWAD	VKQEFGIPYN
A2_CY_94CY	QDTAYFILKL	AGRWPVKVIH	TDNGPNFISA	TVKAACWWAG	IQQEFGIPYN
A2D_97KR	QETAYFILKL	AGRWPVKVIH	TDNGPNFISA	PVKAACWWAG	VQQEFGIPYN
A2G_CD_97C	QETAYFILKL	AGGWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
A_BY_97BL0	QETAYFLLKL	AGRWPVKVVH	TDNGPNFTSS	AVKAACWAN.	IQQEFXIPYN
A_KE_Q23_A	QETAYFLLKL	AGRWPVKIVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
A_SE_SE659	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
A_SE_SE725	QETAYFLLKL	AGRWPVKIVH	TDNGSNFTSA	AFKAACWWAS	IQQEFGIPYN
A_SE_SE753	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VKQEFGIPYN
A_SE_SE853	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN
A_SE_SE889	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN
A_SE_UGSE8	QEAAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAN	VQQEFGIPYN
A_UG_92UG0	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	VKQEFGIPYN
A_UG_U455_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAVCWWAN	IQQEFGIPYN
AC_IN_2130	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
AC_RW_92RW	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	TVKAACWWAG	IQQEFGIPYN
AC_SE_SE94	QETAYFLLKL	AGRWPVRRVH	TDNGSNFTSA	AVKAACWWAN	IQQEFGIPYN
ACD_SE_SE8	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AFKAACWWAS	VQQEFGIPYN
ACG_BE_VI1	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
AD_SE_SE69	QETAYFLLKL	AGRWPVRVVH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
AD_SE_SE71	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN

ADHK_NO_97	QETAYFILKL	AGRWPVKVIH	TDNGSNFISA	AVKAACWWAD	IKQEFGIPYN
ADK_CD_MAL	QETAYFILKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	IKQEFGIPYN
AG_BE_VI11	QETAYFILKL	AGRWPVKILH	TDNGSNFISA	AVKAACWWAD	IKQEFGIPYN
AG_NG_92NG	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AMKAACWWAN	IQQEFGIPYN
AGHU_GA_VI	QETAYFILKL	AGRWPVKVIH	TDNGTNFTSA	AVKAACWWAN	VTQEFGIPYN
AGU_CD_Z32	QETAYFILKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
AJ_BW_BW21	QETAYFLLKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAG	VRQEFGIPYN
B_AU_VH_AF	QETAYFLLKL	AGRWPVKTVH	TDNGPIFIST	AVKAACWWAG	IKQEFGIPYN
B_CN_RL42	QETAYFLLKL	AGRWPVKTIH	TDNGRNFTSN	SVKAACWWAG	IKQEFGIPYN
B_DE_D31_U	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	VKQEFGIPYN
B_DE_HAN_U	QETAYFLLKL	AGRWPVKTVH	TDNGPNFTST	TVKAACWWAG	IKQEFGIPYN
B_FR_HXB2	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTGA	TVRAACWWAG	IKQEFGIPYN
B_GA_OYI	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_GB_CAM1	QETAYFLLKL	AGRWPVKTIH	TDNGGNFIST	TVKAACWWAG	IKQEFGIPYN
B_GB_GB8_A	QETAYFILKL	AGRWPVKTIH	TDNGRNFTST	TVKAACWWAG	IKQEFGIPYN
B_GB_MANC	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_KR_WK_AF	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTSN	TVKAACWAR.	IKQEFGIPYN
B_NL_3202A	QETAYFILKL	AGRWPVTTIH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
B_TW_TWCYS	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTSA	AVKAACWWAG	IKQKFGIPYN
B_US_BC_L0	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_DH123	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_JRCSF	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_MNCG	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_P896	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_RF_M1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_SF2_K	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_WEAU1	QETAYFILKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
B_US_WR27	QETAYFILKL	AXRWPVXTIH	TDNGSNFIST	TVXAAXWWAG	IXQEFGIPYN
B_US_YU2_M	QETAYFLLKL	AGRWPVTTIH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
BF1_BR_93B	QETAYFLLKL	AGRWPVKTIH	TDNGSNFTST	TVKAACWWAG	IKQEFGIPYN
C_BR_92BR0	QETAYFILKL	AGRWPVKVIH	TDNGSNFISN	TVKAACWWAG	IQQEFGIPYN
C_BW_96BW0	QETAYYILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAG	IQQEFGIPYN
C_BW_96BW1	QETAYYILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_BW_96BW1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	TQQEFGIPYN
C_BW_96BW1	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_ET_ETH22	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN9	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_93IN9	QETAYYILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAS	IQQEFGIPYN
C_IN_94IN1	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
C_IN_95IN2	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AG.RPVKVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVRVIH	TDNGSNFTSA	AMKAACWWAN	VQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VQQEFGIPYN
CRF01_AE_C	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAN	VQQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VQQEFGIPYN
CRF01_AE_T	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAN	VRQEFGIPYN
CRF02_AG_F	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_F	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_G	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_N	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_S	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF02_AG_S	QETAYFILKL	AGRWP.KVVH	TDNGSNFTSA	AVKAACWWPK	LHQELGIYN.
CRF03_AB_R	QETAYFVLKL	AGRWPVKIIH	TDNGSNFTST	AVKAACWWAG	IKQEFGIPYN
CRF03_AB_R	QETAYFVLKL	AGRWPVKVIH	TDNGSNFIST	AVKAACWWAG	IKQEFGIPYN
CRF04_cpx	QETAYFILKL	AGRWPVKMIH	ADNGPNFTSA	AVKAACWWAD	INQEFGIPYN
CRF04_cpx	QETAYFILKL	AGRWPVKIIH	TDNGPNFTSA	AVKAACWWAD	VQQEFGIPYN

CRF04_cpx_	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAN	IQQEFVGPYN
CRF05_DF_B	QDTAYFILKL	AGRWPVKMIH	TDNGPNFTSG	AVKAACWWAG	IQQEFGIPYN
CRF05_DF_B	QETAYFILKL	AGRWPVKMVIH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTST	AVKAACWWAN	VTQEFGIPYN
CRF06_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	AVKAACWWAN	VTQEFGIPYN
CRF11_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSS	TVKAACWWAN	IQQEFGIPYN
CRF11_cpx_	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSN	AVKAACWWAG	IQQEFGIPYN
D_CD_84ZR0	QEAAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
D_CD_ELI_K	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
D_CD_NDK_M	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	TVKAACWWAG	IKQEFGIPYN
D_UG_94UG1	QETAYFLLKL	AGRWPVKVVH	TDNGSNFTSA	AVKAACWWAG	IKQEFGIPYN
F1_BE_VI85	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKASCWWAG	ITQEFGIPYN
F1_BR_93BR	QETAYFLLKL	AGRWPVKTIH	TDNGTNFTSA	TVKAACWWAG	IQQEFGIPYN
F1_FI_FIN9	QDTAYFILKL	AGRWPVKMIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN
F1_FR_MP41	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSS	AVKAACWWAG	IQQEFGIPYN
F2_CM_MP25	QEAAYFILKL	AGRWPVKIIH	TDNGSNFTSA	VVKAACWWAG	IQQEFGIPYN
F2KU_BE_VI	QETAFFILKL	AGRWPVKIIH	TDNGSNFISA	TVKAACWWAG	IQQEFGISYN
G_BE_DRCBL	QETAYFILKL	AGRWPVKIIH	TDNGSNFTSA	AVKAACWWAS	ITQEFGIPYN
G_NG_92NG0	QETAYFILKL	AGRWPVKVIH	TDNGPNFISA	AVKAACWWAN	ITQEFGIPYN
G_SE_SE616	QETAYFILKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAN	ITQEFGIPYN
H_BE_VI991	QETAYFILKL	AGRWPVKMIH	TDNGSNFTSA	AVKAACWWAD	IKQEFGIPYN
H_BE_VI997	QETAYFILKL	AGRWPVKMIH	TDNGTNFTST	AVKAACWWAD	IQQDFGIPYN
H_CF_90CF0	KETAYFLLKL	ASRWPVKVIH	TDNGSNFTSA	AVKAACWWAD	IQQEFGIPYN
J_SE_SE702	QEAFFILKL	AGGWPVKAIH	TDNGSNFTSG	AVKAACWWAD	IKQEFGIPYN
J_SE_SE788	QEAFFILKL	AGRWPVKVIH	TDNGSNFTSG	AVKAACWWAD	IKQEFGIPYN
K_CD_EQTB1	QETAYFILKL	AGRWPVRVIH	TDNGSNFTSA	VVKAACWWAD	IKQEFGIPYN
K_CM_MP535	QETAYFILKL	AGRWPVKVIH	TDNGTNFTST	VVKAACWWAG	VKQEFGIPYN
N_CM_YBF30	QETAYFILKL	AGRWPVKVIH	TDNGSNFTSA	TVKAACWWAN	IKQEFGIPYN
O_CM_ANT70	QETAYFLLKL	AARWPVKVIH	TDNGPNFTST	TMKAACWWAN	IQHEFGIPYN
O_CM_MVP51	QETAYFLLKL	AARWPVKVIH	TDNGPNFTSA	AMKAACWWTG	IQHEFGIPYN
O_SN_99SE_	QETAYFLLKL	AARWPVKVIH	TDNGPNFTSA	AMKAACWWAN	IKHEFGIPYN
O_SN_99SE_	QETAYFLLKL	AARWPVKIIH	TDNGPNFTSA	TMKAACWWTG	IKHEFGIPYN
U_CD_83C	QETAYFVLKL	AGRWPVTVIH	TDNGSNFTSA	AVKAACWWAG	IQQEFGIPYN

901

950

00BW0762_1	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRRGGIGGY
00BW0768_2	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW0874_2	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRRGGIGGY
00BW1471_2	PQSQGVVKS	NKELKKIIGQ	VRDQAEHLKT	AVLMAVFIHN	FKRKGGIGGY
00BW1616_2	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW1686_8	PQSQGVVESM	NKELKKIIGQ	VRDQAEHHT	AVQMAVFVHN	FKRKGGIGGY
00BW1759_3	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW1773_2	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW1783_5	PQSQGVVESM	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW1795_6	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW1811_3	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRRGGIGGY
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00BW1921_1	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
00BW2036_1	PQSQGVVESM	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
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00BW3842_8	PQSQGVVESM	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGGIGGY
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00BW3876_9	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
00BW3886_8	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
00BW3891_6	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
00BW3970_2	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
00BW5031_1	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
96BW01B21	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
96BW0407	PQSQGVVESH	NKELEKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
96BW0502	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BW06_J4	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BW11_06	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BW1210	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BW15B03	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BW16_26	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BW17A09	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
96BWM01_5	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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98BWMC12_2	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWMC13_4	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWMC14_a	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM014_1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM018_d	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
98BWM036_a	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
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99BWMC16_8	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A2_CD_97CD	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2_CY_94CY	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2D_97KR	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A2G_CD_97C	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
A_BY_97BL0	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_KE_Q23_A	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE659	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE725	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE753	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE853	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_SE889	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_SE_UGSE8	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_UG_92UG0	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
A_UG_U455_	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
AC_IN_2130	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AC_RW_92RW	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AC_SE_SE94	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
ACD_SE_SE8	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
ACG_BE_VI1	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AD_SE_SE69	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AD_SE_SE71	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
ADHK_NO_97	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
ADK_CD_MAL	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
AG_BE_VI11	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AG_NG_92NG	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AGHU_GA_VI	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AGU_CD_Z32	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
AJ_BW_BW21	PQSQGVVESH	NKELKKIIGQ	VREQAHLKT	AVQMAVFIHN	FKRKGIGGY
B_AU_VH_AF	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_CN_RL42_	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_DE_D31_U	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
B_DE_HAN_U	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY

D_CD_NDK_M	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
D_UG_94UG1	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_BE_VI85	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_BR_93BR	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_FI_FIN9	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F1_FR_MP41	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F2_CM_MP25	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
F2KU_BE_VI	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
G_BE_DRCBL	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
G_NG_92NG0	PQSQGVVESH	NKELKKIIGQ	VGDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
G_SE_SE616	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
H_BE_VI991	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
H_BE_VI997	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
H_CF_90CF0	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
J_SE_SE702	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
J_SE_SE788	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
K_CD_EQTB1	PQSQGVVESH	NKELKKIIGQ	VREQAEHLKT	AVQMAVFIHN	FKRKGIGGY
K_CM_MP535	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
N_CM_YBF30	PQSQGVVESH	NKELKKIIGQ	IRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
O_CM_ANT70	PQSQGVVEAM	NKELKSIIQQ	VRDQAEHLRT	AVQMAVFIHN	FKRKGIGGY
O_CM_MVP51	PQSQGVVEAM	NKELKSIIQQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
O_SN_99SE	PQSQGVVEAM	NKELKSIIQQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
O_SN_99SE	PQSQGVVEAM	NKELKSIIQQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY
U_CD_83C	PQSQGVVESH	NKELKKIIGQ	VRDQAEHLKT	AVQMAVFIHN	FKRKGIGGY

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1000

00BW0762_1	SAGERIIDII	ATDIQTRELQ	KRIIQIONFR	VYYRDSRDPI	WKGPALLWK
00BW0768_2	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW0874_2	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1471_2	SAGERIVDII	ASDIQTKELQ	KQITKIONFR	VYYRDSREPV	WKGPALLWK
00BW1616_2	SAGERIVDII	ATDIQTRELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1686_8	SAGERIIDII	ATDIQTKELQ	KQITKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1759_3	SAGERIIDII	ATDIQTKELQ	KQITKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1773_2	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1783_5	SAGERIIDII	ATDIQTRELQ	KQIIKIONFR	VYYGDSRDPI	WKGPALLWK
00BW1795_6	SAGERIIDII	ATDIQTRELQ	KQIIKIONFR	VYYRDNRPDI	WKGPALLWK
00BW1811_3	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1859_5	SAGERIIDII	ATDIQTRELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1880_2	SAGERIIDII	ATDIQTRELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW1921_1	SAGERIIDII	ATDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPALLWK
00BW2036_1	SAGERIIDII	ATDIQTKELQ	KQITKIONFR	VYYRDSRDPI	WKGPALLWK
00BW2063_6	SAGERIIDII	ATDIQTRELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW2087_2	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW2127_2	SAGERIIDII	ATDIQTKELQ	KRIIQIONFR	VYYRDSRDPI	WKGPALLWK
00BW2128_3	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW2276_7	SAGERIIDII	ATDIQTKELQ	KQITKIONFR	VYYRDSRDPI	WKGPALLWK
00BW3819_3	SAGERIIDII	ATDIQTRELQ	KQIIQIONFR	VYYRDSRDPI	WKGPALLWK
00BW3842_8	SAGERIIDII	ATDIQTKELQ	NQITKIONFR	VYYRDSRDPI	WKGPALLWK
00BW3871_3	SAGERIIDII	ATDIQTKELQ	KQITKIONFR	AYYRDSRDPI	WKGPALLWK
00BW3876_9	SAGERIIDII	ATDIQTKELQ	NQITKIONFR	VYYRDSRDPI	WKGPALLWK
00BW3886_8	SAGERIIDII	ATDIQTKELQ	NQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW3891_6	SAGGRIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW3970_2	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
00BW5031_1	SAGERIIDII	ATDIQTKELQ	KQITKIONFR	VYYRDSRDPI	WKGPALLWK
96BW01B21	SAGERIIDII	ATDIRTKELQ	KQIMKIRNFR	VYYRDSRDPI	WRGPALLWK
96BW0407	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
96BW0502	SAGERIIDII	ATDIQTKELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
96BW06_J4	SAGERIIDII	ATDIQTKELQ	KQITNIQKFR	VYYRDSRDPI	WKGPALLWK
96BW11_06	SAGERIIDMI	ATDIQTRELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK
96BW1210	SAGERIIDII	ATDIQTTELQ	KQIIKIONFR	VYYRDSRDPI	WKGPALLWK

96BW15B03	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLIWK
96BW16_26	TAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
96BW17A09	SAGERIVDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSREP	WKGPAKLLWK
96BWM01_5	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRPDI	WKGPAKLLWK
96BWM03_2	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWM012_2	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWM013_4	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDNRPDI	WKGPAKLLWK
98BWM014_a	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWM014_1	SAGERIIDII	ATDIQTKELQ	KQILNIQKFR	VYYRDSRDPI	WKGPAKLLWK
98BWM018_d	SAGERIIDII	ATDIQTRELQ	RQIIKIQIFR	VYYRDSRDPI	WKGPAKLLWK
98BWM036_a	SAGERIIDII	ATDIQTKELQ	RQILKIQNFR	VYYRDSRDPI	WKGPAKLLWK
98BWM037_d	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSGDPI	WKGPAKLLWK
99BW3932_1	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4642_4	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4745_8	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BW4754_7	SAGERIIDII	ASDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
99BWM016_8	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2_CD_97CD	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2_CY_94CY	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2D_97KR	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A2G_CD_97C	SAGERIIDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_BY_97BL0	SAXERIIDII	ATDIQTKELQ	KXITKIQNFX	VYYRDSRDPI	WKGPAKLLXK
A_KE_Q23_A	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPL	WKGPAKLPWK
A_SE_SE659	SAGERIIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE725	SAGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE753	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE853	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_SE889	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_SE_UGSE8	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
A_UG_92UG0	SAGERIIDII	ASDLQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
A_UG_U455_	SAGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRDPI	WKGPAKLLWK
AC_IN_2130	SAGERIIDII	ATDIQTKELQ	KQISKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_RW_92RW	SAGERIIDII	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AC_SE_SE94	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
ACD_SE_SE8	SVGERIIDII	ATDIQTKELQ	KQITKIQKFR	VYYRDSRNPI	WKGPAKLLWK
ACG_BE_VI1	SARERIIDII	ASDIQTKELQ	KPITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AD_SE_SE69	SAGERIIDII	ATDIQTKELQ	RQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AD_SE_SE71	SAGERIIDII	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
ADHK_NO_97	SAGERIIDXI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
ADK_CD_MAL	SAGERIIDMI	ATDIQTKELQ	KQITKIQNFR	VYYRDNRPDI	WKGPAKLLWK
AG_BE_VI11	SAGERIIDII	ASDIQTKELQ	KXITKIXNFR	VYYRDSRDPI	WKGPAKLLWK
AG_NG_92NG	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AGHU_GA_VI	SAGERIIDII	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AGU_CD_Z32	SAGERIVDII	ASDIQTKELQ	NQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
AJ_BW_BW21	SAGERIIDMI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLLWK
B_AU_VH_AF	SAGERIIDII	ASDIQTKELQ	KQITKVQNFR	VYYRDSRDPL	WKGPAKLLWK
B_CN_RL42_	SAGERIVDII	ATDIQTRELQ	KQITKIQNFR	VYYRGSRDPL	WKGPAKLLWK
B_DE_D31_U	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_DE_HAN_U	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREP	WKGPAKLLWK
B_FR_HXB2_	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRNPL	WKGPAKLLWK
B_GA_OYI_	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSREPL	WKGPAKLLWK
B_GB_CAM1_	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_GB_GB8_A	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_GB_MANC_	SAGGRIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRNPL	WKGPAKLLWK
B_KR_WK_AF	SAGERIIDII	ATDIQTKELQ	KQVTKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_NL_3202A	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_TW_TWCYS	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNRPDI	WKGPAKLLWK
B_US_BC_L0	SAGERIVDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNKDPL	WKGPAKLLWK
B_US_DH123	SAGERIVDII	ASDIQTKELQ	KQITKIQNFR	VYYRDSRDPL	WKGPAKLLWK
B_US_JRCSF	SAGERIIDII	ATDIQTKELQ	KQITKIQNFR	VYYRDNRPDI	WKGPAKLLWK

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B_US_MNCG_	SAGERIVGII	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPL	WKGPAKLWLK
B_US_P896_	SAGERIVDII	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPL	WKGPAKLWLK
B_US_RF_M1	SAGERIVDII	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPL	WKGHAKLLWK
B_US_SF2_K	SAGERIVDII	ATDIQTKELQ	KOITKIQNFR	VYYRDNKDPL	WKGPAKLWLK
B_US_WEAU1	SAGERIIDI	ATDIQTQQQLQ	KOITKIQNFR	VYYRDSRDPL	WKGPAKLWLK
B_US_WR27_	SAGERIIDI	ATDIQXKKXLQ	XQXTIXQNXR	VYYRDSRDPL	WKGPAKLWLK
B_US_YU2_M	SAGERIVDII	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPL	WKGPAKLWLK
BF1_BR_93B	SAGERIVDII	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPL	WKGPAKLWLK
C_BR_92BR0	SAGERIIDI	ATDIQTKELQ	KQIMKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_BW_96BW0	SAGERIIDI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
C_BW_96BW1	SAGERIIDMI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_BW_96BW1	SAGERIIDI	ATDIOTTLELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_BW_96BW1	SAGERIIDI	ATDIQTKBLQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_ET_ETH22	SAGERIIDI	ASDIQTKBLQ	NQILKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_IN_93IN1	SAGERIIDI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_IN_93IN9	SAGERIIDI	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_IN_93IN9	SAGERIIDI	ATDIQTKELQ	KQIIKIHNR	VYYRDSRDPI	WKGPAKLWLK
C_IN_94IN1	SAGERIIDI	STDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
C_IN_95IN2	SAGERIIDI	ATDIQTKELQ	KOITKVQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_C	SAGERIIDI	AITEIQTBEXQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_C	SAGERIIDI	ATDIQTKALQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_C	SAGERIIDI	ATDIQTKELQ	KHITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_T	SAGERIIDI	ATDIQTKBLQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_T	SVGERIIDII	AADIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_T	SAGERIIDI	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_T	SAGERIIDI	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_T	SAGERIIDI	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF01_AE_T	SAGERIIDI	ATDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF02_AG_F	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF02_AG_F	SAGERIIDI	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF02_AG_G	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF02_AG_N	SAGERIIDI	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF02_AG_S	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF02_AG_S	SAGERIIDI	ASDIQTKELQ	KOITNIQKFR	VYYRDSRDPI	WKGPAKLWLK
CRF03_AB_R	SAGERIIDI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF03_AB_R	SAGERIIDI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF04_cpx_	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSREPI	WKGPAKLWLK
CRF04_cpx_	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF04_cpx_	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF05_DF_B	GAGERIIDII	TDDIOTKELQ	KQIIKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
CRF05_DF_B	SAGEGIIDI	STDIQTKELQ	KOITKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
CRF06_cpx_	SAGERIIDI	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF06_cpx_	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF06_cpx_	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF06_cpx_	SAGERIIDI	ASDIQTKELQ	KOITKIRNFR	VYYRDSRDPI	WKGPAKLWLK
CRF11_cpx_	SAGERIVDII	ATDLQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
CRF11_cpx_	SAGERIIDI	ATDLQTKELQ	KOITKIQKFR	VYYRDSRDPI	WKGPAKLWLK
D_CD_84ZR0	SAGERIIDI	ASDIQTRELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
D_CD_ELI_K	SAGERIIDI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
D_CD_NDK_M	SAGERIIDI	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
D_UG_94UG1	SAGERIIDI	ATDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
F1_BE_VI85	SAGERIIDI	STDIQTRELQ	KOITKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
F1_BR_93BR	SAGERTIDII	ATDIQTRELQ	KQIIKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
F1 FI_FIN9	SAGERIIDI	ATDIQTKELQ	KQVTKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
F1_FR_MP41	SAGERIIDI	STDIQTRELQ	KQIIKIQNFR	VYYRDSRDPIV	WKGPAKLWLK
F2_CM_MP25	SAGERIIDI	ATDIQTKELQ	KQISKIQNFR	VYFRDSRDPIV	WKGPAKLWLK
F2KU_BE_VI	SAGERIVDII	ASDIQTRALQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
G_BE_DRCBL	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPI	WKGPAKLWLK
G_NG_92NG0	SAGERIIDI	ASDIQTKELQ	KQIIKIQNFR	VYYRDSRDPI	WKGPAKLWLK
G_SE_SE616	SAGERIIDI	ASDIQTKELQ	KOITKIQNFR	VYYRDSRDPIV	WKGPAKLWLK

H_BE_VI991	SARERIIDI	ATDIPTKELQ	KQISQIQKFR	VYYRDSRDPI	WKGPAKLLWK
H_BE_VI997	SAGERIIDII	ATDIQTKELO	KQISNIQKFR	VYYRDSRDPI	WKGPAKLLWK
H_CF_90CF0	SAGERIIDII	ATDIQTKELO	KQISNIQKFR	VYYRDSRDPI	WKGPAKLLWK
J_SE_SE702	SAGERIIDII	ATDIQTKELO	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
J_SE_SE788	SAGERIIDII	ATDIQTRELO	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK
K_CD_EQTB1	SAGERIIDII	ATDIQTKELO	KQITKIQNFR	VYYRDSRDPI	WKGPAKLPWK
K_CM_MP535	SAGERIVDII	ATDIQTKELO	KQILNIQKFR	VYYRDSREPI	WKGPAKLLWK
N_CM_YBF30	TAGERIIDII	ATDIQTNNLO	TQILKVQNFR	VYYRDSRDPI	WKGPAKLLWK
O_CM_ANT70	TAGERIIDIL	ASQIQTTTELQ	KQILKXHKFR	VYYRDSRDPI	WKGPAQLLWK
O_CM_MVP51	TAGERLIDIL	ASQIQTTTELQ	KQILKINNFR	VYYRDSRDPI	WKGPAQLLWK
O_SN_99SE_	TAGERIIDIL	ASQIQTTTELQ	KQIFKIQKFQ	VYYRDSRDPI	WKGPAQLLWK
O_SN_99SE_	TAGERIIDIL	ASQIQTTTELQ	KQIFKIQKFQ	VYYRDSRDPI	WKGPAQLLWK
U_CD__83C	SAGERIIDII	ATDIQTKELO	KQITKIQNFR	VYYRDSRDPI	WKGPAKLLWK

1001

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00BW0762_1	GE.GAVVIQD	NSDIKVIPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
00BW0768_2	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW0874_2	GE.GAVVIQD	NGDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW1471_2	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
00BW1616_2	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW1686_8	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDEDQ
00BW1759_3	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDEDQ
00BW1773_2	GE.GAVVIQD	NNDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDEDQ
00BW1783_5	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	GQDEN.
00BW1795_6	GE.GAVVLQD	NSEIKVVPRR	KVKIIRDYGK	Q MAGADCMAG	RQDEDQ
00BW1811_3	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDEDQ
00BW1859_5	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	GQDEN.
00BW1880_2	GE.GAVVIQD	KSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAS	RQDED.
00BW1921_1	GE.GAVVIQD	NSDVKVVPRR	KAKIIRDYGK	Q MAGADCVAD	RQDED.
00BW2036_1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAD	RQDED.
00BW2063_6	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW2087_2	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW2127_2	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAS	RQDED.
00BW2128_3	GE.GAVVLQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	GQDEN.
00BW2276_7	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW3819_3	GE.GAVVIQD	NGDIKVVPRR	KAKIIRDYGK	Q MAGADCVAS	RQDEN.
00BW3842_8	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW3871_3	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
00BW3876_9	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
00BW3886_8	GE.GAVVIQD	KGDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
00BW3891_6	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
00BW3970_2	GE.GAVVIQD	NSDIKVVPRR	RAKIIRDYGK	Q MAGADCVAD	RQDED.
00BW5031_1	GE.GAVVIQD	NSDIKAVPRR	KAKIIRDYGQ	Q MAGADCVAG	RQDEN.
96BW01B21	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
96BW0407	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
96BW0502	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	GQDEN.
96BW06_J4	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAS	RQDED.
96BW11_06	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
96BW1210	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
96BW15B03	GEGAVVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDED.
96BW16_26	GE.GAVVLQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	GQDEN.
96BW17A09	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
96BWM01_5	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDEDQ
96BWM03_2	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDEDQ
98BWMC12_2	GD.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
98BWMC13_4	GE.GAVVIQD	NSEIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDEDQ
98BWMC14_a	GE.GAVVIQD	SSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
98BWM014_1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.
98BWM018_d	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	Q MAGADCVAG	RQDEDQ
98BWM036_a	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	Q MAGADCVAG	RQDED.

98BWM037_d GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGADCVAG RQDEDQ
 99BW3932_1 GE.GAVVIQD NSDIKVVPRR KAKIIRKDYGK QMAGADCVAS RQDED.
 99BW4642_4 GE.GAVVIQD NSDIKVVPRR KAKIIRKDYGK QMAGADCVAD RQDED.
 99BW4745_8 GE.GAVVIQD NSDIKVVPRR KVKIIRKDYGK QMAGADCVAG RQDED.
 99BW4754_7 GE.GAVVIQD KSDIKVVPRR KAKIIRKDYGK QMAGDDCVAG RQDED.
 99BWM016_8 GE.GAVVIQD NSDIKVVPRR KAKIIRKDYGK QMAGADCVAG RQDED.
 A2_CD_97CD GE.GAVVIQD NGDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 A2_CY_94CY GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 A2D_97KR GE.GAVVIQD NSDIKVVPRR RAKIIRDYGK QMAGDDCVAG RQDED.
 A2G_CD_97C GE.GAVVIQD NNEIKVVPRR KTKILRDYGK QMAGDDCVAG RQDED.
 A_BY_97BL0 GE.GAVVIQD NXDIKVVPRR KAKIIXDXXK QMAGXDCVAS RQDED.
 A_KE_Q23_A GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 A_SE_SE659 GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 A_SE_SE725 GE.GAVVIQD NNDIKVVPRR KAKILRDYGK QMAGDDCVAG RQDED.
 A_SE_SE753 GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGDDCVAG RQDED.
 A_SE_SE853 GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 A_SE_SE889 GE.GAVLIQD NSDIKVVPRR KAKIIRDYGK QMAGDGCVAS RQDED.
 A_SE_UGSE8 GE.GAVVIQD QSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 A_UG_92UG0 GE.GAVVIQD NSDIKVVPRR KVKIIRKDYGK QMAGDDCVAG RQDED.
 A_UG_U455_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCMAG RQDED.
 AC_IN_2130 GE.GAVVIQD NSDIKVVPRR KAKIIRKDYGK QMAGADCVAG RQDED.
 AC_RW_92RW GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 AC_SE_SE94 GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGDDCVAG RQDED.
 ACD_SE_SE8 GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDEDW
 ACG_BE_VI1 GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDGCVAS RQDED.
 AD_SE_SE69 GE.GAVVIQD NSEIKVVPRR KVKIIRDYGK QMAGDDCVAS RQDED.
 AD_SE_SE71 GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 ADHK_NO_97 GE.GAVVIQD NGDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 ADK_CD_MAL GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 AG_BE_VI11 GE.GAVAIQD NNEIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 AG_NG_92NG GE.GAVVIQD NSEIKVVPRR KVKIIRKDYGK QMAGGDCVAS RQDED.
 AGHU_GA_VI GE.GAVVIQD NSEIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 AGU_CD_Z32 GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 AJ_BW_BW21 GE.GAVVIQD NSEIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 B_AU_VH_AF GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_CN_RL42_ GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGDDCVAS RQDED.
 B_DE_D31_U GE.GAVVIQD NSEIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 B_DE_HAN_U GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMGSDDCVAS RQDED.
 B_FR_HXB2_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_GA_OYI_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_GB_CAM1_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_GB_GB8_A GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_GB_MANC_ GE.GAVVIQD NSEIKVVPRR KVKIIRDYGK QMAGDDCVAG RQDED.
 B_KR_WK_AF GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_NL_3202A GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_TW_TWCYS GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 B_US_BC_L0_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_DH123 GE.GAVVIQD KSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_JRCSE GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGDDCVAS RQDED.
 B_US_MNCG_ GE.GAVVIQD NNDIKVVPRR KAKVIRDYGK QTAGDDCVAS RQDED.
 B_US_P896_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_RF_M1_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_SF2_K_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_WEAU1_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_WR27_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAS RQDED.
 B_US_YU2_M_ GE.GAVVIQD NSDIKVVPRR KAKIIRDYGK QMAGDDCVAG RQDED.
 BF1_BR_93B GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGGDCVAS RQDED.
 C_BR_92BR0 GE.GAVVLQD NSDIKVVPRR KVKIIRKDYGK QMAGADCMAS RQDED.
 C_BW_96BW0 GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGADCVAG RQDED.
 C_BW_96BW1 GE.GAVVIQD NSDIKVVPRR KVKIIRDYGK QMAGADCVAG RQDED.

C_BW_96BW1	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_BW_96BW1	GEGAVVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGADCVAG	RQDED.
C_ET_ETH22	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN9	GE.GAVVLQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_93IN9	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_94IN1	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
C_IN_95IN2	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGADCVAG	RQDED.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDEN.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDEN.
CRF01_AE_C	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF01_AE_T	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_F	GE.GAVVIQD	KSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_F	GE.GAVVIQD	KSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_G	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_N	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF02_AG_S	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF03_AB_R	GE.GAVVIQD	NNDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
CRF03_AB_R	GE.GAVVIQD	NNDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGNDCVAG	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF04_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF05_DF_B	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF05_DF_B	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF06_cpx_	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF11_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
CRF11_cpx_	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
D_CD_84ZR0	GE.GAVVIQD	NSDIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
D_CD_ELI_K	GE.GAVVIQD	KSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
D_CD_NDK_M	GE.GAVVIQD	NSDIKVVPRR	KVKIIRDYGK	QMAGDDCVAS	RQDED.
D_UG_94UG1	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAS	RQDED.
F1_BE_VI85	GE.GAVVIQD	NSEIKIVPRR	KAKIIRDYGK	QMAVDDCVAG	RQDED.
F1_BR_93BR	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F1_FI_FIN9	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F1_FR_MP41	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F2_CM_MP25	GE.GAVVIQD	NNEIKVIPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
F2KU_BE_VI	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
G_BE_DRCBL	GE.GAVVIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
G_NG_92NG0	GE.GAVVIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
G_SE_SE616	GE.GAVVIQD	NNEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
H_BE_VI991	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
H_BE_VI997	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
H_CF_90CF0	GE.GAVVIQD	NSEIKVVPRR	EAKIIRDYGK	QMAGDDCVAS	RQDED.
J_SE_SE702	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
J_SE_SE788	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
K_CD_EQTB1	GE.GAVVIN.	.SEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
K_CM_MP535	GE.GAVVIQD	NSEIKVVPRR	KAKIIRDYGK	QMAGDDCVAG	RQDED.
N_CM_YBF30	GE.GAVVIQD	NGDIKVVPRR	KAKIIRDYGK	QMAGDGCVAS	GQDENQ
O_CM_ANT70	GE.GAVVIQD	KGDIKVVPRR	KAKIIRDYGK	QMAGTDSMAS	GQTESE
O_CM_MVP51	GE.GAVVIQD	KGDIKVVPRR	KAKIIRDYGK	QMAGTDSMAN	RQTESE
O_SN_99SE_	GE.GAVVIQD	KGDIKVVPRR	KAKIIRHYGK	QMAGTDSMAS	GQTESE

60453026 032803

O_SN_99SE_ GE.GAVVIQD KGDIKVPPRR KAKIIRHYGK QMAGTDSMAS GQTESE
U_CD__83C GE.GAVVIQD NSBIKVPPRR KAKIIRDYGK QMAGDDCVAS RQDEN.

Table 15. HIV Rev Sequence Alignment
GCG Multiple Sequence File.
Written by Omega 1.1

Name: 00BW0762_1	Len: 129	Check: 4903	Weight: 1.00
Name: 00BW0768_2	Len: 129	Check: 5102	Weight: 1.00
Name: 00BW0874_2	Len: 129	Check: 5815	Weight: 1.00
Name: 00BW1471_2	Len: 129	Check: 4144	Weight: 1.00
Name: 00BW1616_2	Len: 129	Check: 5298	Weight: 1.00
Name: 00BW1686_8	Len: 129	Check: 3871	Weight: 1.00
Name: 00BW1759_3	Len: 129	Check: 4976	Weight: 1.00
Name: 00BW1773_2	Len: 129	Check: 5775	Weight: 1.00
Name: 00BW1783_5	Len: 129	Check: 6142	Weight: 1.00
Name: 00BW1795_6	Len: 129	Check: 5055	Weight: 1.00
Name: 00BW1811_3	Len: 129	Check: 5804	Weight: 1.00
Name: 00BW1859_5	Len: 129	Check: 5252	Weight: 1.00
Name: 00BW1880_2	Len: 129	Check: 4995	Weight: 1.00
Name: 00BW1921_1	Len: 129	Check: 6482	Weight: 1.00
Name: 00BW2036_1	Len: 129	Check: 4770	Weight: 1.00
Name: 00BW2063_6	Len: 129	Check: 5384	Weight: 1.00
Name: 00BW2087_2	Len: 129	Check: 4848	Weight: 1.00
Name: 00BW2127_2	Len: 129	Check: 5783	Weight: 1.00
Name: 00BW2276_7	Len: 129	Check: 5364	Weight: 1.00
Name: 00BW3819_3	Len: 129	Check: 5712	Weight: 1.00
Name: 00BW3842_8	Len: 129	Check: 5586	Weight: 1.00
Name: 00BW3871_3	Len: 129	Check: 5299	Weight: 1.00
Name: 00BW3876_9	Len: 129	Check: 4423	Weight: 1.00
Name: 00BW3886_8	Len: 129	Check: 5415	Weight: 1.00
Name: 00BW3891_6	Len: 129	Check: 5426	Weight: 1.00
Name: 00BW3970_2	Len: 129	Check: 2613	Weight: 1.00
Name: 00BW5031_1	Len: 129	Check: 4597	Weight: 1.00
Name: 96BW01B21	Len: 129	Check: 5653	Weight: 1.00
Name: 96BW0407	Len: 129	Check: 4310	Weight: 1.00
Name: 96BW0502	Len: 129	Check: 4675	Weight: 1.00
Name: 96BW06_J4	Len: 129	Check: 5079	Weight: 1.00
Name: 96BW11_06	Len: 129	Check: 5939	Weight: 1.00
Name: 96BW1210	Len: 129	Check: 5666	Weight: 1.00
Name: 96BW15B03	Len: 129	Check: 5102	Weight: 1.00
Name: 96BW16_26	Len: 129	Check: 5675	Weight: 1.00
Name: 96BW17A09	Len: 129	Check: 2825	Weight: 1.00
Name: 96BWMO1_5	Len: 129	Check: 5636	Weight: 1.00
Name: 96BWMO3_2	Len: 129	Check: 6552	Weight: 1.00
Name: 98BWMC12_2	Len: 129	Check: 3043	Weight: 1.00
Name: 98BWMC13_4	Len: 129	Check: 5518	Weight: 1.00
Name: 98BWMC14_a	Len: 129	Check: 4358	Weight: 1.00
Name: 98BWMO14_1	Len: 129	Check: 7531	Weight: 1.00
Name: 98BWMO18_d	Len: 129	Check: 5291	Weight: 1.00
Name: 98BWMO36_a	Len: 129	Check: 6801	Weight: 1.00
Name: 98BWMO37_d	Len: 129	Check: 4790	Weight: 1.00
Name: 99BW3932_1	Len: 129	Check: 5736	Weight: 1.00
Name: 99BW4642_4	Len: 129	Check: 6464	Weight: 1.00
Name: 99BW4745_8	Len: 129	Check: 6181	Weight: 1.00
Name: 99BW4754_7	Len: 129	Check: 5182	Weight: 1.00
Name: 99BWMC16_8	Len: 129	Check: 4245	Weight: 1.00
Name: A2_CD_97CD	Len: 129	Check: 2625	Weight: 1.00
Name: A2_CY_94CY	Len: 129	Check: 4125	Weight: 1.00
Name: A2D_97KR	Len: 129	Check: 4114	Weight: 1.00
Name: A2G_CD_97C	Len: 129	Check: 1115	Weight: 1.00
Name: A_BY_97BL0	Len: 129	Check: 9470	Weight: 1.00
Name: A_KE_Q23_A	Len: 129	Check: 2684	Weight: 1.00

Name: A_SE_SE659	Len: 129	Check: 4659	Weight: 1.00
Name: A_SE_SE725	Len: 129	Check: 4491	Weight: 1.00
Name: A_SE_SE753	Len: 129	Check: 3636	Weight: 1.00
Name: A_SE_SE853	Len: 129	Check: 1862	Weight: 1.00
Name: A_SE_SE889	Len: 129	Check: 2798	Weight: 1.00
Name: A_SE_UGSE8	Len: 129	Check: 6865	Weight: 1.00
Name: A_UG_92UG0	Len: 129	Check: 4427	Weight: 1.00
Name: A_UG_U455	Len: 129	Check: 3229	Weight: 1.00
Name: AC_IN_2130	Len: 129	Check: 5110	Weight: 1.00
Name: AC_RW_92RW	Len: 129	Check: 5015	Weight: 1.00
Name: AC_SE_SE94	Len: 129	Check: 7976	Weight: 1.00
Name: ACD_SE_SE8	Len: 129	Check: 2296	Weight: 1.00
Name: ACG_BE_VI1	Len: 129	Check: 3968	Weight: 1.00
Name: AD_SE_SE69	Len: 129	Check: 4558	Weight: 1.00
Name: AD_SE_SE71	Len: 129	Check: 2678	Weight: 1.00
Name: ADHK_NO_97	Len: 129	Check: 1890	Weight: 1.00
Name: ADK_CD_MAL	Len: 129	Check: 5260	Weight: 1.00
Name: AG_BE_VI11	Len: 129	Check: 4003	Weight: 1.00
Name: AG_NG_92NG	Len: 129	Check: 5027	Weight: 1.00
Name: AGHU_GA_VI	Len: 129	Check: 1978	Weight: 1.00
Name: AGU_CD_Z32	Len: 129	Check: 1958	Weight: 1.00
Name: AJ_BW_BW21	Len: 129	Check: 2263	Weight: 1.00
Name: B_AU_VH_AF	Len: 129	Check: 4074	Weight: 1.00
Name: B_CN_RL42	Len: 129	Check: 4483	Weight: 1.00
Name: B_DE_D31_U	Len: 129	Check: 5079	Weight: 1.00
Name: B_DE_HAN_U	Len: 129	Check: 4550	Weight: 1.00
Name: B_FR_HXB2	Len: 129	Check: 3649	Weight: 1.00
Name: B_GA_OYI_M	Len: 129	Check: 3334	Weight: 1.00
Name: B_GB_CAM1	Len: 129	Check: 3865	Weight: 1.00
Name: B_GB_GB8_A	Len: 129	Check: 3083	Weight: 1.00
Name: B_GB_MANC	Len: 129	Check: 5502	Weight: 1.00
Name: B_KR_WK_AF	Len: 129	Check: 4156	Weight: 1.00
Name: B_NL_3202A	Len: 129	Check: 3826	Weight: 1.00
Name: B_TW_TWCYS	Len: 129	Check: 3546	Weight: 1.00
Name: B_US_BC_LO	Len: 129	Check: 4674	Weight: 1.00
Name: B_US_DH123	Len: 129	Check: 4202	Weight: 1.00
Name: B_US_JRCSE	Len: 129	Check: 3217	Weight: 1.00
Name: B_US_MNCG	Len: 129	Check: 3512	Weight: 1.00
Name: B_US_P896	Len: 129	Check: 3297	Weight: 1.00
Name: B_US_RF_M1	Len: 129	Check: 5527	Weight: 1.00
Name: B_US_SF2_K	Len: 129	Check: 3616	Weight: 1.00
Name: B_US_WEAU1	Len: 129	Check: 4435	Weight: 1.00
Name: B_US_WR27	Len: 129	Check: 812	Weight: 1.00
Name: B_US_YU2_M	Len: 129	Check: 4948	Weight: 1.00
Name: BF1_BR_93B	Len: 129	Check: 3645	Weight: 1.00
Name: C_BR_92BR0	Len: 129	Check: 4262	Weight: 1.00
Name: C_BW_96BW0	Len: 129	Check: 4323	Weight: 1.00
Name: C_BW_96BW1	Len: 129	Check: 3054	Weight: 1.00
Name: C_BW_96BW1	Len: 129	Check: 3900	Weight: 1.00
Name: C_BW_96BW1	Len: 129	Check: 4051	Weight: 1.00
Name: C_ET_ETH22	Len: 129	Check: 3843	Weight: 1.00
Name: C_IN_93IN1	Len: 129	Check: 2878	Weight: 1.00
Name: C_IN_93IN9	Len: 129	Check: 4499	Weight: 1.00
Name: C_IN_93IN9	Len: 129	Check: 3994	Weight: 1.00
Name: C_IN_94IN1	Len: 129	Check: 4362	Weight: 1.00
Name: C_IN_95IN2	Len: 129	Check: 3765	Weight: 1.00
Name: CRF01_AE_C	Len: 129	Check: 4444	Weight: 1.00
Name: CRF01_AE_C	Len: 129	Check: 3760	Weight: 1.00
Name: CRF01_AE_C	Len: 129	Check: 3562	Weight: 1.00
Name: CRF01_AE_T	Len: 129	Check: 5676	Weight: 1.00

Name: CRF01_AE_T	Len: 129	Check: 6090	Weight: 1.00
Name: CRF01_AE_T	Len: 129	Check: 6846	Weight: 1.00
Name: CRF01_AE_T	Len: 129	Check: 5393	Weight: 1.00
Name: CRF01_AE_T	Len: 129	Check: 6189	Weight: 1.00
Name: CRF01_AE_T	Len: 129	Check: 5202	Weight: 1.00
Name: CRF02_AG_F	Len: 129	Check: 5063	Weight: 1.00
Name: CRF02_AG_F	Len: 129	Check: 3731	Weight: 1.00
Name: CRF02_AG_G	Len: 129	Check: 2202	Weight: 1.00
Name: CRF02_AG_N	Len: 129	Check: 4873	Weight: 1.00
Name: CRF02_AG_S	Len: 129	Check: 3995	Weight: 1.00
Name: CRF02_AG_S	Len: 129	Check: 6502	Weight: 1.00
Name: CRF03_AB_R	Len: 129	Check: 2858	Weight: 1.00
Name: CRF03_AB_R	Len: 129	Check: 2808	Weight: 1.00
Name: CRF04_cpx_	Len: 129	Check: 3912	Weight: 1.00
Name: CRF04_cpx_	Len: 129	Check: 3700	Weight: 1.00
Name: CRF04_cpx_	Len: 129	Check: 3297	Weight: 1.00
Name: CRF05_DF_B	Len: 129	Check: 3974	Weight: 1.00
Name: CRF05_DF_B	Len: 129	Check: 4062	Weight: 1.00
Name: CRF06_cpx_	Len: 129	Check: 2954	Weight: 1.00
Name: CRF06_cpx_	Len: 129	Check: 1655	Weight: 1.00
Name: CRF06_cpx_	Len: 129	Check: 2327	Weight: 1.00
Name: CRF06_cpx_	Len: 129	Check: 2706	Weight: 1.00
Name: CRF11_cpx_	Len: 129	Check: 2064	Weight: 1.00
Name: CRF11_cpx_	Len: 129	Check: 1685	Weight: 1.00
Name: D_CD_84ZR0	Len: 129	Check: 4305	Weight: 1.00
Name: D_CD_ELI_K	Len: 129	Check: 4483	Weight: 1.00
Name: D_CD_NDK_M	Len: 129	Check: 3024	Weight: 1.00
Name: D_UG_94UG1	Len: 129	Check: 3298	Weight: 1.00
Name: F1_BE_VI85	Len: 129	Check: 2602	Weight: 1.00
Name: F1_BR_93BR	Len: 129	Check: 2572	Weight: 1.00
Name: F1_FI_FIN9	Len: 129	Check: 3253	Weight: 1.00
Name: F1_FR_MP41	Len: 129	Check: 2465	Weight: 1.00
Name: F2_CM_MP25	Len: 129	Check: 2231	Weight: 1.00
Name: F2KU_BE_VI	Len: 129	Check: 461	Weight: 1.00
Name: G_BE_DRCBL	Len: 129	Check: 3194	Weight: 1.00
Name: G_NG_92NG0	Len: 129	Check: 4325	Weight: 1.00
Name: G_SE_SE616	Len: 129	Check: 2614	Weight: 1.00
Name: H_BE_VI991	Len: 129	Check: 2347	Weight: 1.00
Name: H_BE_VI997	Len: 129	Check: 1680	Weight: 1.00
Name: H_CF_90CF0	Len: 129	Check: 2751	Weight: 1.00
Name: J_SE_SE702	Len: 129	Check: 2099	Weight: 1.00
Name: J_SE_SE788	Len: 129	Check: 2149	Weight: 1.00
Name: K_CD_EQTB1	Len: 129	Check: 3510	Weight: 1.00
Name: K_CM_MP535	Len: 129	Check: 2798	Weight: 1.00
Name: N_CM_YBF30	Len: 129	Check: 3973	Weight: 1.00
Name: O_CM_ANT70	Len: 129	Check: 9677	Weight: 1.00
Name: O_CM_MVP51	Len: 129	Check: 8852	Weight: 1.00
Name: O_SN_MP129	Len: 129	Check: 1678	Weight: 1.00
Name: O_SN_MP130	Len: 129	Check: 2242	Weight: 1.00
Name: U_CD_83C	Len: 129	Check: 9312	Weight: 1.00

00BW0762_1	MAGRSGD...	NDTLLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
00BW0768_2	MAGRSEDS..	.DATLLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARKNRRRRWR
00BW0874_2	MAGRSGD...	SDEALLQAVR	IIKVLQSNP	YPK.PEGTRQ	ARKNRRRRWR
00BW1471_2	MAGRSGD...	SDEALLQAVR	IIRILYQSNP	YPKPEG.TRQ	ARKNRRRRWR
00BW1616_2	MAGRSGDS..	.DEALLQAVR	TIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR
00BW1686_8	MAGRSGDS..	.DEALLQAIK	SIKILYQSNP	YPE.PQGTRQ	AQRNRRRRWR
00BW1759_3	MAGRSGD...	NDEAVLQAIR	IIKILYQSNP	YPK.PRQTRQ	AQKNRRRRWR
00BW1773_2	MAGRSGDS..	.DEALLQAVK	IIKILYQSNP	YPE.PKGTRQ	ARKNRRRRWR

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00BW1783_5  MAGRSGD... SDEAVLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW1795_6  MAGRSGD... GDAALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW1811_3  MAGRSGD... SDEELLQVAR IIKILYQSNP YPE.PRGTRO ARKNRRRRRWR
00BW1859_5  MAGRSGD... DAALLQAAK IIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
00BW1880_2  MAGRSGD... NDEALLQAVR IIKILYQSNP FPK.PEGTRQ ARKNRRRRRWR
00BW1921_1  MAGRSGD... NDEALLQAVR IIKILYQSNP YPE.PQGTRO ARKNRRRRRWR
00BW2036_1  MAGRSGD... DEALLQAIR LIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
00BW2063_6  MAGRSGDN.D ADAALLQAVK IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW2087_2  MAGRSGD... SDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW2127_2  MAGRSGD... NDEARLQVVK IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW2276_7  MAGRSGD... SDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW3819_3  MAGRSGD... SDELLKAVR LIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW3842_8  MAGRSGD... DEALLRVVR IIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
00BW3871_3  MAGRSGD... DEALLQAIR TIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
00BW3876_9  MAGRSGD... DEALLHAVR TIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
00BW3886_8  MAGRSGD... DEALLQAVR IIKILYQSNP YPE.HQGTRO ARKNRRRRRWR
00BW3891_6  MAGRSGD... DEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
00BW3970_2  MAGRSGD... DEALLQAVK IIKILYQSDP YPK.PEGTRQ ARKNRRRRRWR
00BW5031_1  MAGRSGDN... DEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
96BW01B21  MAGRSGD... SDEALLQAVR IIRILYQSNP YPE.PRGTRO ARKNRRRRRWR
96BW0407  MAGRSGD... SDEALLQAVK IIKILYQSNP YPK.PEEIRQ ARKNRRRRRWR
96BW0502  MAGRSGD... DEALLQAVK AIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
96BW06_J4  MAGRSGD... DEALLQAVR IIKILYQSNP SPE.PKGNRQ ARKNRRRRRWR
96BW11_06  MAGRSGD... NDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
96BW1210  MAGRSGD... SDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
96BW15B03  MAGRSGD... DEALLHAVR IIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
96BW16_26  MAGRSGD... DAALLQAVR IIKILYQSNP YPK.PKGTRQ ARKNRRRRRWR
96BW17A09  MAGRSGD... NDEALLQAMG IIKILYQSNP YPKPEG.TRR ARKNRRRRRWR
96BWMO1_5  MAGRSGD... SDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
96BWMO3_2  MAGRSGD... SDEALLQAVR TIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
98BWMC12_2  MAGRSGD... DEALLQAVR IIKILYQSNP QPK.PEGTRQ ARKNRRRRRWR
98BWMC13_4  MAGRSGD... SDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
98BWMC14_a  MAGRSGD... DEALLQAVR IIKILYQSNP PPE.RRGIGQ ARKNRRRRRWR
98BWMO14_1  MAGRSGD... DDERLLQAVR IIKILYQSNP YPS.PEGTRQ ARKNRRRRRWR
98BWMO18_d  MAGRSGD... SDEALLQAVR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
98BWMO36_a  MAGRSGV... SDEALLQAVK IIKILYQSNP YPNNPEGSQ ARKNRRRRRWR
98BWMO37_d  MAGRSGD... SDEALLQAVR IIKILYQSNR YPK.PEGTRQ ARKNRRRRRWR
99BW3932_1  MAGRSGD... PDEALLQAIR IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
99BW4642_4  MAGRSGD... DAALLQAVR IIKILYQSNP YPE.PKGTRQ ARKNRRRRRWR
99BW4745_8  MAGRSGD... DEALLQAVR IIKILYQSNP YPK.PKETRO ARKNRRRRRWR
99BW4754_7  MAGRSGD... NDAALLLAVQ TIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
99BWMC16_8  MAGRSGD... DEALLQAVR IIKILYQSNP CPE.PRGTRO ARKNRRRRRWR
A2_CD_97CD  MAGRSGD... PDEDLIRAIR IIKILYQSNP YPKPRG.TRQ ARKNRRRRRWR
A2_CY_94CY  TAGRSDD... PDESLLQAIR TIKILYQSNP YPKPRG.SRQ ARKNRRRRRWR
A2D_97KR  MAGRSGD... PDEDLLRAVR AIRILYQSNP SPDPRG.SRQ ARKNRRRRRWR
A2G_CD_97C  MAGRSGS... TDEELLQAAR IIKILYQSNP YPPPEG.TRQ ARKNRRRRRWR
A_BY_97BL0  MAGRSGG... TDAELLTAVR IIXFLYQSNP YPTPRK.TRQ AXKNQRRRXR
A_KE_Q23_A  MAGRSGD... SDEELLRAVR IIKILYQSNP YPKPKG.SRQ ARKNRRRRRWR
A_SE_SE659  MAGRSGP... GDEELLKAIR IIKILYQSNP YPKPRG.TRQ ARKNRRRRRWR
A_SE_SE725  MAGRSGD... SDEELLRAVR IIKILYQSNP YPRPKG.SRQ AQKNRRRRRWR
A_SE_SE753  MAGRSGN... SDEELLRAIR IIKILYQSNP YPKPKG.SRQ ARKNRRRRRWR
A_SE_SE853  MAGRSGN... SDEELLRAIR IIKILYQSNP HPKPRG.SRQ ARKNRRRRRWR
A_SE_SE889  MAGRSGD... SDEELLKAVR IIKILYQSNP YPKPRG.TRQ ARKNRRRRRWR
A_SE_UGSE8  MAGRSGD... SDEELLKAVR TIKILYQSNP YQPKG.SRQ ARKNRRRRRWR
A_UG_92UG0  MAGRSGN... PDEELLRAIR IIKILYQSNP YPEPKG.TRQ ARKNRRRRRWR
A_UG_U455_  MARRSGN... PDEDLLKAVR IIKILYQSNP CPNPRG.SRQ ARKNRRRRRWR
AC_IN_2130  MAGRSGD... SDEELLQVVR IIKILYQSNP YPKPRG.TRQ ARKNRRRRRWR
AC_RW_92RW  MAGRSGD... SDETLLQAVK IIKILYQSNP YPK.PEGTRQ ARKNRRRRRWR
AC_SE_SE94  MAGRSGD... SDEALLQAVR IIKILYQSNP YPKPRG.TRQ ARKNRRRRRWR
ACD_SE_SE8  MAGRSGD... SDEDLLRAIR IIKILYQSNP YPKPRG.SRQ ARKNRRRRRWR

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ACG_BE_VI1	MAGRSGA...	SDEELLRAVR	IVKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
AD_SE_SE69	MAGRSGD...	SDEXLLKAVR	LIKTLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
AD_SE_SE71	MAGRSGN...	SDEELLQAAR	IIKILYQSNP	YPKPKG.SRQ	ARKNRRRRWR
ADHK_NO_97	MAGRSGD...	RDADLLKAVR	IIKILYQSNP	YPE.PTGSRQ	ARRNRRRRWR
ADK_CD_MAL	MAGRSGD...	SDEELLRAIR	LIKILYQSNP	PPNTEGTTRQ	ARRNRRRRWR
AG_BE_VI11	MAGRTGS...	TDEELLKAVR	TIKILYQSNP	YPSSEG.SRQ	ARKNRRRRWR
AG_NG_92NG	MAGRSGD...	ADEELLRVTR	IIKILYQSNP	YPPPEG.TRQ	ARKNRRRRWR
AGHU_GA_VI	MAGRSGA...	SDEELLKAVR	IIKILYQSNP	FPE.PTGTRQ	ARRNRRRRWR
AGU_CD_Z32	MAGRSGD...	SDEELLKIVR	IIKILYQGNP	YPPPEG.TRQ	ARRNRRRRWR
AJ_BW_BW21	MAGRSGD...	NDEQLLLAIR	IIKILYKSNP	YPKPNG.SRQ	ARRNRRRRWR
B_AU_VH_AF	MAGRSGD...	SDDELLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_CN_RL42	MAGRSED...	SDEELLKTVR	LIKLLYQSNP	LPSPEG.TRQ	ARRNRRRRWR
B_DE_D31_U	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_DE_HAN_U	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSNEG.TPT	ARRNRRRRWR
B_FR_HXB2	MAGRSGD...	SDEELIRTVR	LIKLLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
B_GA_OYI_M	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
B_GB_CAM1	MAGRSGD...	SDEELLKAVR	LIKLLYQSNP	LPSSKG.TRQ	ARRNRRRRWR
B_GB_GB8_A	MAGRSGD...	SDEDFLKTVR	FIKFLYQSNP	PPNPKG.TRQ	ARRNRRRRWR
B_GB_MANC	MAGRSGD...	SDEELLQTVK	LVKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_KR_WK_AF	MAGRSGD...	SDEELLRTIR	IIKFLYQSNP	LPEPEG.TRQ	ARRNRRRRWR
B_NL_3202A	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_TW_TWCYS	MAGRSGD...	SDEELLRTVR	LIKLIYQSNP	PPNPEG.TRQ	ARRNRRRRWR
B_US_BC_L0	MAGRSGD...	SDEELLKTVR	LIKLLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
B_US_DH123	MAGRSGE...	SDEDLLNTRV	LIKLLYQSNP	LPSLEG.TRQ	ARRNRRRRWR
B_US_JRCFS	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSNEG.TRQ	ARRNRRRRWR
B_US_MNCG	MAGRSGD...	SDEELLKTVR	LIKFLYQSNP	PPSSEG.TRQ	ARRNRRRRWR
B_US_P896	MAGRSGD...	SDEDLLKTVR	LIKFLYQSNP	PPSLEG.TRQ	ARRNRRRRWR
B_US_RF_M1	MAGRSGD...	SDEDLLKAVR	LIKSLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_US_SF2_K	MAGRSGD...	SDEELLRTVR	LIKLLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_US_WEAU1	MAGRSGD...	SDEDLLKTVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
B_US_WR27	MAGRSGD...	SDEELLQKV	LIRFLYQSNP	PPSSEG.TRQ	ARRNRRRRWR
B_US_YU2_M	MAGRSGD...	SDEDLLRTVR	LIKVLVQSNP	PPSSEG.TRQ	ARRNRRRRWR
BF1_BR_93B	MAGRSGD...	SDTELLKAVS	YIKILYQSNP	LPKPKG.TRQ	ARRNRRRRWR
C_BR_92BR0	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
C_BW_96BW0	MAGRSGD...	SDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
C_BW_96BW1	MAGRSGD...	NDEALLQAVR	IIKILYQSNP	YPK.PEGTRQ	ARRNRRRRWR
C_BW_96BW1	MAGRSGD...	SDEALLQAVR	IIKILYQNNP	YPK.PEGTRQ	ARRNRRRRWR
C_ET_ETH22	MAGRSGD...	.DEALLHAVR	IIKILYQSNP	YPE.PKGTRQ	ARRNRRRRWR
C_IN_93IN1	MAGRSGDS...	.DEALLQAVR	IIKILYQSNP	YPT.PEGTRQ	ARRNRRRRWR
C_IN_93IN9	MAGRSGDS...	.DEELLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARRNRRRRWR
C_IN_93IN9	MAGRSGDS...	.DEALLRAVR	IIKILYQSNP	YPE.PRGTRQ	ARRNRRRRWR
C_IN_94IN1	MAGRSGDS...	.DEALLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARRNRRRRWR
C_IN_95IN2	MAGRSGDS...	.DEALLKAVR	IIKILYQSNP	YPE.PRGTRQ	ARRNRRRRWR
CRF01_AE_C	MAGRSGN...	TDEDLLQAVR	IIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
CRF01_AE_C	MAGRSGS...	TDEDLLRTVR	IIKILYQSNP	YPPAEG.TRQ	ARRNRRRRWR
CRF01_AE_C	MAGRSGS...	TDEELLRAAR	AIKILFQSNP	YPSSEG.TRQ	ARRNRRRRWR
CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	YPSSEG.TRQ	ARRNRRRRWR
CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKVLYQSNP	YPSSEG.TRQ	ARRNRRRRWR
CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	YPSSEGGTRQ	ARRNRRRRWR
CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKLLYBSNP	PPSSEG.TRQ	ARRNRRRRWR
CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IIKILYQSNP	PPSSEG.TRQ	ARRNRRRRWR
CRF01_AE_T	MAGRSGS...	TDEELLRAVR	IINILYQSNP	LPSSEG.SRQ	ARRNRRRRWR
CRF02_AG_F	MAGRSGD...	ADEELLRVVR	IIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
CRF02_AG_F	MAGRSGD...	ADEELLRVVR	IVKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
CRF02_AG_G	MAGRSGD...	ADEELLRVIR	IIKILYQSNP	YPKPEG.TRQ	ARRNRRRRWR
CRF02_AG_N	MAGRSGD...	ADEELLRAVR	IIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
CRF02_AG_S	MAGRSGN...	ADEELLRAVR	TIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
CRF02_AG_S	MAGRSGD...	ADEGLLRAVR	IIRILYQSNP	YPPPEG.SRQ	ARRNRRRRWR
CRF03_AB_R	MAGRSGD...	SDEELLKTIR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR

CRF03_AB_R	MAGRSGD...	SDEDLLKTIR	LIKFLYQSNP	PPNPEG.TRQ	ARRNRRRRWR
CRF04_cpx	MAGRSGN...	IDEDLFKAAR	AIKILYQSNP	YPNNPTGTRO	ARRNRRRRWR
CRF04_cpx	MAGRSG...	SNEDLLGSVG	IVKILYQSNP	YPN.PTGTRK	ARRNRRRRWR
CRF04_cpx	MAGRSGS...	TDEDLLKAVG	IVKILYQSNP	YPNNTAGTRQ	ARRNRRRRWR
CRF05_DF_B	MAGRSGD...	RDEDLLKAVR	LIKILYQSNP	LPSPEG.TRQ	ARRNRRRRWR
CRF05_DF_B	MAGRSGD...	RDEDLLKAVR	LIKFLYQSNP	PPRPEG.TRQ	ARRNRRRRWR
CRF06_cpx	MAGRSGD...	SDDRLLLA VR	IIKILYQSNP	YKPNG.SRQ	ARRNRRRRWR
CRF06_cpx	MAGRSGD...	NDEQLLLAVR	IIKILYQSNP	YKPNG.GRQ	ARRNRRRRWR
CRF06_cpx	MAGRSGD...	NDEQLLLAVR	TIKILYQSNP	YKPSG.SRQ	ARRNRRRRWR
CRF06_cpx	MAGRSGD...	SDEQLLWAVR	VIKILYQSNP	YKLSG.SRQ	ARRNRRRRWR
CRF11_cpx	MAGRSGD...	NDEQLLTAVK	IIKILYQSNP	QPNPTG.SRQ	ARRNRRRRWR
CRF11_cpx	MAGRSGD...	SDAQLLAAAR	IIKILYQSSP	YKPPAG.TRQ	ARRNRRRRWR
D_CD_84ZR0	MAGRSGD...	SDEDLLTAVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
D_CD_ELI_K	MAGRSGD...	SDEDLLKAVR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
D_CD_NDK_M	MAGRSGD...	SDENLLKAIR	LIKFLYQSNP	PPSPEG.TRQ	ARRNRRRRWR
D_UC_94UG1	MAGRSGD...	RDEELLQAVR	LIKILYQSNP	PPSPEG.TRQ	ARRNRRRRWR
F1_BE_VI85	MAGRSGD...	SDTELLKAVK	CIKILYQSNP	YKPEG.TRQ	ARRNRRRRWR
F1_BR_93BR	MAGRSGD...	SDQELLKAVR	YIKILYQSNP	YKPEG.TRQ	ARRNRRRRWR
F1_FI_FIN9	MAGRSGD...	SDTELLKAVK	YIKILYQSNP	YPSPDG.TRQ	ARRNRRRRWR
F1_FR_MP41	MAGRSGD...	NDEELLRAVR	AIKILYQSNP	YKPEG.TRQ	ARRNRRRRWR
F2_CM_MP25	MAGRSGD...	RDEELLKAVR	YIKILYQSNP	YKLEG.TRK	ARRNRRRRWR
F2KU_BE_VI	MAGRSGD...	SDEELLKAVR	LIKILYQSNP	YKPEG.TRQ	ARRNRRRRWR
G_BE_DRCBL	MAGRSGS...	TDEELLTAVR	IIKLLYQSNP	SPPPEG.TRQ	ARRNRRRRWR
G_NG_92NG0	MAGRSGD...	PDEELLRAVR	IIKTLYQSNP	YPSPAG.TRQ	ARRNRRRRWR
G_SE_SE616	MAGRSGS...	TDEELLRAVR	AIKILYQSNP	YPPPEG.TRQ	ARRNRRRRWR
H_BE_VI991	MAGRSGD...	NDEGLLRACR	IIRLLYQSNP	YPE.PAGTRQ	AQRNRRRRWR
H_BE_VI997	MAGRSGA...	GDEQLPQVCK	IIKIIYQSNP	YPE.PAGTRQ	ARRNRRRRWR
H_CF_90CF0	MAGRSGA...	SDTELLQVCK	IIKILYQSNP	CPE.PTGTRQ	ARRNRRRRWR
J_SE_SE702	MAGRSGD...	NDDQLLLAVR	IIKILYQSNP	YSKPNG.SRQ	ARRNRRRRWR
J_SE_SE788	MAGRSGD...	SDDQLLLAVR	LIKILYQSNP	YKPNG.SRQ	ARRNRRRRWR
K_CD_EQTB1	MAGRSGD...	SEQQLTPVR	IIKILYQSNP	YKPEG.TRQ	ARRNRRRRWR
K_CM_MP535	MAGRSGD...	PDEQLTTVR	TIKILYQSNP	YPNLEG.SRQ	TRRNRRRRWR
N_CM_YBF30	MAGRSGVN...	.DEELLRAVR	VIKILYQSNP	YPNSKG.TRQ	ARRNRRRRWR
O_CM_ANT70	MAGRSED...	.DQ.LLQAIQ	IIKILYQSNP	QPSPRG.SRN	ARRNRRRRWR
O_CM_MVP51	MAGRSEE...	.DQQLLQAIQ	IIKILYQSNP	CPTPAG.SRN	ARRNRRRRWR
O_SN_MP129	MAGRSDG...	.DQPLLRAIQ	IIKILYQSNP	HTSPTG.SRS	ARRNRRRRWR
O_SN_MP130	MAGRSDG...	.DQPLLRAIQ	IIKILYQSNP	HPSPTTGSTS	ARRNRRRRWR
U_CD_83C	MAGRSGE...	SDEELLRAVR	IIKILYQSNP	PPNPEG.TRQ	ARRNRRRRWR

51

100

00BW0762_1	ARQRQIHSIS	ERILSTVLGR	PAEPVPFQLP	PIERLHIGCS	ESGGTSGTQQ
00BW0768_2	ARQRQINSIS	ERILSTCLGR	PAEAVPLQLP	PIERLHIGCN	ESGGTSGTQQ
00BW0874_2	ARQRQINSIS	GRILSACLGR	PTEPVPFQLP	PIERLHINCS	ENGGTSGTQQ
00BW1471_2	ARQRQIRAI	ERILDTCLGR	LTEPVHLPLP	PLERLHLDCS	EDCEPTGTEQ
00BW1616_2	ARQRQIHSIS	ERILSACLGR	SAEPVPFQLP	PIERLHIDCS	BSSGNSG...
00BW1686_8	ARQRQIHSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTFGTQQ
00BW1759_3	ARQRQIDSIS	ERVLTSTVLGR	PTEPVPFQLP	PIERLDIGDS	ESGGTSGTER
00BW1773_2	ARQRQIREIS	QRILSTYLGR	PAEPVPLLLP	PIERLHIDCS	ESGGTSGTQQ
00BW1783_5	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLHIGDS	KSSGTSGTQQ
00BW1795_6	ARQRQIHSIS	ERILSTCLGR	PAEPVPFLLP	PLERLHIGDS	ESSGTSGTQQ
00BW1811_3	ARQRQIREIS	ERILCTCLGR	STEPVPFLLP	PIERLHIGDS	EGSGTSGTQQ
00BW1859_5	ARQRQIHTIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
00BW1880_2	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLHIGDS	ESSGTSGTQR
00BW1921_1	ARQRQINSIS	ERILTCLGR	SEEPVPLQLP	PIERLNIGGS	ESSGTSGTQQ
00BW2036_1	ARQRQIDSIS	ARILSTCLGR	PAEPVPFQLP	PIERLNIGDN	ESGGTSGTQQ
00BW2063_6	ARQRQIHSIS	ERILSTCLGR	SEEPVPLLLP	PIERLRIGDS	ESSGTSGTQQ
00BW2087_2	ARQRQIHSIS	ERILTTLGR	SAEPVPFQLP	PIERLNINCS	EGSGTSGTQQ
00BW2127_2	ARQRQIHSIS	ERILSTCLGR	STEPVPFQLP	PIERLNIGDS	EGSGTSGTQR
00BW2276_7	ARQRQIHTIS	ERILSTCLGR	PAEPVPLQLP	PIERLYIGDS	EGGTSGTQQ
00BW3819_3	ARQRQIHSIS	ERILSACLGR	PAEPVPFQLP	PIERLNIGDS	EGDRTYGTQQ

00BW3842_8	ARQRQIDSIS	GRLSTCLGR	SAEPVPLQLP	PIERLNIGDS	ESGGTSGTQQ
00BW3871_3	ARQRQINSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTSGTQQ
00BW3876_9	ARQKQIHSIS	ERILSACLGR	SAEPVPLQLP	PIERLHIGGS	ESGGTSGTQQ
00BW3886_8	ARQRQINSIT	ERILSDCLGR	SAEPVPLQLP	PIERLHIVDS	ESGGTSGTQQ
00BW3891_6	ARQRQIHSLS	ERILSTCLGR	SAEPVPLQLP	PIERLHIGDS	ESGGTSGTQQ
00BW3970_2	ARQKEIHSLS	ERILSTCLGR	PAEPVPLQLP	PLERLHIDCS	ESGGTSGTQ.
00BW5031_1	ARQRQIHSIG	ERILSTCLGR	SAEPVPLQLP	PLERLHIDCS	ESSGTPGTQQ
96BW01B21	ARQRQIHSIS	ERILTTCLGR	FTEPVPFQLP	PIERLHIGDS	ESGGTSGTQQ
96BW0407	ARQRQIHSIS	ERILSTCLGR	PTEPVPFQLP	PIERLHIDCS	ESSGASGTQR
96BW0502	ARQRQIHSLS	ERILSACLGR	PAEPVPFQLP	PIERLHIDCS	KSVGTSG...
96BW06_J4	ARQRQINSIS	ERILSTCLGR	SAEPVPFQLP	PIERLHIGGS	ESGGTSGTQQ
96BW11_06	TRQKQINSIS	ERILSTCLGR	SAEPVPFLLP	PIERLHISDS	ESSGTSGTQQ
96BW1210	ARQRQIHSIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIGGS	ENSGTTGTQQ
96BW15B03	ARQRQIDSIS	TRILSTCLGR	PEEPVPFQLP	PIERLNIGDS	ESGGTSGTQQ
96BW16_26	ARQRQIRAIS	ARIFSACLGR	PAEPVPLQLP	PIERLHIGSS	ESGGTSGTQ.
96BW17A09	ARQRQIHSIS	ERILSTCLGR	PTEPVHLPLP	PLERLHLDCS	EDCEPTGTEQ
96BWM01_5	ARQRQINSIS	ERILSACLGR	PAEPVPFLLP	PIERLHIGDS	ESSGTSGTQQ
96BWM03_2	ARQRQIHSIS	ERILSACLGR	PTEPVPFQLP	PIERLSIGDS	ESSGTSGTQQ
98BWMC12_2	ARQKHIHSIS	ERILSDCLGR	SAEPVPLQLP	PIERLHIDCS	ESGGTSGTQQ
98BWMC13_4	ARQRQINSIS	ERILSTCLGR	STEPVPFLLP	PIERLHIGDS	ESSGTSGTQQ
98BWMC14_a	ARQTQINSLS	ERIVSTCLGR	PAERAPFQLP	PIEKLHIDCS	ESGGTPG...
98BWM014_1	ARQRQIRALS	ERILSTVLR	PTEPVPFQLP	PIERLNINCS	ESSGTSGTQQ
98BWM018_d	ARQRQINSIS	ERILSTCLGR	PAEPVPFQLP	PIERLHIDCS	ESSGTSGTQH
98BWM036_a	ARQRQIHSIS	ERILSSCLGR	PTEPVPFQLP	PIERLHIGDS	ESGGTYGTQQ
98BWM037_d	ARQRQIHSIS	ERILSTCLGR	SAEPVPLQLP	PIERLHIADS	KGGGTSGIQQ
99BW3932_1	ARQRQIHSIS	ERILFTCLGR	STEPVPFQLP	PIERLNIGDS	ESGGTYGTQ
99BW4642_4	ARQRQISSLS	ERILSTCLGR	SAEPVPLQLP	PIERLHIDCS	ESSGTSGTQQ
99BW4745_8	ARQNQIRAIS	KRILSTCLGR	PAEPVPLQLP	PLERLHIGDS	ESGGTSGTQQ
99BW4754_7	ARQRQIHSIS	ERILSNCLGR	PAEPVPFQLP	PIEGLHIDCN	ESSGTSGTQQ
99BWMC16_8	ARQRQIDSIS	QRILSDCLGG	PAEPVSFQLP	PIERLNIDCN	ESGGTSGTQQ
A2_CD_97CD	ARQRQIDSIS	ERILSTCLGR	PTEPVPLQLP	PLERLHLDCS	EDCGTCGTQQ
A2_CY_94CY	ARQRQIDSIS	ERVLRTCLGR	PTEPVPLQLP	PLERLHIDCS	EDCGTSGTLQ
A2D_97KR	ARQRQIRAIS	ERILSACLGR	PTEPVPLQLP	PLERLHLDCS	EDCGTSGTQQ
A2G_CD_97C	ARQRQIREIS	ERILSTCLGR	PTEPVPLLLP	PLERLHLDCS	EDGGTAETQQ
A_BY_97BL0	ARQRQINSIS	KRIFSTCXGR	SXEPVSLQLP	PIERLHLDCS	EDCXTSETQQ
A_KE_Q23_A	ARQRQIDSIS	ERILSTCLGR	PTEPVPLQLP	PLERLHLDCS	EDCGTSGTQQ
A_SE_SE659	ARQRQIDSIS	ERILSACLGR	STEPVPLQLP	PLERLNLDCC	EDCGTSGTQQ
A_SE_SE725	ARQRQIDSIS	ERILSTCLGR	SEEPVPLQLP	SLETLHLDCS	DDCGTSGTQQ
A_SE_SE753	ARQRQIDSIS	ERILNACLGG	STEPVPLQLP	PLERLNLDCC	EDCGTSGTQQ
A_SE_SE853	ARQRQIDSIS	ERILSTCLGR	SAEPVPLQLP	PLEGLHLDCS	EDCGTSGTQQ
A_SE_SE889	ARQKQIDSLS	ERILSTCLGR	PQEPVPLLLP	PIERLHLDCS	EDCGTSGTQQ
A_SE_UGSE8	ARQRQIDSLS	QRILSACLGR	SEEPVPLQLP	PLERLHLDCS	EDCGTSGTG.
A_UG_92UG0	ARQRQIDTSL	ERVLSTCLGR	PAEPVPLQLP	PIERLHLDCS	EDCGTSGTQQ
A_UG_U455_	ARQRQIDSLS	ERILSDCLGR	PAEPVPLQLP	PIERLRLDCS	ESCGTSGTQQ
AC_IN_2130	ARQRQIDSIS	ERILSTFCLGR	SAEPVPLQLP	PLERLHLDCQ	EDCGTSGTQQ
AC_RW_92RW	ARQRQIHSIS	ERILSTCLGR	PTEPVPFQLP	PIERLTIDCS	EDGGTSGTQQ
AC_SE_SE94	ARQRQIDSIS	ERILSTCLGR	SAEPVPLQLP	PLERLHLD..SGTQQ
ACD_SE_SE8	ARQRQIDSIS	QRILSTCLGR	SEEPVPLQLP	PLERLNLDCC	EDCGTSGTQQ
ACG_BE_VI1	ARQRHIHSLS	ERILCTCLGR	SEEPVHLPLP	PLEGLTLDCN	ESSGTSGTEG
AD_SE_SE69	ARQRQINSIG	ERILSTYLGR	SQEPVPLQLP	PLERLTLCNCI	EDCGTSGTQQ
AD_SE_SE71	ARQNQIDSIS	KRILSNCLGR	PAEPVPLQLP	PLERLNLNCS	KDCGTSGTQQ
ADHK_NO_97	ARQXQIHSIG	ERVLATCMGR	PAEPVPLQLP	PLERLTLDSS	EDCDIAGKQQ
ADK_CD_MAL	ARQRQINSIG	ERILSTYLGR	PEEPVPLQLP	PLERLTLCNCN	EDCGTSGTQQ
AG_BE_VI11	ARQRHIQAIS	RRILDACLGR	PAEPVPLQLP	PLERLSLDCS	KDIGTSGTQR
AG_NG_92NG	ARQRQISALS	ERILSTCLGR	PAEPVPLQLP	PIERLSLDCS	EDSRTPETQQ
AGHU_GA_VI	ARQKQIHSIG	ERVLATYLGR	PAEPVPLQLP	PLERLTLDSCS	EDCGTSGEKG
AGU_CD_Z32	ARQRQIHSIG	ERILTTCLGR	STEPVPFLLP	PIERLRIDCS	EDRGDSDPQG
AJ_BW_BW21	ARQNQIDSIS	ERILSTCLGR	PTEPVPFQLP	PIERLRLDCS	EDCGHSGTQQ
B_AU_VH_AF	ARQRQIRQIS	GWILSTYLGR	PAEPVPLQLP	PLERLTLDSCS	KDCGTSGTQQ
B_CN_RL42_	ARQRQIREIS	DRILVTYLG	STEPVPLQLP	PLERLTLDSCS	KDCGTSGTQQ

B_DE_D31_U	QRQRQIQSIS	ERILSTYLGR	PEQPVPLPLP	PLERLTLDSCS	EDCGTSGTQG
B_DE_HAN_U	ERQRQIRISIS	ERILSTFLGR	PAEPVPLQLP	PLERLTLDSCS	EDCGNSGTQG
B_FR_HXB2	ERQRQIHSIS	ERILGTYLGR	SAEPVPLQLP	PLERLTLDSCN	EDCGTSGTQG
B_GA_OYI_M	ERQRQIRKIS	GWILSTYLGR	SAEPVPLQLP	PLERLNLDSCS	EDCGTSGTQG
B_GB_CAM1	ERQRHIRAIS	NWILSTHLGR	PAEPVPLQLP	PLERLTLDSCS	KDCGTSGTQG
B_GB_GB8_A	ARQRQIHQIG	EWILSAFLGR	PAEPVPLQLP	PIERLTLDSCD	EDCGTSGTQG
B_GB_MANC	GRQRQIQSLS	AWILSTRLGR	STQPVPLQLP	PLERLTLDSCS	EDCGTSGTQG
B_KR_WK_AF	RRQWWIQSLS	GWILNTHLGR	PAEPVPLQLP	PLERLTLDSCN	EECGTSGTQG
B_NL_3202A	ERQRQIRISIS	ERILSTYLGR	SAEPVPLQLP	PLERLTLDSCD	EDCGTSGTQG
B_TW_TWCYS	ERQRQIRTIS	GWILSNYLGR	PAEPVPLQLP	PLERLTLDSCD	EDCGTSGTQG
B_US_BC_L0	ERQRQIRISIS	ERILSTFLGR	SAEPVPLQLP	PLERLTLDSCD	EDCGTSGTQG
B_US_DH123	QRQRQIQSIS	GWILSNHLGR	PADAVPLQLP	PLERLTLDSCN	EDCGTSGTQG
B_US_JRCSF	ERQRQIRTIS	ERILSTYLGR	PAEPVPLQLP	PLERLTLDSCN	EDCGTSGTQG
B_US_MNCG	ERQRHIRSIS	AWILSNYLGR	PAEPVPLQLP	P.QRLTLDSCS	EDCGTSGTQG
B_US_P896	ERQRQIRISIS	ERILGTFLGR	FEEPVPPLPLP	PLEKLTLDSCN	EDCGTSGTQG
B_US_RF_M1	ERQRQIRRCIS	EWILDTYLGR	SVDPVQLQLP	PLERLTLDSCS	EDCGTSGTQG
B_US_SF2_K	ERQRQIRISIS	GWILSTYLGR	SAEPVPLQLP	PLERLTLDSCS	EDCGNSGAQG
B_US_WEAU1	ERQRQIRKIS	GWILNTYLGR	PTEPVPLPLP	PLDRLTLDCK	EDCGTSGTQG
B_US_WR27	.RQRQIQSLS	AWIISTHLGR	PAEPVPLQLP	PLERLTLDSCS	EDCGTSGTQG
B_US_YU2_M	ERQRQIRISIS	GWLLSNYLGR	PTEPVPLQLP	PLERLTLDSCN	EDCGTSGTQG
BF1_BR_93B	ARQRQIREIS	ERILSSCLGR	PEEPVPLQLP	PLERLHINCS	EDCGQGTTEE
C_BR_92BR0	ARQRQIHSIS	ERILSTCVGR	PAEPVPLQLP	PIERLNINCS	ESGGTSGTQQ
C_BW_96BW0	ARQRQIHSIS	ERILSTCLGR	PTEPVPLQLP	PIERLHIDCS	ESSGASGTQQ
C_BW_96BW1	ARQKQINSIS	ERILSTCLGR	SAEPVPFLLP	PIERLHISDS	ESGGTSGTQQ
C_BW_96BW1	ARQRQIHSIS	ERILSTCLGR	PAEPVPLQLP	PIERLHIGGS	ENSGTTGTQQ
C_BW_96BW1	ARQRQIDSIS	TRILSTCLGR	PEEPVPFLQLP	PIERLNIGDS	ESGGTSGTQQ
C_ET_ETH22	ARQRQIHTLS	ERILSNFLGR	PAEPVPLQLP	PLERLNLDSCS	EDSGTSGTQQ
C_IN_93IN1	ARQRQIHSIS	ERILSTCLGR	STEPVPLQLP	PIERLHIGGS	ESGGTSGTQQ
C_IN_93IN9	ARQRQIHSLS	ERILSACLGR	PAEPVPLQLP	PLERLHISGS	ESGGTSGTQQ
C_IN_93IN9	ARQKQIHSLS	ERILSTCLGR	SAEPVPLQLP	PLERLHISGS	ESGGTSGTQQ
C_IN_94IN1	ARQRQIHSIS	ERILSACLGR	PAEPVPLQLP	PIERLHISGS	ESGGTSGTQQ
C_IN_95IN2	ARQRQIHSIS	ERILSTFLGR	PAEPVPLQLP	PIERLHISGS	ESAGTSGTPQ
CRF01_AE_C	RRQRQIHSLS	ERILVACVGR	STEPVPLQLP	PLERLHIDCS	EDCGTSGTQQ
CRF01_AE_C	ARQRQIHKIG	ERILSTCLGR	SPEPVPLQLP	PLERLHLDSCS	EDCGTSGTQQ
CRF01_AE_C	ARQRQIRALS	ERILSACLGR	SAEPVPLQLP	PLERLHLDSCS	EDCGTSGTQQ
CRF01_AE_T	ARQRQIRAIS	BRILITCLGR	STEPVPLQLP	PLERLHLDSCN	EDCGTSGTQQ
CRF01_AE_T	ARQRQIRAIS	BRILNACVGR	STEPVPLQLP	PLERLHLDSCS	EDCGTSGTQQ
CRF01_AE_T	ARQRQIRAIS	BRILSTCLGR	STEPVPLQLP	PLERLHLDSCS	EDCGTSGTQQ
CRF01_AE_T	ARQRQIREIS	ERILSSCVGR	STEPVPLPLP	PLERLHLDSCS	EDCGTSGTQQ
CRF01_AE_T	ARQRQISAIS	ERILSTCLGR	STEPVPLQLP	PVERLNLDSCS	EDGGTSGTQQ
CRF01_AE_T	ARQRQISAIS	ERILSACLGR	STEPVSLPLP	PLERLHLDSCS	EDCGTSGTQQ
CRF02_AG_F	ARQRQIRAIS	ERFLSTCLGR	SAEPVPLQLP	PIERLCLDSCS	EGCGTSGTQQ
CRF02_AG_F	ARQRQIRAIS	QRILSTCLGR	SAEPVPLQLP	PLERLCLDSCS	EGCGTSGTQQ
CRF02_AG_G	ARQRQIHSLS	ERILSTCLGR	PEEPVSFQLP	PLERLNLDSCS	EDCGNSGTQS
CRF02_AG_N	ARQRQIRAIS	ERILSTCLGR	SAEPVPLQLP	PIERLNLDSCS	EDCGTSGTQL
CRF02_AG_S	ARQRQIRAIS	ERILSTCLGR	SAEPVPLQLP	PIERLRLDSCS	EDCGTSGTQG
CRF02_AG_S	ARQRQVRAIS	ERILSTCLGR	PAEPVPLPLP	PIERLCLDSCS	EDSGTSGTQQ
CRF03_AB_R	ERQRHIHSIS	EQILSTYLGR	PEEPVLLHLP	PLERLTLDSCS	EDCGTSGTQG
CRF03_AB_R	ERQRHIHSIS	QRILSTYLGR	PEEPVPLHLP	PLERLTLDSCS	EDCGTSGTQG
CRF04_cpx	ARQKQIHSLS	ERILATYLGR	PAEPVPLQLP	PLEKLTNLCS	EDCGTSGDKG
CRF04_cpx	ARQKQIHSIS	ERVLATYLGR	PAEPVPLQLP	PLEKLTNLCS	EDCGTSGEKG
CRF04_cpx	ARQNRIHSIS	ERILAACLGR	PAEPVPLQLP	PIEKLTLDSCS	EDCGTSGDKG
CRF05_DF_B	ARQRQINSIG	ERLLSTYLGR	SEEPVPLQLP	PLERLNLDSCS	EDCGTSGTQG
CRF05_DF_B	ARQRQIRISIA	DRIVDTYLGR	PEEPVPLQLP	PLERLNLDSCS	EDCGTSGTQG
CRF06_cpx	ARQNQIDSIS	ERVLSTCLGR	SAEPVPLQLP	PIERLRLDSCS	EDCGNSGTQG
CRF06_cpx	ARQNQIDSIS	ERILSTCLGR	PTEPVPLQLP	PIERLRLDSCS	EDCGNSGTQG
CRF06_cpx	ARQKQIDSIS	ERILSTCLGR	SAEPVPLQLP	PIERLRLDSCS	EDCGNSGTQG
CRF06_cpx	ARQNQIDSIS	ERILSSCLGR	SEEPVPLQLP	PIERLRLDCT	EDCGNSGTQG
CRF11_cpx	ARQNQIDSIS	QRILSDCLGR	SEEPVPLQLP	PIERLHLDSCS	EDCGNPGTQG
CRF11_cpx	ARQNQLHSIS	QRILSTCLGR	SEEPVPLPLP	PIERLHLDSCS	EDCGNSGTQG

D_CD_84ZR0	ARQRYIHSIG	ERILSTYLGR	SEEPVPLQLP	PLERINLNCS	EDCGTSGTQG
D_CD_ELI_K	ARQRQIREIA	ERILGTYLGR	PAEPVPLQLP	PLERLNLNCS	EDCRTSGTQG
D_CD_NDK_M	ARQRQIHSIG	ERIICTFLGR	PEEPVPLQLP	PLERLNLNCS	EDCGTSGTQG
D_UG_94UG1	ARQRQIHSIG	ERIISTYLGR	FEPPVPLQLP	PLERLNLNCS	EDCGTSGTQG
F1_BE_VI85	ARQRQIRALS	DRILSSCLGR	SEEPVPLQLP	PLERLNLNCS	EDCGQGPPEG
F1_BR_93BR	ARQRQIREIS	DRILSSCLGR	PAEPVPLQLP	PLERLNHNCS	EDCGQGAEEG
F1_FI_FIN9	ARQRQIRAIS	ERILSSCLGR	LEEPVPLQLP	PLERLNHNCS	EDCGQGTEEG
F1_FR_MP41	ARQKQIRSIS	ERILVACLGR	PEEPVPLQLP	PLERLNHNCS	KDCGQGTNEG
F2_CM_MP25	ARQRQIHQIS	ERILSTCLGR	LQEPVRLQLP	LLEKLHNCS	EDCGQGTEKG
F2KU_BE_VI	ARQRQIHSIS	QRILSTCLGR	PAEPVPFQLP	PLERLNLDCS	EDSGREGAEGE
G_BE_DRCBL	ARQRQIHSIS	ERILSTCLGR	PEEPVPLQLP	PLERLHLDCS	EDSGTSGTQQ
G_NG_92NG0	ARQRQIHSIS	ERILSACLGR	PAEPVPFQLP	PLEGLSLDCS	KDGGTSGTQQ
G_SE_SE616	ARQRQIS AIS	ERILTAYLGR	PAEPVPLQLP	PLERLHLDCS	EDSGTSGTQQ
H_BE_VI991	ARQRQIHSIG	ERVLATCLGG	PAEPVPLQLP	PLERLTLDCS	EDCGTSGEKG
H_BE_VI997	ARQRQIR AIS	ERILTDC LGR	PPEPVPLQLP	PLERLTLD CN	KDCGTSGEKG
H_CF_90CF0	ARQRQIREIS	ERILTCLGR	PPEPVT LQLP	PLERLT LNCS	EDCGTSGEKG
J_SE_SE702	ARQNQIDSIS	ERILSSCLGR	PAEPVPLQLP	PIERLRLDCS	EDCGNSGTQG
J_SE_SE788	ARQNQIDSIS	ERIPSSCLGR	PAEPVPLQLP	PIERLRLDCS	EDCGNSGTQG
K_CD_EQTB1	ARQRQIREIS	QVRLSSCLGR	STEPVPLQLP	PLERLSLNCD	EDSGQGTETE
K_CM_MP535	ARQKQISSIS	ERLLSACLGR	SAEPVPLQLP	PIEKLNLNCD	EDPGKGTEGG
N_CM_YBF30	ARQRQIR AIS	ERILSSCLGG	PPEPVDLPLP	PLDRLTLDTE	EDSGTPGTES
O_CM_ANT70	RRQAQVDTLA	ARVLATVVHG	PQNNNIVDLP	PLEQLSIRDP	EGDQLSEAWT
O_CM_MVP51	RRQAQVDSL A	TRILATVVHG	SQDNNLV DLP	PLEQLNIRDP	EADRLPGTGT
O_SN_MP129	TRHAHVDTLA	ARILATVVHG	PQDNNLV ELP	PLEQLSIRDP	DGDQPSGTWT
O_SN_MP130	KRQAQIDT LA	ARILATVVHG	PQDNNLV ELP	PLEQLSIRDP	DGDQPSGTWT
U_CD_83C	RRQQQIRSIS	ERILSTCLGR	PAEPVHLQLP	PLERLNLDCSKGTATG

	101		129
00BW0762_1	PQGTPEG MGN	P.....
00BW0768_2	SQGTSEG VGS	P.....
00BW0874_2	SQGTTEG VGN	P.....
00BW1471_2	SQGITEG VGS	P.....
00BW1616_2TOGVGS	P.....
00BW1686_8	SQGATEG VGN	P.....
00BW1759_3VGS	P.....
00BW1773_2	SQGTTEG VGS	P.....
00BW1783_5	SQGTTEG VGN	P.....
00BW1795_6	SQGTPEG VGN	P.....
00BW1811_3	SQGTPEG VGN	P.....
00BW1859_5	SQGTTEG VGS	P.....
00BW1880_2	SQGTPEG VGN	P.....
00BW1921_1	SQGTTEG VGN	P.....
00BW2036_1	SQGTTEG VGS	P.....
00BW2063_6	SQGTPEG VGN	P.....
00BW2087_2	PQGTTEG VGN	P.....
00BW2127_2VGS	P.....
00BW2276_7	SQGTTEG VGS	P.....
00BW3819_3	SQGTTEG VGS	P.....
00BW3842_8	PQGTTEG VGS	P.....
00BW3871_3	SQGTTEG VGN	P.....
00BW3876_9	SQGTKEG VGS	P.....
00BW3886_8	SQGTTEG VGS	P.....
00BW3891_6	SQGTTEG VGS	P.....
00BW3970_2GVGH	P.....
00BW5031_1	PQGDTEG VGR	P.....
96BW01B21	SQGTTEG VGN	P.....
96BW0407	SQGTTEG VGN	P.....
96BW0502TEGVGS	P.....
96BW06_J4	SQGPTEG VGS	P.....
96BW11_06	SQGTPEG VGN	P.....

96BW1210 SQGTTEGVGS P.....
 96BW15B03 SQGTTEGVGS P.....
 96BW16_26GVGS P.....
 96BW17A09 SQGATEGVGS P.....
 96BWM01_5 SQGTPEGVGN P.....
 96BWM03_2 SQGTTEGVGS S.....
 98BWM012_2 SQGTARGVGS P.....
 98BWM013_4 SHGTPEGVGN P.....
 98BWM014_aTQGVGN P.....
 98BWM014_1 SLGTTEGVGS P.....
 98BWM018_d SQGTTEGVGN P.....
 98BWM036_a PQGTTEGVGN P.....
 98BWM037_d PQGTTEGVGS P.....
 99BW3932_1 SQGTTEGVGS P.....
 99BW4642_4 SQGTTEGVGS P.....
 99BW4745_8 SQGTTEGVGS P.....
 99BW4754_7 SQGTPEGVGN S.....
 99BWM016_8 SQGTTEGVGS P.....
 A2_CD_97CD SQGAETGVGR PQTSVESSGI LGS GIEDX.
 A2_CY_94CY SQGTETGVGR SQESVESSVI LGS GTEEX.
 A2D_97KR PQGTETGVGR PQISVEPSVV LGS GTEEX.
 A2G_CD_97C PQGTETGVGG .TIFVESSVI LGS RTKEQX
 A_BY_97BL0 SQXTETXVXX PQISXESSXI XXSGTKEX.
 A_KE_Q23_A SQGAETGVGR HQVSVESPVI LGS GTKNX.
 A_SE_SE659 SQGVETGVGR PQVSGESPVI LGS GTKNX.
 A_SE_SE725 SQGVETGVGR PQVPGEPTV LGS GTKTX.
 A_SE_SE753 SQGIETGVGR PQVSVESPVI LGS GTKEX.
 A_SE_SE853VGR PQVSVESPGV LDS GTKNX.
 A_SE_SE889 SQGAETGVGG PQVSEESSII LGS GTKTX.
 A_SE_UGSB8TQVSGESSVV LDS GTKDX.
 A_UG_92UG0 SQGVETGVGR TQVSGESPVV LGS GTKNX.
 A_UG_U455 PQGTETGVGG PQISVESSAV LGS GTKNX.
 AC_IN_2130 SQGVETGVGR PQVSVESPGI LGS GTKNX.
 AC_RW_92RW SQGTTEGVGN PVS RKSCAVL GSGTKKEX.
 AC_SE_SE94 SQGTETGVGR PQVSVESSAI LGPGTKNX.
 ACD_SE_SE8VGS NQISVESPAV LDS GTKEX.
 ACG_BE_VI1VGS SQTSGEHPVI LES GTKEX.
 AD_SE_SE69VGS PQIPVEPPAV LDS GTKEX.
 AD_SE_SE71VGS PQIPVESPAI LDSGTENX.
 ADHK_NO_97VGD PQIPGESSAV LGTGTKEX.
 ADK_CD_MALVGS PQISVESPAI LGS GTEEX.
 AG_BE_VI11 SQGTETGVGR PQIFVESSGV LGS GTKEX.
 AG_NG_92NG SPGTETGVGG PQISVESPVV LGS GTKEX.
 AGHU_GA_VIVGS PQISVESPTV LGTGAKEX.
 AGU_CD_Z32VGD SQIPGESCDL LGS GTKEX.
 AJ_BW_BW21VGD PQVSGESCPI LGE GTKEX.
 B_AU_VH_AFVGG PQVLVESPAV LESGAAEX.
 B_CN_RL42VGS PQILVESPAV LDS GTKEX.
 B_DE_D31_UVGS PQILVESPAV LES GTKEX.
 B_DE_HAN_UVGS PQVLVESPAV LEPGTKEX.
 B_FR_HXB2VGS PQILVESPTV LES GTKEX.
 B_GA_OYI_MVGS PEILVESPAV LEPGTKEX.
 B_GB_CAM1VGS PQILVESPAV LES GTKEX.
 B_GB_GB8_AVGS PQVLVESPAV LDPGTKEX.
 B_GB_MANCVGN PQVLVESPAV LESGSKEX.
 B_KR_WK_AFVGN PQILVESPAV LES GTKEX.
 B_NL_3202AVGS PQILVESPAV LES GTKEX.
 B_TW_TWCYSVGS PQIFVESPTV LDS GTKEX.
 B_US_BC_L0VGS PQVLVESPTV LEPGTKEX.
 B_US_DH123VGT PQILVESPAV LES GTKEX.

B_US_JRCSEVGN PEILVESPTV LESGTKEX.
 B_US_MNCGVGS PQILVESPTV LESGTKEX.
 B_US_P896VGS PQILVESPAI LEPGTKEX.
 B_US_RF_M1VGS PQVLVESPAV LESGAKEX.
 B_US_SF2_KVGS PQILVESPAV LDSGTKEX.
 B_US_WEAU1VGS SQILLES PAV LEPGTKEX.
 B_US_WR27VGD PQILGESPTV LGSGAKEX.
 B_US_YU2_MVGS PQILVESPPV LDSGTKEX.
 BF1_BR_93BVGS PQTSGESRAV LESGTKEX.
 C_BR_92BR0 PQGNTERVGN PVFGRPCAVL ESRVKKEX.
 C_BW_96BW0 SQGTTEGVGN PVSGKSCAIL GSRAKKEX.
 C_BW_96BW1 SQGTPEGVGN PISGKSCAVL GARAKKEX.
 C_BW_96BW1 SQGTTEGVGS PISGKSCAVL GSGTKKEX.
 C_BW_96BW1 SQGTTEGVGS PVSGKSCAVL GSGTKKEX.
 C_ET_ETH22 SQGTTEGVGN PISGKPCAVL GSGAKKEX.
 C_IN_93IN1L..GS PISGKSCAVL GSGAKKEX.
 C_IN_93IN9 SQGTTERVGS PISGKSCAVL GSGAKKEX.
 C_IN_93IN9 SQGTTEGVGS PISGKSCAVL GYRAKKEX.
 C_IN_94IN1 SQGTTERVGS PISGKSCAVL GSGAKKEX.
 C_IN_95IN2 SQGTTEGVGS PISGKSCTVL GSGAKKEX.
 CRF01_AE_C SQGTETGVGG PQISGESSVI LGSGTKNX.
 CRF01_AE_C STGTETEVR PISGESSVI LGSGTKNX.
 CRF01_AE_C SRTGTGVGR PQISGESSVI LGSGTENX.
 CRF01_AE_T SQGTETGVGR PQISGESSVI LGPGTKNX.
 CRF01_AE_T SQGTETGVGR PQISGESSVI LGSGTKNX.
 CRF01_AE_T SQGTETGVGR PQISGESSVI LGPGTKNX.
 CRF01_AE_T SQGTETGVGR PQISGESSVI LGPGTKNX.
 CRF01_AE_T SQGTETGVGR PQISGESSVI LGPGTKNX.
 CRF01_AE_T SQGTETGVGR PQISVSSGI LGPGTKNX.
 CRF02_AG_F PQGTETGVGS PPISGESSTI LGSGTKEX.
 CRF02_AG_F SQGTETGLGS PQISGESSTI LGAGTKEX.
 CRF02_AG_GVAD PQIPGESRAI LGSGTKEX.
 CRF02_AG_N SQGTETGVGS PQISVESYII LGSGTKEX.
 CRF02_AG_SVGS PQISVSSIV LGSGTKEX.
 CRF02_AG_S SQGTETGVGS PQISVSSIV LGSGTKEX.
 CRF03_AB_RVGS PQILVESPTV LDSGTKEX.
 CRF03_AB_RVGS PQILVESPTV LDSGTKEX.
 CRF04_cpxVGS PQVSVELPAV LGTGAKEX.
 CRF04_cpxVGS PQVSVEPPAV LGTGAKEX.
 CRF04_cpxVGN PQVPVEPPAV LGTGDKEX.
 CRF05_DF_BVGS PQISVEPPAI LESGTKEX.
 CRF05_DF_BVGS PQISVESPTV LESGAKEX.
 CRF06_cpxVGN PQISGEPDML LGTGTTX.
 CRF06_cpxVGD PQIPGEPGVV LGTGTKEX.
 CRF06_cpxVGD PQIPVEPGVL LGTGTKEX.
 CRF06_cpxVGD PQIPGEPGVV LGTGTKEX.
 CRF11_cpxVGD SQISGESDTV LGPRTEEX.
 CRF11_cpxVGE SQIPGESSTV LGPRTEEX.
 D_CD_84ZR0VGS PQISVESPAI LESRTEEX.
 D_CD_ELI_KVGH PQISVESPTV LESGTEEQX.
 D_CD_NDK_MVGS PQIPVEPPAV LESGTEEX.
 D_UG_94UG1VGS HQISVESPAV LDSGTKEX.
 F1_BE_VI85VGS SQISGESHAV LESGTKEX.
 F1_BR_93BRVGS SQISGESHTV LGSGTKEX.
 F1_FI_FIN9VGS PQISGEHHTV LESGTKEX.
 F1_FR_MP41VGN PQISMEPRTV LESGTKEX.
 F2_CM_MP25VGS PQISVESRAV LGSGTKEX.
 F2KU_BE_VILGN PQIPVEPCAV LGSGTKEX.
 G_BE_DRCBL SQGTETGVGS PQIFVSSVV LGSGTKEX.
 G_NG_92NG0 PQGTETGVGR PQVLVEPPVV LGSGTKEX.

G_SE_SE616 PQGTETGVGR .SIFVESSVV LGQGTKEX.
 H_BE_VI991VGS PQTSGESPAV LGTGAKEX.
 H_BE_VI997KGG PQIPVESSTV LGTGTKEX.
 H_CF_90CF0EGS PQISLESSTI LGTGTKEX.
 J_SE_SE702VGD PQISGEPCMV LGAGTKEX.
 J_SE_SE788VGD PQISGEPCMV LGAGTKEX.
 K_CD_EQTB1LGS PQIPVEPDTV LGSGDKEX.
 K_CM_MP535LGS PQISVEPCTV LESGTKEX.
 N_CM_YBF30 QQG.TATTET QNTLVGNTCI LGKRVKGX.
 O_CM_ANT70 VDPR.AEDNC LQNLCSNTI LATRIAEX.
 O_CM_MVP51 VDPG.TKDNS LT.LWSCNAI LATRIEKX.
 O_SN_MP129 VDSG.TEDNC LQTLHSCNTI LATRVAEX.
 O_SN_MP130 VDPG.TEDNC LQNLHSCNTI LATRVAEX.
 U_CD__83CVGS TQIPGESCAV LGSGTKE..

Table 16. HIV Tat Alignment
GCG Multiple Sequence File.
Written by Omega 1.1

Name: 00BW0762_1	Len: 108	Check: 5728	Weight: 1.00
Name: 00BW0768_2	Len: 108	Check: 4583	Weight: 1.00
Name: 00BW0874_2	Len: 108	Check: 5462	Weight: 1.00
Name: 00BW1471_2	Len: 108	Check: 4359	Weight: 1.00
Name: 00BW1616_2	Len: 108	Check: 5389	Weight: 1.00
Name: 00BW1686_8	Len: 108	Check: 6742	Weight: 1.00
Name: 00BW1759_3	Len: 108	Check: 6187	Weight: 1.00
Name: 00BW1773_2	Len: 108	Check: 5566	Weight: 1.00
Name: 00BW1783_5	Len: 108	Check: 6579	Weight: 1.00
Name: 00BW1795_6	Len: 108	Check: 6027	Weight: 1.00
Name: 00BW1811_3	Len: 108	Check: 4928	Weight: 1.00
Name: 00BW1859_5	Len: 108	Check: 6153	Weight: 1.00
Name: 00BW1880_2	Len: 108	Check: 6898	Weight: 1.00
Name: 00BW1921_1	Len: 108	Check: 6286	Weight: 1.00
Name: 00BW2036_1	Len: 108	Check: 4808	Weight: 1.00
Name: 00BW2063_6	Len: 108	Check: 7492	Weight: 1.00
Name: 00BW2087_2	Len: 108	Check: 4005	Weight: 1.00
Name: 00BW2127_2	Len: 108	Check: 6532	Weight: 1.00
Name: 00BW2276_7	Len: 108	Check: 7138	Weight: 1.00
Name: 00BW3819_3	Len: 108	Check: 4977	Weight: 1.00
Name: 00BW3842_8	Len: 108	Check: 5730	Weight: 1.00
Name: 00BW3871_3	Len: 108	Check: 7576	Weight: 1.00
Name: 00BW3876_9	Len: 108	Check: 4797	Weight: 1.00
Name: 00BW3886_8	Len: 108	Check: 7443	Weight: 1.00
Name: 00BW3891_6	Len: 108	Check: 5634	Weight: 1.00
Name: 00BW3970_2	Len: 108	Check: 5984	Weight: 1.00
Name: 00BW5031_1	Len: 108	Check: 8884	Weight: 1.00
Name: 96BW01B21	Len: 108	Check: 6237	Weight: 1.00
Name: 96BW0407	Len: 108	Check: 5097	Weight: 1.00
Name: 96BW0502	Len: 108	Check: 5303	Weight: 1.00
Name: 96BW06_J4	Len: 108	Check: 5679	Weight: 1.00
Name: 96BW11_06	Len: 108	Check: 7244	Weight: 1.00
Name: 96BW1210	Len: 108	Check: 5043	Weight: 1.00
Name: 96BW15B03	Len: 108	Check: 5056	Weight: 1.00
Name: 96BW16_26	Len: 108	Check: 5774	Weight: 1.00
Name: 96BW17A09	Len: 108	Check: 4288	Weight: 1.00
Name: 96BWM01_5	Len: 108	Check: 6335	Weight: 1.00
Name: 96BWM03_2	Len: 108	Check: 5085	Weight: 1.00
Name: 98BWM012_2	Len: 108	Check: 5048	Weight: 1.00
Name: 98BWM013_4	Len: 108	Check: 5714	Weight: 1.00
Name: 98BWM014_a	Len: 108	Check: 6475	Weight: 1.00
Name: 98BWM014_1	Len: 108	Check: 5085	Weight: 1.00
Name: 98BWM018_d	Len: 108	Check: 4268	Weight: 1.00
Name: 98BWM036_a	Len: 108	Check: 6665	Weight: 1.00
Name: 98BWM037_d	Len: 108	Check: 5564	Weight: 1.00
Name: 99BW3932_1	Len: 108	Check: 5875	Weight: 1.00
Name: 99BW4642_4	Len: 108	Check: 6405	Weight: 1.00
Name: 99BW4745_8	Len: 108	Check: 4857	Weight: 1.00
Name: 99BW4754_7	Len: 108	Check: 5219	Weight: 1.00
Name: 99BWM016_8	Len: 108	Check: 4870	Weight: 1.00
Name: A2_CD_97	Len: 108	Check: 4523	Weight: 1.00
Name: A2_CY_94	Len: 108	Check: 3933	Weight: 1.00
Name: A2D_97_9	Len: 108	Check: 4676	Weight: 1.00
Name: A2G_CD_9	Len: 108	Check: 2213	Weight: 1.00
Name: A_BY_97_97	Len: 108	Check: 4264	Weight: 1.00
Name: A_KE_93_Q2	Len: 108	Check: 3668	Weight: 1.00

Name: A_SE_93_SE	Len: 108	Check: 4159	Weight: 1.00
Name: A_SE_94_SE	Len: 108	Check: 4323	Weight: 1.00
Name: A_SE_94_SE	Len: 108	Check: 3099	Weight: 1.00
Name: A_SE_95_SE	Len: 108	Check: 3717	Weight: 1.00
Name: A_SE_95_SE	Len: 108	Check: 4178	Weight: 1.00
Name: A_SE_95_UG	Len: 108	Check: 3954	Weight: 1.00
Name: A_UG_85_U4	Len: 108	Check: 3663	Weight: 1.00
Name: A_UG_92_92	Len: 108	Check: 4315	Weight: 1.00
Name: AC_IN_95_2	Len: 108	Check: 5100	Weight: 1.00
Name: AC_RW_92_9	Len: 108	Check: 4062	Weight: 1.00
Name: AC_SE_96_S	Len: 108	Check: 6001	Weight: 1.00
Name: ACD_SE_95_	Len: 108	Check: 4767	Weight: 1.00
Name: ACG_BE_ V	Len: 108	Check: 5568	Weight: 1.00
Name: AD_SE_93_S	Len: 108	Check: 4456	Weight: 1.00
Name: AD_SE_95_S	Len: 108	Check: 4850	Weight: 1.00
Name: ADHK_NO_97	Len: 108	Check: 6557	Weight: 1.00
Name: ADK_CD_85_	Len: 108	Check: 4622	Weight: 1.00
Name: AG_BE_ VI	Len: 108	Check: 3720	Weight: 1.00
Name: AG_NG_92_9	Len: 108	Check: 4790	Weight: 1.00
Name: AGHU_GA_	Len: 108	Check: 4548	Weight: 1.00
Name: AGU_CD_76_	Len: 108	Check: 7456	Weight: 1.00
Name: AJ_BW_98_B	Len: 108	Check: 4086	Weight: 1.00
Name: B_AU_ VH	Len: 108	Check: 5824	Weight: 1.00
Name: B_CN_ RL4	Len: 108	Check: 3342	Weight: 1.00
Name: B_DE_86_D3	Len: 108	Check: 4538	Weight: 1.00
Name: B_DE_86_HA	Len: 108	Check: 5673	Weight: 1.00
Name: B_FR_83_HX	Len: 108	Check: 2953	Weight: 1.00
Name: B_GA_ OYI	Len: 108	Check: 5056	Weight: 1.00
Name: B_GB_ CAM	Len: 108	Check: 4131	Weight: 1.00
Name: B_GB_ GB8	Len: 108	Check: 7783	Weight: 1.00
Name: B_GB_59_MA	Len: 108	Check: 5562	Weight: 1.00
Name: B_KR_ WK	Len: 108	Check: 6702	Weight: 1.00
Name: B_NL_86_32	Len: 108	Check: 5027	Weight: 1.00
Name: B_TW_ TWC	Len: 108	Check: 6611	Weight: 1.00
Name: B_US_ DH1	Len: 108	Check: 5131	Weight: 1.00
Name: B_US_ P89	Len: 108	Check: 5087	Weight: 1.00
Name: B_US_83_RF	Len: 108	Check: 7745	Weight: 1.00
Name: B_US_83_SF	Len: 108	Check: 4303	Weight: 1.00
Name: B_US_84_MN	Len: 108	Check: 4888	Weight: 1.00
Name: B_US_86_JR	Len: 108	Check: 5959	Weight: 1.00
Name: B_US_86_YU	Len: 108	Check: 6104	Weight: 1.00
Name: B_US_87_BC	Len: 108	Check: 5602	Weight: 1.00
Name: B_US_88_WR	Len: 108	Check: 5031	Weight: 1.00
Name: B_US_90_WE	Len: 108	Check: 5035	Weight: 1.00
Name: BF1_BR_93_	Len: 108	Check: 3381	Weight: 1.00
Name: C_BR_92_92	Len: 108	Check: 6035	Weight: 1.00
Name: C_BW_96_96	Len: 108	Check: 5570	Weight: 1.00
Name: C_BW_96_96	Len: 108	Check: 7348	Weight: 1.00
Name: C_BW_96_96	Len: 108	Check: 5043	Weight: 1.00
Name: C_BW_96_96	Len: 108	Check: 5056	Weight: 1.00
Name: C_ET_86_ET	Len: 108	Check: 4199	Weight: 1.00
Name: C_IN_93_93	Len: 108	Check: 5957	Weight: 1.00
Name: C_IN_93_93	Len: 108	Check: 4573	Weight: 1.00
Name: C_IN_93_93	Len: 108	Check: 5361	Weight: 1.00
Name: C_IN_94_94	Len: 108	Check: 5479	Weight: 1.00
Name: C_IN_95_95	Len: 108	Check: 5697	Weight: 1.00
Name: CRF01_AE_C	Len: 108	Check: 2633	Weight: 1.00
Name: CRF01_AE_C	Len: 108	Check: 4093	Weight: 1.00
Name: CRF01_AE_C	Len: 108	Check: 2957	Weight: 1.00
Name: CRF01_AE_T	Len: 108	Check: 2478	Weight: 1.00

Name: CRF01_AE_T	Len: 108	Check: 1857	Weight: 1.00
Name: CRF01_AE_T	Len: 108	Check: 1204	Weight: 1.00
Name: CRF01_AE_T	Len: 108	Check: 2024	Weight: 1.00
Name: CRF01_AE_T	Len: 108	Check: 913	Weight: 1.00
Name: CRF01_AE_T	Len: 108	Check: 1446	Weight: 1.00
Name: CRF02_AG_F	Len: 108	Check: 4840	Weight: 1.00
Name: CRF02_AG_F	Len: 108	Check: 6283	Weight: 1.00
Name: CRF02_AG_G	Len: 108	Check: 4683	Weight: 1.00
Name: CRF02_AG_N	Len: 108	Check: 3989	Weight: 1.00
Name: CRF02_AG_S	Len: 108	Check: 3401	Weight: 1.00
Name: CRF02_AG_S	Len: 108	Check: 4884	Weight: 1.00
Name: CRF03_AB_R	Len: 108	Check: 2749	Weight: 1.00
Name: CRF03_AB_R	Len: 108	Check: 3199	Weight: 1.00
Name: CRF04_cpx_	Len: 108	Check: 2779	Weight: 1.00
Name: CRF04_cpx_	Len: 108	Check: 2140	Weight: 1.00
Name: CRF04_cpx_	Len: 108	Check: 4857	Weight: 1.00
Name: CRF05_DF_B	Len: 108	Check: 6229	Weight: 1.00
Name: CRF05_DF_B	Len: 108	Check: 4828	Weight: 1.00
Name: CRF06_cpx_	Len: 108	Check: 4652	Weight: 1.00
Name: CRF06_cpx_	Len: 108	Check: 5232	Weight: 1.00
Name: CRF06_cpx_	Len: 108	Check: 4871	Weight: 1.00
Name: CRF06_cpx_	Len: 108	Check: 5747	Weight: 1.00
Name: CRF11_cpx_	Len: 108	Check: 4101	Weight: 1.00
Name: CRF11_cpx_	Len: 108	Check: 3288	Weight: 1.00
Name: D_CD_83_EL	Len: 108	Check: 3640	Weight: 1.00
Name: D_CD_83_ND	Len: 108	Check: 4658	Weight: 1.00
Name: D_CD_84_84	Len: 108	Check: 6447	Weight: 1.00
Name: D_UG_94_94	Len: 108	Check: 6559	Weight: 1.00
Name: F1_BE_93_V	Len: 108	Check: 4812	Weight: 1.00
Name: F1_BR_93_9	Len: 108	Check: 4376	Weight: 1.00
Name: F1_FI_93_F	Len: 108	Check: 4918	Weight: 1.00
Name: F1_FR_96_M	Len: 108	Check: 3934	Weight: 1.00
Name: F2_CM_95_M	Len: 108	Check: 5318	Weight: 1.00
Name: F2KU_BE_94	Len: 108	Check: 4644	Weight: 1.00
Name: G_BE_96_DR	Len: 108	Check: 4391	Weight: 1.00
Name: G_NG_92_92	Len: 108	Check: 5855	Weight: 1.00
Name: G_SE_93_SE	Len: 108	Check: 2420	Weight: 1.00
Name: H_BE_VI9	Len: 108	Check: 5780	Weight: 1.00
Name: H_BE_VI9	Len: 108	Check: 2472	Weight: 1.00
Name: H_CF_90_90	Len: 108	Check: 3026	Weight: 1.00
Name: J_SE_93_SE	Len: 108	Check: 4542	Weight: 1.00
Name: J_SE_94_SE	Len: 108	Check: 4057	Weight: 1.00
Name: K_CD_97_EQ	Len: 108	Check: 2222	Weight: 1.00
Name: K_CM_96_MP	Len: 108	Check: 4681	Weight: 1.00
Name: N_CM_95_YB	Len: 108	Check: 3679	Weight: 1.00
Name: O_CM_ANT	Len: 108	Check: 1276	Weight: 1.00
Name: O_CM_91_MV	Len: 108	Check: 814	Weight: 1.00
Name: O_SN_99S	Len: 108	Check: 9132	Weight: 1.00
Name: O_SN_99S	Len: 108	Check: 2342	Weight: 1.00
Name: U_CD_83C	Len: 108	Check: 4773	Weight: 1.00

00BW0762_1	...MEQVDPN	LEPWNHPGSQ	PKTPCNKCFC	KSCSYHCLVC	FQTKGLGISY	50
00BW0768_2	...MDPVDPN	LEPWNHPGSQ	PKTACNNCYC	KYCSYHCLVC	FQKKGLGISY	
00BW0874_2	...MEPVDPN	LEPWNHPGSQ	PKTACNSCYC	KHCCYHCRVC	FLTKGLGISY	
00BW1471_2	...MDPVDPK	LEPWNHPGSQ	PKTACNTCYC	KKCCYHCQVC	FLNKGLGISY	
00BW1616_2	...MEPIDPN	LEPWNHPGSQ	PSTACNKCVC	KQCCYHCPAC	FLTKGLGISY	
00BW1686_8	...MEPVDPK	LEPWNHPGSQ	PTTPCTTCFC	KVCSYHCLVC	FQTKGLGIYY	
00BW1759_3	...MEPIDPN	LEPWNHPGSQ	PKTACNKCVC	KSCSYHCLVC	FQKKGLGISY	
00BW1773_2	...MEPVDPN	LEPWNHPGSQ	PKTPCTKCVC	KLCSYHCLVC	FQTKGLSISY	

00BW1783_5	...MEPVDPN	LEPWNHPGSQ	PKTPCTKCYC	KKCSYHCLVC	FQTKGLGISY
00BW1795_6	...MEPVDPN	LEPWNHPGSQ	PKTPCNHCYC	KHCSYHCLVC	FQTKGLGISY
00BW1811_3	...MEPVDPN	LEPWKHPGSQ	PKTACNTCYC	KRCSYHCPVC	FLTKGLGISY
00BW1859_5	...MEPVDPN	LEPWNHPGSQ	PKTACNKCYC	KRCSYHCLVC	FQTKGLGISY
00BW1880_2	...MEPVDPN	LEPWNHPGSQ	PQTPCNKCYC	KRCSYHCLVC	FQTKGLGISY
00BW1921_1	...MEPIDPK	LEPWNHPGSQ	PNTPTCTPCYC	KKCSYHCLVC	FQTKGLGIYY
00BW2036_1	...MEPVDPK	LEPWNHPGSQ	PKTPCNKCYC	KKCSYHCLVC	FQTKGLGISY
00BW2063_6	...MEIVDPN	LDPWDHPGSQ	PSTPCNKCYC	KYCSYHCLVC	FQTKGLGISY
00BW2087_2	...MEPIDPN	LEPWNHPGSQ	PKTACNKCF	KRCCYHCPAC	FLTKGLGISY
00BW2127_2	...MEPVDPN	LEPWNHPGSQ	PKTACSPCYC	KNCSYHCLVC	FQTKGLGISY
00BW2276_7	...MEPVDPN	LEPWKHPGSQ	PKTACTSCYC	KRCSYHCLVC	FQTKGLGISY
00BW3819_3	...MEPVDPN	LEPWNHPGSQ	PKTACNQCYC	KHCCYHCLVC	FQTKGLGISY
00BW3842_8	...MEPVDPK	LEPWNHPGSQ	PRTPCNKCF	KVCSYHCQSC	FLTKGLGISY
00BW3871_3	...MDPVDPN	LEPWNHPGSQ	PKTPCNNCYC	KKCSYHCPVC	FQTKGLGIYY
00BW3876_9	...MELIDPK	LEPWNHPGSQ	PAAPCNNCYC	KHCSYHCLVC	FQTKGLGISY
00BW3886_8	...MEPIDPN	LEPWNHPGSQ	PKTPCNKCYC	KHCSYHCLVC	FQTKGLGISY
00BW3891_6	...MEPVDPN	LEPWNHPGSQ	PNTACNKCYC	KQCSYHCLVC	FQKKGLGISY
00BW3970_2	...MEPVDPN	LEPWNHPGSQ	PKTACNSCYC	KKCSYHCPVC	FLTKGLGIYY
00BW5031_1	...MEPVDPN	LEPWNHPGSQ	PKTPCNKCYC	KQCSYHCPVC	FLTKGLGIYY
96BW01B21	...MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KHCSYHCLVC	FQTKGLGIYY
96BW0407	...MEPIDPN	LEPWNHPGSQ	PKTACNKCYC	KHCSYHCLVC	FQTKGLGISY
96BW0502	...MEPVDPN	LEPWKHPGSQ	PRTACTKCYC	KYCCYHCLVC	FQTKGLGISY
96BW06_J4	...MEPVDPK	LEPWNHPGSQ	PKTPCNTCYC	KKCSYHCLVC	FQKKGLGIYY
96BW11_06	...MEQVDPN	LEPWNHPGSQ	PKTPCNNCYC	KYCSYHCLVC	FQTKGLGISY
96BW1210	...MEPVDPN	LEPWNHPGSQ	PKIACNKCYC	KACCYHCLVC	FQTKGLGISY
96BW15B03	...MEPVDPK	LEPWNHPGSQ	PKTPCTKCF	KGCSYHCLVC	FQTKGLGISY
96BW16_26	...MEPVDPK	LEPWNHPGSQ	PKTACNKCYC	KRCSYHCLVC	FQTKGLGISY
96BW17A09	...MDPVDPN	LEPWNHPGSQ	PKTACNTCYC	KKCCYHCQVC	FLNKGLGISY
96BWM01_5	...MEPVDPN	LEPWKHPGSQ	PETPCNKCYC	KSCSYHCLVC	FQKKGLGISY
96BWM03_2	...MEPVDPN	LEPWNHPGSQ	PKTACNNCCC	KRCSYHCLVC	FQKKGLGISY
98BWMC12_2	...MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KRCCYHCQRC	FLTKGLGISY
98BWMC13_4	...MEPVDPN	LEPWNHPGSQ	PKTSCNNCYC	KKCSYHCLVC	FQKKGLGISY
98BWMC14_a	...MDPVDPK	LEPWNHPGSQ	PSTPCNTCF	KKCSYHCLVC	FQKKGLGIYY
98BWM014_1	...MEPIDPN	LEPWNHPGSQ	PKTACNKCHC	KRCCYHCTVC	FLTKGLGISY
98BWM018_d	...MEPIDPN	LEPWNHPGSQ	PKTDCNKCYC	KRCCYHCLVC	FQKKGLGISH
98BWM036_a	...MEPVDPN	LEPWNHPGSQ	PRTACNTCYC	KKCSYHCLVC	FQKKGLGISY
98BWM037_d	...MEPVDPN	LEPWNHPGSQ	PKTACNKCYC	KHCSYHCLVC	FQTKGLGISY
99BW3932_1	...MEPVDPN	LEPWNHPGSQ	PKTACNKCYC	KSCSYHCPVC	FLSKGLGISY
99BW4642_4	...MEPVDPN	LEPWNHPGSQ	PKTPCTTCFC	KRCSYHCLVC	FQTKGLGIYY
99BW4745_8	...MEPVDPN	LEPWNHPGSQ	PSTACNKCYC	KHCSYHCLVC	FQTKGLAISY
99BW4754_7	...MEPVDPN	LEPWNHPGSQ	PETPCNKCF	KACSYHCLVC	FQKKGLGISY
99BWMC16_8	...MDPVDPN	LEPWNHPGSQ	PKTACNRCYC	KKCSYHCLVC	FHTKGLGISY
A2_CD_97	...MEPVDPN	LEPWNHPGSQ	PKTACNNCYC	KKCCYHCQRC	FLNKGLGISY
A2_CY_94	...MEPVDPK	LEPWNHPGSQ	PKTACTKCYC	KRCCYHCQLC	FINKGLGISY
A2D_97_9	...MDPVDPN	LEPWNHPGSQ	PRTACNKCYC	KRCCYHCPVC	FLNKGLGISY
A2G_CD_9	...MDPVDPN	LEPWNHPGSQ	PKTACNKCYC	KACCWHCQVC	FLNKGLGISY
A_BY_97_97	...XDPVDPN	LEPXNHXXSQ	PKTXCRNCYC	KKCCWHCQIC	FLKKGLGISY
A_KE_93_Q2	...MDPVDPN	LEPWNHPGSQ	PTTACNKCYC	KKCCYHCQVC	FLNKGLGISY
A_SE_93_SE	...MDPVDPN	LEPWNHPGSQ	PSTACNKCYC	KICCYHCPVC	FLNKGLGISY
A_SE_94_SE	...MDPVDPN	LEPWNHPGSQ	PTTPCSKCYC	KKCCYHCIVC	FQNKGLGISY
A_SE_94_SE	...MDPVDPN	LEPWNHPGSQ	PTTACNKCYC	KKCCYHCQAC	FLNKGLGISY
A_SE_95_SE	...MEPVDPN	LEPWNHPGSQ	PTTPCTKCYC	KKCCYHCPAC	FLNKGLGISY
A_SE_95_SE	...MDPVDPN	LEPWNHPGSQ	PATACSACYC	KKCCYHCPVC	FLNKGLGISY
A_SE_95_UG	...MDPVDPN	LEPWNHPGSQ	PTTPCNKYFC	KRCCYHCLVC	FQHKGLGISY
A_UG_85_U4	...MEPVDPN	LEPWKHPGSQ	PTTACSNCYC	KVCCWHCQLC	FLKKGLGISY
A_UG_92_92	...MDPVDPN	LEPWNHPGSQ	PKTPCNKCYC	KVCCYHCQCC	FLNKGLGISY
AC_IN_95_2	...MEPVDPN	LEPWNHPGSQ	PRTACNNCYC	KRCSYHCLVC	FQKKGLGISY
AC_RW_92_9	...MEPVDPK	LEPWNHPGSQ	PKTACNNCYC	KHCSYHCLVC	FQAKGLGISY
AC_SE_96_S	...MEPIDPN	LEPWNHPGSQ	PKTACNRCYC	KRCSYHCLVC	FQTKGLGISY
ACD_SE_95_	...MDLVDPN	LEPWNHPGSQ	PTTPCSKCYC	KKCCYHCQHC	FITKGLGISY

00453026 032203

[illegible]

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CRF03_AB_R    ...MEPVDP R LEPWKHPGSQ PKTACTNCCYK KKCCCLHCQVC FMKKGLGISY
CRF04_cpx_    ...MEPVDPD LEPWNHPGSQ PTTDCNKCFC KKCCWHCQVC FLKKGLGISY
CRF04_cpx_    MEAVDLVYPN LEPWNHPGSQ PTTACNKCFC KKCCWHCQAC FLKKGLGISY
CRF04_cpx_    ...MEPVDPN LEPWNHPGSQ PTTACTKCFC KVCCYHCQVC FLRKGLGISY
CRF05_DF_B    ...MDPVDPN LEPWNHPGSQ PRTACNQCYC KMCCYHCQNC FITKGLGISY
CRF05_DF_B    ...MDPVDPN LEPWNHPGSQ PRTACNQCHC KKCCYHCQVC FITKGLGISY
CRF06_cpx_    ...MEPVDPK IEPWNQPGSR PKTACTKCYC KKCCYHCPVC FLNKGLGISY
CRF06_cpx_    ...MEPVDPN IEPWNQPGSR PKTACTPCYC KKCCYHCQVC FLNKGLGISY
CRF06_cpx_    ...MEPVDPK IEPWNQPGSR PKTACTSCYC KRCCYHCPLC FLNKGLGISY
CRF06_cpx_    ...MEPVDPN IEPWNQPGSR PKTACTSCYC KQCCYHCPVC FLNKGLGISY
CRF11_cpx_    ...MEPVDPN IEPWNQPGSR PKTACNQCYC KRCCYHCQVC FLKKGLGIYY
CRF11_cpx_    ...MEPGDIN IDPWNQPGSQ PKTACNQCYC KRCCYHCQHC FLKKGLGISY
D_CD_83_EL    ...MDPVDPN LEPWNHPGSQ PRTPCNKCHC KKCCYHCPVC FLNKGLGISY
D_CD_83_ND    ...MDPVDPN LESWNHPGSQ PRTACNKCCHC KKCCYHCQVC FITKGLGISY
D_CD_84_84    ...MDPVDPN IDPWNHPGSQ PRTACNCCYC KKCCYHCQVC FITKGLGISY
D_UG_94_94    ...MEPVDPN LEPWNHPGSQ PRTPCNKCYC KRCCYHCYVC FVTKGLGISY
F1_BE_93_V    ...MEPVDPN LDPWNHPGSQ PTTPTCTRCYC KRCCFHCQWC FTTKGLGISY
F1_BR_93_9    ...MELVDPN LDPWNHPGSQ PTTPTCTRCYC KWCCFHCYWC FTTKGLGISY
F1_FI_93_F    ...MELVDPN LDPWNHPGSQ PTTPTCTRCYC KRCCFHCYWC FATKGLGISY
F1_FR_96_M    ...MELVDPN LDPWNHPGSQ PTTPTCTRCYC KWCCFHCYWC FATKGLGISY
F2_CM_95_M    ...MEVVDPN LDPWKHPGSQ PETPCNKCYC KKCCFHCQVC FTRKGLGISY
F2KU_BE_94    ...MEQVDPN LDPWNHPGSQ PKTACNCCYC KKCCFHCQVC FTTKGLGISY
G_BE_96_DR    ...MDPVDPK LEPWKHPGSQ PKTACNCCYC KS.VAALQVC FLNKGLGISY
G_NG_92_92    ...MDPVDPK LEPWNHPGSQ PTTPTCTRCYC KVCCWHCQVC FLNKGLGISY
G_SE_93_SE    ...MDPVDPN LEPWNHPGSQ PKTACNKCFC KVCCWHCQVC FLNKGLGISY
H_BE_VI9      ...MDPVDPN QEPWNHPGSQ PRTACNCCYC KKCCYHCQVC FLKKGLGIYY
H_BE_VI9      ...MDPVDPN QEPWNHPGNQ PKTACNCCYC KQCSFHCQVC FLKKGLGISY
H_CF_90_90    ...MDPVDPK LEPWNHPGSQ PRTACNCCYC KKCCYHCQMC FLKKGLGISY
J_SE_93_SE    ...MEPVDPN REPWNHPGSQ PKTACTNCCYC KKCCYHCQVC FLQKGLGISY
J_SE_94_SE    ...MEPVDPN REPWNHPGSQ PKTACTNCCYC KKCCYHCQVC FLQKGLGISY
K_CD_97_EQ    ...MEPVDPN IEPWNQPGSQ PKTACNQCYC KKCCYHCQVC FLQKGLGICY
K_CM_96_MP    ...MDPVDPN IEPWNQPGSQ PKTACNQCYC KRCCYHCQVC FLKKGLGISN
N_CM_95_YB    ...MEPVDPK LEPWNHPGSQ PKTACNCCYC KRCCYHCLYC FTKKGLGISY
O_CM_ANT      ...MDPVDPK VPPWHHPGSQ PQIPCNCCYC KRCCYHCYVC FVRKGLGISY
O_CM_91_MV    ...MDPVDPK MPPWHHPGSQ PQTPCNCCYC KRCCYHCYVC FTKKGLGISH
O_SN_99S      ...MDPVDPK MPPWHHPGSQ PQTPCNCCYC KACCYHCYVC FASKGLGISY
O_SN_99S      ...MDPVDPK MPPWHHPGSQ PQTPCNCCYC KACCYHCYVC FASKGLGLSY
U_CD_83C      ...MDPVDPK LEPWNHPGSQ PKTACNCCYC KRCCLHCQVC FMTKGLGISY

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51

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00BW0762_1    GRKKRRQRR. .HAPPGSKDH QNPISKQPLP .QTRGDPTGS BESKKKVESK
00BW0768_2    GRKKRGQRR. .NAPPSSEDH QDLISKQPLS .QTRGDPTGS BESKKKAESK
00BW0874_2    GRKKRRQRR. .SAPPSGEDH QSSLPKQPLP .QARGNPTGS BESKKKVESK
00BW1471_2    GRKKRRQRR. .SAPPSKDH QDPLSKQPLS .QTRGDPTGS KESKKKVESK
00BW1616_2    GRKKRRQRR. .STPPSSKDH QNPVSKQPLP .RTQGNSTGS BESKKKVESK
00BW1686_8    GRKKRRQRR. .SAPPSNKEH QDPIPKQPLP .RTPGDPTGP BESKKKVESK
00BW1759_3    GRKKRRQRR. .SGPPSNKDH QNLVSKQPLS .QTQRDPTGS BESKKKVESK
00BW1773_2    GRKKRRQRR. .STPPSSSEDH QDLISKQPLP .RTQGDPTGS BESKKKVESK
00BW1783_5    GRKKRRQRR. .SGPPSSSEDH QNPISKQPLS .QTRGDPTGS KESKKKVESK
00BW1795_6    GRKKRRRRR. .SAPPSSEDH QNPISKQPLS .QTRGDPTGS BESKKKVESK
00BW1811_3    GRKKRRQRR. .RAPPSSEDH QNPISKQPLS .RTQGDPTGS BESKKKVESK
00BW1859_5    GRKKRGQRR. .SAPSSSEDH QDNISKQPLP .RTQGDPTGS BESKKKVESK
00BW1880_2    GRKKRRQRR. .SAPPSSEDH QNPISKQPLP .QTRGDSTGS BESKKKVESK
00BW1921_1    GRKKRRQRR. .SAPPSKDH QNPLSKQPLP .RTPGNSTGS BESKKKVESK
00BW2036_1    GRKKRGQRR. .STPPSNKAH QNLISKQPLP .RTQGDSTGS BESKKKVESK
00BW2063_6    GRKKWRQRRG RSAPSSSKDH QDLISKQPLP .QTRGDPTSS KESKKKVESK
00BW2087_2    GRKKRRQRR. .SAPPSSEDH QNPISKQPLP .QTRGNPTGS BESKKKVESK
00BW2127_2    GRKKRRQRR. .SAPPSSEDH QDPIKQPLP .QTRGDPTGS BEPKKKVESK
00BW2276_7    GRKKRRQRR. .SAPPSSEDH QNHISKQPLP .QTRGDQDTS BESKKKVESK
00BW3819_3    GRKKRRQRR. .RSPQSSEAH QDPIKQPLP .QARGDPTGS BESKKKVESK

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100

00BW3842_8	GRKKRGQRR.	.SAPSSSEDH	QNPIPKQPLP	.RTQGNSTGS	EESKKKVESK
00BW3871_3	GRKKRRQRR.	.SAPPSNKDH	QNPISKQPLP	.RTQGNSTGS	EESKKKVESK
00BW3876_9	GRKKRRQRR.	.STPPRSEDH	QNLILKQPLP	.RTQGNPTGP	EESKKKVESK
00BW3886_8	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTPGNSTGS	EESKKKVSGK
00BW3891_6	GRKKRRQRR.	.SAPPSSEDH	QNPISKQPLS	.QTRGDSTGS	EESKKKVESK
00BW3970_2	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.QTRGNQSTGS	EESKKKVESK
00BW5031_1	GRKKRRQRR.	.SAPSSSENH	QNPVSKQPLP	.QARGNSTGS	EESKKKVESK
96BW01B21	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
96BW0407	GRKKRRQRR.	.STPPSEDH	QNPVSKQPLS	.QTRGDPTGS	EESKKKVESK
96BW0502	GRKKRRQRR.	.STPPSSESH	QNLISEQPLP	.RTQGNPTGS	EESKKKVESK
96BW06_J4	GRKKRRQRR.	.SAPSSSEDH	QDPISKQPPF	.RTQGESTGS	EESKKEVESK
96BW11_06	GRKKRRQRR.	.SAPPSKDH	QNPVSKQPLP	.QTRGDPTGS	KESKRKVENK
96BW1210	GRKKRRQRR.	.SAPPSSEDH	QDLVPKQPLS	.QARGNPTSS	KESKKKVESK
96BW15B03	GRKKRGQRR.	.SAPPRSEDH	QNLISKQPLP	.RTQGDSTGS	EESKKKVESK
96BW16_26	GRKKRRQRR.	.SAPPSSEDH	QNPISKQPLP	.QTQGDPTGS	EESKKKVESK
96BW17A09	GRKKRRQRR.	.SAPPSNGDH	QNPISKQPLP	.QTRGDPTGS	KESKKEVESK
96BWM01_5	GRKKRRQRR.	.SAPPSSEDH	QDLVSKQPLP	.QTRGDPTGS	KESKKKVESK
96BWM03_2	GRKKRGQRR.	.SAPPSKDH	QNPVSKQPLP	.QTRGNSTGS	EESKKKVESK
98BWMC12_2	GRKKRRQRR.	.SAPPSCKDH	QNPLPEQPST	.QTRGDSTGS	EESKKKVESK
98BWMC13_4	GRKKRRQRR.	.SAPASSEDH	QDLISKQLLP	.QTRGDPTGS	KESKKKVESK
98BWMC14_a	GRKKRRQRR.	.STPPSSKDH	QNPVSKQPTS	.RTQGDWTGS	IESEKKVESK
98BWM014_1	GRKKRRRRR.	.KAPPSSEDH	QNLVSKQPLP	.QSRGNPTGS	EESKKKVESK
98BWM018_d	GRKKRRQRR.	.SAPPSKDH	QNPIPKQPLP	.QTRGDQSTGS	EESKKKVESK
98BWM036_a	GRKKRSQRR.	.STPPSEDH	QDPISKQPLP	.QPRGIPSTGS	EESKKKVESK
98BWM037_d	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLS	.QTRGDPTGP	EESKKKVESK
99BW3932_1	GRKKRRPRR.	.SAPPSNKDH	QDLVSKQPLP	.QTRGDPTGS	EESKKKVESK
99BW4642_4	GRKKRCQRRR.	.STPSSSKDH	QDLVPKQPLP	.RTQGNSTGS	EESKKKVESK
99BW4745_8	GRKKRRQRR.	.SAPPSSEDH	QNLVSKQPLP	.QAQGDPTGS	EESKKKVESK
99BW4754_7	GRKKRRQRR.	.SAPPSSTDH	QTPISKQPLP	.QTRGDQSTGS	EESKKKVESK
99BWMC16_8	GRKKRRQRR.	.SAPPSSEDH	QNPISKQPLP	.RTQGDSTGS	EESKKKVESK
A2_CD_97	GRKKRRPRR.	.GPDQGNTH	QNPVPKQSLP	.QTQRDSTGP	EESKKKVESK
A2_CY_94	GRKKRRPRR.	.KPSPSNKDH	QNPIPKQSLP	.QAQRVPTGP	EESKKEVESK
A2D_97_9	GRKKRRPRR.	.RPPQGGTGH	QNPIPEQSLP	.RPQRIPTGT	EESKTEVESK
A2G_CD_9	GRKKRKHRR.	.GAPPGSKDH	QNPIPKQPLP	TTRG.NPTGP	KESKKEVASK
A_BY_97_97	GRKKRRHRR.	.GTSHSSKDH	XIPISKQPLP	HTQK.DQTGX	EESKKKXESK
A_KE_93_Q2	GRKKRRQRR.	.GAPQSSKDH	QNSIQKQPIP	QTQG.VSTGP	KESKKKMESK
A_SE_93_SE	GRKKRTRRR.	.GAPQSNKDH	QNPISKQPIP	QTQG.DSTGP	EESKKKVESK
A_SE_94_SE	GRKKRRQRR.	.RTPQSSKDH	QNPIPKQPIP	QTQC.VSTGP	EESKKKVESK
A_SE_94_SE	GRKKRKQRR.	.GAPQSNKDH	QNPQQQSIP	QTQG.IPTGP	EESKKKVESK
A_SE_95_SE	GRKKRKQRR.	.GTPQGNKDH	QNPIPKQSTP	QTQG.ISTGP	EESKKKVESK
A_SE_95_SE	GRKKRRQRR.	.RTPQSSKDH	QNPVPKQSIP	QAQG.DSTGP	EESKKKVESK
A_SE_95_UG	GRKKRRQRR.	.GTPQSSKDH	QDPIPKQSIP	PAQG.IPTGP	EESKKKVESK
A_UG_85_U4	GKKRKPRR.	.GPPQGSKDH	QTLIPKQPLP	QSQR.VSAGQ	EESKKKVESK
A_UG_92_92	GRKKRKPRR.	.GTPQSNKDH	QNPIPKQPIP	RTQG.DSTGP	EESKKKVESK
AC_IN_95_2	GRKKWRQRR.	.RAPPSEDH	QNLISKQPIP	.QTQGDSTGP	EESKKKMESK
AC_RW_92_9	GRKKRRQRR.	.NAPPSEDH	QNPISKQPLS	.QTRGDPTGS	EESKKKVESK
AC_SE_96_S	GRKKRRQRR.	.SAPPSKDH	QNPISKQSIP	.QTQGDPTGP	EESKKKVESK
ACD_SE_95	GRKKRRQRR.	.GPPQSNKDH	QNPVQKQPIP	QTQR.ESTGP	EESKKKVESK
ACG_BE_V	GRKKRSQRR.	.RAPPSEDR	QNLISKQPLS	.QTRGDPTGP	EESKKEVESK
AD_SE_93_S	GRKKRRQRR.	.XTPEGGAH	QDPIPKQPS	QPRGD.PTGP	KEKKK.VASK
AD_SE_95_S	GRKKRKQRR.	.GAPPSKDH	QNPIPKQPIP	QTQG.ISTGP	KESKKEVESK
ADHK_NO_97	GRKKRRPRR.	.RPPKSSQDH	QDFIPKQPLS	.RTHGEPTGP	KEKKK.VASK
ADK_CD_85	GRKKRRQRR.	.RPPQGNQAH	QDPLPEQPS	QHRGDHPTGP	KEKKK.VESK
AG_BE_VI	GRKNRKHRR.	.GTPQGSKDH	QNPVPKQSLP	LIRG.IPTGP	EESKKEVASK
AG_NG_92_9	GRKKRRRRR.	.GTPQSHQDH	QNPVPKQPLP	TTRG.NPTGP	KESKKEVESK
AGHU_GA	GRKKRSQRR.	.RAPKSSPDH	QNLVPKQPPS	.RTNGNPTGP	KEKKK.VASK
AGU_CD_76	GRKKRRQRR.	.GTPQDRKDH	QNPVPRQPLP	TTRG.NPTGP	KESKKEVESK
AJ_BW_98_B	GRKKRRQRR.	.TAPPGNKNH	QDLVQEPLS	.QTQRKSTGP	EESKKEVESK
B_AU_VH	GRKKRRQRR.	.RAPEDSQTH	QVSLSKQAP	QPRGD.PTGP	KESKKKVESK
B_CN_RL4	GRKKRRQRR.	.RAPQDSQTH	QASLSKQPAS	QPRGD.PAGP	KESKKKVESE

B_DE_86_D3	GRKKRRQRR.	.RAPEDSQTH	QVSLSKQPAS	QPRGD . PTGP	KESKKKVETE
B_DE_86_HA	GRKKRRQRR.	.RAPQDSQTH	QVSLPKQPSS	QQRGD . PDSP	KKSKKKVERE
B_FR_83_HX	GRKKRRQRR.	.RAHQNSQTH	QASLSKQPTS	QPRGD . PTGP	KE . KKKVERE
B_GA_OYI	GRKKRRQRR.	.RAPQDSKTH	QVSLSKQPAS	QPRGD . PTGP	KESKKKVETE
B_GB_CAM	GRKKRRQRR.	.RTPQSSKTH	QASLSKQPAS	QFQGD . PTGP	KESKKKVEGE
B_GB_GB8	GRKKRRQRR.	.RLPEDSQIH	QVSLPKQPTS	QPQGD . PTGP	KESKKKVESK
B_GB_59_MA	GRKKRRQRR.	.RAPPDSQTR	QVSLSKQPTS	QPRGD . PTGP	EESKKKVETE
B_KR_WK	GRKKRRQRR.	.RAPQDNKNH	QVSLSKQPTS	RARGD . PTGQ	EESKEKVEKE
B_NL_86_32	GRKKRRQRR.	.RSPQDSETH	QVSLSKQPAS	QPRGD . PTGP	KESKKKVETE
B_TW_TWC	GRKKRRQRR.	.RTPQNSQTH	QADLSKQPTS	QPRGD . QTGQ	KESTKKVERE
B_US_DH1	GRKKRRQRR.	.RSPQHSQTD	QASLSKQPAS	QPRGD . PTGP	KESKKKVETE
B_US_P89	GRKKRRQRR.	.RPPQDSQTH	QVSLSKQPSS	QPRGD . PTGP	KEQKKKVETE
B_US_83_RF	GRKKRRQRR.	.GPPQGSQTH	QVSLSKQPTS	QPRGD . PTGP	KESKEKVERE
B_US_83_SF	GRKKRRQRR.	.RAPQDSQTH	QASLSKQPAS	QSRGD . PTGP	TESKKKVETE
B_US_84_MN	GRKKRRQRR.	.RAPEDSQTH	QVSLPKQPAP	QPRGD . PTGP	KESKKKVETE
B_US_86_JR	GRKKRRQRR.	.RPPQDSQTH	QVSLPKQPSS	QQRGD . PTGP	KESKKKVETE
B_US_86_YU	GRKKRRQRR.	.RPPQDSQTH	QSSLSKQPTS	QLRGD . PTGP	TESKKKVETE
B_US_87_BC	GRKKRRQRR.	.RAPQDSQTH	QASLSKQPTS	QPRGD . PTGP	KESKKKVETE
B_US_88_WR	GRKKRRQRR.	.RAPPEGLTH	QVPLSKQPSS	QFRGD . PTGP	KESKKKVETE
B_US_90_WE	GRKKRRQRR.	.RSPQNSQTH	QDLSKQPTS	QPRGD . PTGP	KESKKKVETE
BF1_BR_93	GRKKRRQRR.	.RTPQSSQLH	QDPVPKQPAS	QAQGN . PTGP	KESKKEVESQ
C_BR_92_92	GRKKRRQRR.	.SAPPSSEDH	QNPPIKQPLP	.QTRGDQTGS	EESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSEDH	QNPVSKQPLP	.QTRGDPTGL	EESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSKDH	QNPVSKQPLP	.QTRGDPTGS	KESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSEDH	QDLVPKQPLS	.QARGNPTSS	KESKKKVESK
C_BW_96_96	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTQGDSTGS	EESKKKVESK
C_ET_86_ET	GRKKRRQRR.	.RAPQSSKDH	QNLISKQPLS	.HTRGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.RAPQSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_93_93	GRKKRRQRR.	.SAPPSSEDH	QNLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_94_94	GRKKRRQRR.	.SAPPSSEDH	QDLISKQPLP	.RTQGDPTGS	EESKKKVESK
C_IN_95_95	GRKKRRQRR.	.SAPPSSEDH	QNPISKQPLP	.RTPGDPTGS	EESKKKVESK
CRF01_AE_C	GRKKRRKHRR.	.GPPPGSKDH	QNPPIKQPLP	TTRG . NPTGP	KESKKEVASK
CRF01_AE_C	GRKKRRKHRR.	.GPSQDSKDH	QNSIPKQPLP	TSRG . NPTGP	KESKKEVASK
CRF01_AE_C	GRKKRRKHRR.	.GTPQGSKGH	QDPISKQPLP	IIRG . NPTGP	KESKKEVASK
CRF01_AE_T	GRKKRRKHRR.	.GTPQSSKDH	QNPPIKQPLP	IIRR . NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRRKHRR.	.GTPQSRKDH	QHPIPEQPLS	IIRG . NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRRKHRR.	.GTPQSSKDH	QSPIPEQPLP	IIRG . NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRRKHRR.	.GTPQSRKDH	QYPIPEQPLP	IIRG . NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRRKHRR.	.GTPQSSKDH	QTPIRKQPPS	IIRG . NPTDP	KESKKEVASK
CRF01_AE_T	GRKKRRKHRR.	.RTPQSSKDH	QYPIPEQPPS	IIRG . IPTDP	KESKKEVASK
CRF02_AG_F	GRKKRRRRR.	.GTPQSRQDH	QNPVPKQPLP	TTRG . DPTDP	KESKKEVASK
CRF02_AG_F	GRKKRRRRR.	.GTPQSRQDR	QNPVSKQPLP	TTRG . NPTGP	KESKKEVASK
CRF02_AG_G	GRKKRRRRR.	.GTPQSHQDH	QNPVSKQSLP	QTRG . DPTGP	KESKKEVASK
CRF02_AG_N	GRKKRRRRR.	.GTPQSRQDH	QNPVPKQPLP	TTRG . NPTDP	KESKKEVASK
CRF02_AG_S	GRKKRRRRR.	.GTPQSRQDN	QDPVPKQPLP	TTRG . NPAGP	KESKKEVASK
CRF02_AG_S	GRKKRRRRR.	.GTPQSRQDH	QNPVPKQPLP	TTRG . EQTGP	KESKKEVASK
CRF03_AB_R	GRKKRRQRR.	.RAPQDNQTD	QVSLPKQPAS	QPRGD . PTGP	KE . KKKMERE
CRF03_AB_R	GRKKRRQRR.	.RPPQDNQTD	QVSLPKQPAS	QPRGD . PTGP	KE . KKKVERE
CRF04_cpx_	GRKKRRKHRR.	.GSLQGSKGH	QNLIPKQPLS	QQPNGDSTGP	EEQKKKVASK
CRF04_cpx_	GRKKRRKRNE.	.DLLGFSRDR	QNPPIKQPLS	Q . PNGNPEGP	KEQKKKVASK
CRF04_cpx_	GRKKRRKHRR.	.RPPQGSRDR	QNPPIKQPLS	QQHSGDPTGP	KEQKEAVASK
CRF05_DF_B	GRKKRRPRR.	.RPPQGSQAH	QDPVEQPPS	QPRGD . PTGP	KKQKKEVESK
CRF05_DF_B	GRKKRRSRR.	.RPPQGGQAH	QIPVEQPPS	QARGD . PTGQ	KEQKKKVASK
CRF06_cpx_	GRKKRRQRR.	.QAPPQSKNH	QDPVSKQPLS	.QTQREQTGP	EKSKEVESK
CRF06_cpx_	GRKKRRQRR.	.TAPPQSKNH	QDPVPKQPLS	.QTQRGPTGP	EKSKEVESK
CRF06_cpx_	GRKKRRQRR.	.TAPPQSKNH	QDPVPKQPLS	.QTQRKSTGP	EESKKEVESK
CRF06_cpx_	GRKKRRQRR.	.TAPLGSKSH	QDPVPKQPLS	.QTQRESTGP	EKSKEVESK
CRF11_cpx_	GRKKRRQRR.	.AASHSENH	QDPIPKQPST	.QPNRKPTGP	EESKKEVESK
CRF11_cpx_	GRKKWRQRR.	.TASRSSKNH	QDPIPEQPLP	.QASRNPTGP	EKPKEVESK

D_CD_83_EL	GRKKRRQRR.	.GPPQGGQAH	QVPIPKQPSS	QPRGD.	PTGP	KEQKKKVESE
D_CD_83_ND	GRKKRRQRR.	.KPPQGDQAH	QVPIPEQPSS	QSRGD.	PTGP	K.KKKKVESE
D_CD_84_84	GRKKRRQRR.	.RPPHSSQTH	QDPIPKQPSS	QPRGD.	PTGQ	KEKKK.VESK
D_UG_94_94	GRKKRRPRR.	.RTPPGGQAN	QDPVPKQPSS	QPRGN.	PTGP	KEKKK.VESE
F1_BE_93_V	GRKKRRQRH.	.RTPQSSQVH	QNSLPKQPLS	QARGD.	PTGP	KESKKEVESK
F1_BR_93_9	GRKKRRQRP.	.RTPQSSQIH	QDFVPKQPLS	QARGN.	PTGP	KESKKEVESK
F1_FI_93_F	GRKKRRQRH.	.RTPQSSQIH	QDPVPKQPLS	QPRRN.	PTGP	KESKKEVESK
F1_FR_96_M	GRKKRRQRR.	.RTPQSSQSH	KNPIPEQPLS	QARGD.	PTGP	KESKKEVESK
F2_CM_95_M	GRKKRRQRR.	.RTPQSGEVH	QDPVSKQPLS	QTRGD.	PKGP	EESKKKVESK
F2KU_BE_94	GRKKRRQRR.	.RTPQSSQAH	QNPISKQPLS	QARGD.	PTGP	KEPKKEVESK
G_BE_96_DR	GRKKRKHRR.	.GTPHSSKDH	QTPVPKQPLS	TTRG.	NPTGP	QESKKEVESK
G_NG_92_92	GRKKRRPRR.	.GTPQSGSKH	QNPVPKQPLP	ITSG.	NPTGS	EKPKKEVASK
G_SE_93_SE	GRKKRKHRR.	.GTPQSSKSH	QDPVPKQPLP	TTRG.	NPTGP	KESKKEVASK
H_BE_VI9	GRKKRRQRR.	.GTPKSLQDH	QTLIPKQPLS	.RTSGDPTGP		EKKKK.VASK
H_BE_VI9	GRKKRSRRR.	.ATPASVQDH	QNHIPKQPLS	.RTRGDPTGP		KEKKK.VASK
H_CF_90_90	GRKKRSQRH.	.RTPASLQDH	QNSISKQPLS	.RTHGDPTGP		KEQKKEVASK
J_SE_93_SE	GRKKRRQRR.	.SAPPGSKTH	QDLIPKQPLS	.QTQRKPTGP		EESKKEVESK
J_SE_94_SE	GRKKRRQRR.	.SAPPGSKNH	QDLIPEQPLF	.QTQRKPTGP		EESKKEVESK
K_CD_97_EQ	GREKRRQRT.	.TTPYASKNH	KDPIPKQPLP	.QARGDPTGP		KESKKEVESK
K_CM_96_MP	GRKKRRPRR.	.RTPYNSSENH	QDPLRKQPLS	.QPRGEQTD		KESKKEVESK
N_CM_95_YB	GRKKRSQRR.	.RTPQSSKSH	QDLIPEQPLS	.QQQGDQTD		KKQKEALESK
O_CM_ANT	GRKK...RGR	PAAAS.HPDH	KDPVPKQSPT	ITK.RKQERQ		EEQEEVEKK
O_CM_91_MV	GRKK...RRR	PAAAASYPDN	KDPVPEQSLS	HTG.RKQKRQ		EEQEKKEVEKE
O_SN_99S	GRKK...RRR	PAAAAARHPDN	QDIVPEQLTY	ITN.RKQKRQ		EEQEKEVENE
O_SN_99S	GRKK...RRR	PAAAAARNPDN	QDIVPEQPPP	ITNNRKHKRQ		EEQEKEVEKE
U_CD_83C	GRKKRGKRR.	.RTPQSGPNH	QNIIVSKQPSS	QPRGD.	PTGQ	EEPKKKVEKK

	101	108
00BW0762_1	TETDPFD.	
00BW0768_2	TKTDQFD.	
00BW0874_2	TKTDQFD.	
00BW1471_2	TEADPCD.	
00BW1616_2	TETDPFD.	
00BW1686_8	TKTDPFDD.	
00BW1759_3	TETDRFD.	
00BW1773_2	TETDPD..	
00BW1783_5	TETDPFD.	
00BW1795_6	TETDPFD.	
00BW1811_3	TETDPD..	
00BW1859_5	TETDPYD.	
00BW1880_2	TETNPFDD.	
00BW1921_1	TEADQFD.	
00BW2036_1	TEADRFDD.	
00BW2063_6	TETDPFD.	
00BW2087_2	TERDPFD.	
00BW2127_2	TTTDPFD.	
00BW2276_7	TETDPYD.	
00BW3819_3	TKTDPFDD.	
00BW3842_8	TETDRFD.	
00BW3871_3	TKTDQFD.	
00BW3876_9	TKADPFDD.	
00BW3886_8	AETDQFDY	
00BW3891_6	TETDPFA.	
00BW3970_2	TERDPFA.	
00BW5031_1	TETDPFDW	
96BW01B21	TKTDPFDD.	
96BW0407	TEADPFDD.	
96BW0502	TEADPFA.	
96BW06_J4	TETDQFD.	
96BW11_06	TETDQFD.	

96BW1210 TETDPFD.
 96BW15B03 TETDRFD.
 96BW16_26 TETDPCD.
 96BW17A09 TEADPFDD.
 96BWM01_5 TKTDQFD.
 96BWM03_2 TETDPFD.
 98BWM012_2 TKAHPFD.
 98BWM013_4 TETDQFD.
 98BWM014_a TDTQFA.
 98BWM014_1 TETDPCA.
 98BWM018_d TETDQFD.
 98BWM036_a TETDPFD.
 98BWM037_d TETDPFD.
 99BW3932_1 TETDPFD.
 99BW4642_4 TETDQFA.
 99BW4745_8 TEPDPCD.
 99BW4754_7 TETDPFD.
 99BWM016_8 TEADRFDD.
 A2_CD_97 AETDRFD.
 A2_CY_94 AETDRFD.
 A2D_97_9 AETDPCD.
 A2G_CD_9 TETDPD..
 A_BY_97_97 AETDQFD.
 A_KE_93_Q2 AEADRFDD.
 A_SE_93_SE AETDRFD.
 A_SE_94_SE AEADRFDD.
 A_SE_94_SE AETDRFD.
 A_SE_95_SE TEADRFDD.
 A_SE_95_SE TETDRFA.
 A_SE_95_UG AETDRFA.
 A_UG_85_U4 AKTDRFA.
 A_UG_92_92 TEADRYA.
 AC_IN_95_2 AKTDRFD.
 AC_RW_92_9 TEADPFDD.
 AC_SE_96_S TETDRFD.
 ACD_SE_95_ AETDRFD.
 ACG_BE_V TETHPLA.
 AD_SE_93_S AEADQFDW
 AD_SE_95_S TEPDRFD.
 ADHK_NO_97 TXTDPFDDW
 ADK_CD_85_ AEADQFDW
 AG_BE_VI TETHPGD.
 AG_NG_92_9 TETDQCA.
 AGHU_GA_ AEADPFDDW
 AGU_CD_76_ TETDPFAW
 AJ_BW_98_B AKPDRFD.
 B_AU_VH_ TETNPSD.
 B_CN_RL4 TETDPRD.
 B_DE_86_D3 TETDPID.
 B_DE_86_HA TEADPFDD.
 B_FR_83_HX TETDPFD.
 B_GA_OYI TETDPED.
 B_GB_CAM TETHPGD.
 B_GB_GB8 TETDPSDW
 B_GB_59_MA TETDPVA.
 B_KR_WK_ TVVDPVT.
 B_NL_86_32 TETDPVD.
 B_TW_TWC TETDPNDQ
 B_US_DH1 TETDPVH.
 B_US_P89 TETDPVH.

B_US_83_RF	TETDPAVQ
B_US_83_SF	TETDPFD.
B_US_84_MN	TETHPVD.
B_US_86_JR	TETDPDN.
B_US_86_YU	TETDPVH.
B_US_87_BC	TETDPVD.
B_US_88_WR	TETDPIA.
B_US_90_WE	TETDPED.
BF1_BR_93	AKTDPD..
C_BR_92_92	TETDPFD.
C_BW_96_96	TETDPFD.
C_BW_96_96	TETDQFD.
C_BW_96_96	TETDPFD.
C_BW_96_96	TETDRFD.
C_ET_86_ET	AETDPYA.
C_IN_93_93	TKTDPFD.
C_IN_93_93	AKTDPFA.
C_IN_93_93	TKTDPFA.
C_IN_94_94	TTSDPFD.
C_IN_95_95	TKTDPFD.
CRF01_AE_C	AKTDPFA.
CRF01_AE_C	AETDPDW.
CRF01_AE_C	TKTDPCA.
CRF01_AE_T	AETDQCD.
CRF01_AE_T	AETDPCD.
CRF01_AE_T	AETDPCD.
CRF01_AE_T	AETDPCD.
CRF01_AE_T	AETDPD..
CRF01_AE_T	AETDQCD.
CRF02_AG_F	TETDQGD.
CRF02_AG_F	TKTDPCD.
CRF02_AG_G	TETDPFA.
CRF02_AG_N	TKTDPCD.
CRF02_AG_S	TETDPCD.
CRF02_AG_S	TETGPCD.
CRF03_AB_R	TETHPFD.
CRF03_AB_R	TETHPFD.
CRF04_cpx	TEADPFA.
CRF04_cpx	TEADPFD.
CRF04_cpx	TESNPFD.
CRF05_DF_B	TEADQFDW
CRF05_DF_B	AETDPFDC
CRF06_cpx	AEPDRFD.
CRF06_cpx	AEPDRFD.
CRF06_cpx	AETDRFD.
CRF06_cpx	TEPDRFD.
CRF11_cpx	AEPDRFD.
CRF11_cpx	AEPAPFD.
D_CD_83_EL	AETDPDC.
D_CD_83_ND	AETDPFDW
D_CD_84_84	TEVHPFDW
D_UG_94_94	TEADPFDW
F1_BE_93_V	AKTDPCA.
F1_BR_93_9	AKTDPD..
F1_FI_93_F	AKTDPCD.
F1_FR_96_M	TETDPFD.
F2_CM_95_M	TKTDPSD.
F2KU_BE_94	TETDPLD.
G_BE_96_DR	TETDPFD.
G_NG_92_92	TETDPLD.

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G_SE_93_SE	AEADQCD.
H_BE__VI9	TETDPFDW
H_BE__VI9	TEADPCD.
H_CF_90_90	TETDPD..
J_SE_93_SE	AEPDRFD.
J_SE_94_SE	AEPDRFD.
K_CD_97_EQ	TKTDPD..
K_CM_96_MP	TKTDQFD.
N_CM_95_YB	TEADPCD.
O_CM__ANT	AGPGGYPR
O_CM_91_MV	TGPGSQPC
O_SN__99S	ACP.RYPG
O_SN__99S	TGSDRYPR
U_CD__83C	TTTDPFD.

Table 17. HIV Vif Sequence Alignment
 GCG Multiple Sequence File.
 Written by Omega 1.1

Name: 00BW0762_1	Len: 194	Check: 4675	Weight: 1.00
Name: 00BW0768_2	Len: 194	Check: 4961	Weight: 1.00
Name: 00BW0874_2	Len: 194	Check: 3755	Weight: 1.00
Name: 00BW1471_2	Len: 194	Check: 3843	Weight: 1.00
Name: 00BW1616_2	Len: 194	Check: 4613	Weight: 1.00
Name: 00BW1686_8	Len: 194	Check: 4096	Weight: 1.00
Name: 00BW1759_3	Len: 194	Check: 3523	Weight: 1.00
Name: 00BW1773_2	Len: 194	Check: 4446	Weight: 1.00
Name: 00BW1783_5	Len: 194	Check: 3151	Weight: 1.00
Name: 00BW1795_6	Len: 194	Check: 4892	Weight: 1.00
Name: 00BW1811_3	Len: 194	Check: 3877	Weight: 1.00
Name: 00BW1859_5	Len: 194	Check: 3290	Weight: 1.00
Name: 00BW1880_2	Len: 194	Check: 2555	Weight: 1.00
Name: 00BW1921_1	Len: 194	Check: 4284	Weight: 1.00
Name: 00BW2036_1	Len: 194	Check: 4019	Weight: 1.00
Name: 00BW2063_6	Len: 194	Check: 4165	Weight: 1.00
Name: 00BW2087_2	Len: 194	Check: 5068	Weight: 1.00
Name: 00BW2127_2	Len: 194	Check: 5231	Weight: 1.00
Name: 00BW2128_3	Len: 194	Check: 5469	Weight: 1.00
Name: 00BW2276_7	Len: 194	Check: 5547	Weight: 1.00
Name: 00BW3819_3	Len: 194	Check: 1251	Weight: 1.00
Name: 00BW3842_8	Len: 194	Check: 4197	Weight: 1.00
Name: 00BW3871_3	Len: 194	Check: 3487	Weight: 1.00
Name: 00BW3876_9	Len: 194	Check: 4432	Weight: 1.00
Name: 00BW3886_8	Len: 194	Check: 5175	Weight: 1.00
Name: 00BW3891_6	Len: 194	Check: 3845	Weight: 1.00
Name: 00BW3970_2	Len: 194	Check: 2268	Weight: 1.00
Name: 00BW5031_1	Len: 194	Check: 3711	Weight: 1.00
Name: 96BW01B21	Len: 194	Check: 4602	Weight: 1.00
Name: 96BW0407	Len: 194	Check: 5108	Weight: 1.00
Name: 96BW0502	Len: 194	Check: 4385	Weight: 1.00
Name: 96BW06_J4	Len: 194	Check: 5371	Weight: 1.00
Name: 96BW11_06	Len: 194	Check: 6037	Weight: 1.00
Name: 96BW1210	Len: 194	Check: 4343	Weight: 1.00
Name: 96BW15B03	Len: 194	Check: 5690	Weight: 1.00
Name: 96BW16_26	Len: 194	Check: 4471	Weight: 1.00
Name: 96BW17A09	Len: 194	Check: 3907	Weight: 1.00
Name: 96BWM01_5	Len: 194	Check: 5608	Weight: 1.00
Name: 96BWM03_2	Len: 194	Check: 3079	Weight: 1.00
Name: 98BWMC12_2	Len: 194	Check: 5336	Weight: 1.00
Name: 98BWMC13_4	Len: 194	Check: 5304	Weight: 1.00
Name: 98BWMC14_a	Len: 194	Check: 3984	Weight: 1.00
Name: 98BWM014_1	Len: 194	Check: 2480	Weight: 1.00
Name: 98BWM018_d	Len: 194	Check: 2801	Weight: 1.00
Name: 98BWM036_a	Len: 194	Check: 3762	Weight: 1.00
Name: 98BWM037_d	Len: 194	Check: 4971	Weight: 1.00
Name: 99BW3932_1	Len: 194	Check: 4165	Weight: 1.00
Name: 99BW4642_4	Len: 194	Check: 2912	Weight: 1.00
Name: 99BW4745_8	Len: 194	Check: 5323	Weight: 1.00
Name: 99BW4754_7	Len: 194	Check: 3964	Weight: 1.00
Name: 99BWMC16_8	Len: 194	Check: 6325	Weight: 1.00
Name: A2_CD_97CD	Len: 194	Check: 5849	Weight: 1.00
Name: A2_CY_94CY	Len: 194	Check: 5097	Weight: 1.00
Name: A2D_97KR	Len: 194	Check: 3871	Weight: 1.00
Name: A2G_CD_97C	Len: 194	Check: 5705	Weight: 1.00
Name: A_BY_97BL0	Len: 194	Check: 8467	Weight: 1.00

Name: A_KE_Q23_A	Len: 194	Check: 5053	Weight: 1.00
Name: A_SE_SE659	Len: 194	Check: 3808	Weight: 1.00
Name: A_SE_SE725	Len: 194	Check: 5856	Weight: 1.00
Name: A_SE_SE753	Len: 194	Check: 5873	Weight: 1.00
Name: A_SE_SE853	Len: 194	Check: 5523	Weight: 1.00
Name: A_SE_SE889	Len: 194	Check: 3207	Weight: 1.00
Name: A_SE_UGSE8	Len: 194	Check: 5837	Weight: 1.00
Name: A_UG_92UG0	Len: 194	Check: 5055	Weight: 1.00
Name: A_UG_U455_	Len: 194	Check: 5386	Weight: 1.00
Name: AC_IN_2130	Len: 194	Check: 3540	Weight: 1.00
Name: AC_RW_92RW	Len: 194	Check: 3664	Weight: 1.00
Name: AC_SE_SE94	Len: 194	Check: 4187	Weight: 1.00
Name: ACD_SE_SE8	Len: 194	Check: 4653	Weight: 1.00
Name: ACG_BE_VI1	Len: 194	Check: 6680	Weight: 1.00
Name: AD_SE_SE69	Len: 194	Check: 6416	Weight: 1.00
Name: AD_SE_SE71	Len: 194	Check: 8542	Weight: 1.00
Name: ADHK_NO_97	Len: 194	Check: 1255	Weight: 1.00
Name: ADK_CD_MAL	Len: 194	Check: 5519	Weight: 1.00
Name: AG_BE_VI11	Len: 194	Check: 7396	Weight: 1.00
Name: AG_NG_92NG	Len: 194	Check: 7120	Weight: 1.00
Name: AGHU_GA_VI	Len: 194	Check: 5827	Weight: 1.00
Name: AGU_CD_Z32	Len: 194	Check: 4744	Weight: 1.00
Name: AJ_BW_BW21	Len: 194	Check: 4938	Weight: 1.00
Name: B_AU_VH_AF	Len: 194	Check: 6911	Weight: 1.00
Name: B_CN_RL42	Len: 194	Check: 6101	Weight: 1.00
Name: B_DE_D31_U	Len: 194	Check: 3568	Weight: 1.00
Name: B_DE_HAN_U	Len: 194	Check: 6199	Weight: 1.00
Name: B_FR_HXB2_	Len: 194	Check: 4714	Weight: 1.00
Name: B_GA_OYI_	Len: 194	Check: 4534	Weight: 1.00
Name: B_GB_CAM1_	Len: 194	Check: 4796	Weight: 1.00
Name: B_GB_GB8_A	Len: 194	Check: 6277	Weight: 1.00
Name: B_GB_MANC	Len: 194	Check: 4800	Weight: 1.00
Name: B_KR_WK_AF	Len: 194	Check: 3856	Weight: 1.00
Name: B_NL_3202A	Len: 194	Check: 4181	Weight: 1.00
Name: B_TW_TWCYS	Len: 194	Check: 5670	Weight: 1.00
Name: B_US_BC_L0	Len: 194	Check: 4644	Weight: 1.00
Name: B_US_DH123	Len: 194	Check: 5023	Weight: 1.00
Name: B_US_JRCFS	Len: 194	Check: 6235	Weight: 1.00
Name: B_US_MNCG_	Len: 194	Check: 2067	Weight: 1.00
Name: B_US_P896_	Len: 194	Check: 6322	Weight: 1.00
Name: B_US_RF_M1	Len: 194	Check: 5045	Weight: 1.00
Name: B_US_SF2_K	Len: 194	Check: 3723	Weight: 1.00
Name: B_US_WEAU1	Len: 194	Check: 4222	Weight: 1.00
Name: B_US_WR27_	Len: 194	Check: 7503	Weight: 1.00
Name: B_US_YU2_M	Len: 194	Check: 5093	Weight: 1.00
Name: BF1_BR_93B	Len: 194	Check: 4341	Weight: 1.00
Name: C_BR_92BR0	Len: 194	Check: 5265	Weight: 1.00
Name: C_BW_96BW0	Len: 194	Check: 5846	Weight: 1.00
Name: C_BW_96BW1	Len: 194	Check: 3799	Weight: 1.00
Name: C_BW_96BW1	Len: 194	Check: 4343	Weight: 1.00
Name: C_BW_96BW1	Len: 194	Check: 5690	Weight: 1.00
Name: C_ET_ETH22	Len: 194	Check: 4205	Weight: 1.00
Name: C_IN_93IN1	Len: 194	Check: 3033	Weight: 1.00
Name: C_IN_93IN9	Len: 194	Check: 3201	Weight: 1.00
Name: C_IN_93IN9	Len: 194	Check: 4905	Weight: 1.00
Name: C_IN_94IN1	Len: 194	Check: 3129	Weight: 1.00
Name: C_IN_95IN2	Len: 194	Check: 3351	Weight: 1.00
Name: CRF01_AE_C	Len: 194	Check: 6355	Weight: 1.00
Name: CRF01_AE_C	Len: 194	Check: 2596	Weight: 1.00
Name: CRF01_AE_C	Len: 194	Check: 4412	Weight: 1.00

Name: CRF01_AE_T	Len: 194	Check: 5882	Weight: 1.00
Name: CRF01_AE_T	Len: 194	Check: 5558	Weight: 1.00
Name: CRF01_AE_T	Len: 194	Check: 5926	Weight: 1.00
Name: CRF01_AE_T	Len: 194	Check: 5579	Weight: 1.00
Name: CRF01_AE_T	Len: 194	Check: 2960	Weight: 1.00
Name: CRF01_AE_T	Len: 194	Check: 5867	Weight: 1.00
Name: CRF02_AG_F	Len: 194	Check: 1879	Weight: 1.00
Name: CRF02_AG_F	Len: 194	Check: 3893	Weight: 1.00
Name: CRF02_AG_G	Len: 194	Check: 5632	Weight: 1.00
Name: CRF02_AG_N	Len: 194	Check: 3187	Weight: 1.00
Name: CRF02_AG_S	Len: 194	Check: 5274	Weight: 1.00
Name: CRF02_AG_S	Len: 194	Check: 5177	Weight: 1.00
Name: CRF03_AB_R	Len: 194	Check: 5215	Weight: 1.00
Name: CRF03_AB_R	Len: 194	Check: 5211	Weight: 1.00
Name: CRF04_cpx_	Len: 194	Check: 2914	Weight: 1.00
Name: CRF04_cpx_	Len: 194	Check: 5450	Weight: 1.00
Name: CRF04_cpx_	Len: 194	Check: 4358	Weight: 1.00
Name: CRF05_DF_B	Len: 194	Check: 7168	Weight: 1.00
Name: CRF05_DF_B	Len: 194	Check: 5710	Weight: 1.00
Name: CRF06_cpx_	Len: 194	Check: 4977	Weight: 1.00
Name: CRF06_cpx_	Len: 194	Check: 5603	Weight: 1.00
Name: CRF06_cpx_	Len: 194	Check: 4458	Weight: 1.00
Name: CRF06_cpx_	Len: 194	Check: 3711	Weight: 1.00
Name: CRF11_cpx_	Len: 194	Check: 4246	Weight: 1.00
Name: CRF11_cpx_	Len: 194	Check: 7186	Weight: 1.00
Name: D_CD_84ZR0	Len: 194	Check: 4173	Weight: 1.00
Name: D_CD_ELI_K	Len: 194	Check: 5080	Weight: 1.00
Name: D_CD_NDK_M	Len: 194	Check: 4285	Weight: 1.00
Name: D_UG_94UG1	Len: 194	Check: 3203	Weight: 1.00
Name: F1_BE_VI85	Len: 194	Check: 5281	Weight: 1.00
Name: F1_BR_93BR	Len: 194	Check: 2780	Weight: 1.00
Name: F1_FI_FIN9	Len: 194	Check: 3522	Weight: 1.00
Name: F1_FR_MP41	Len: 194	Check: 3777	Weight: 1.00
Name: F2_CM_MP25	Len: 194	Check: 5402	Weight: 1.00
Name: F2KU_BE_VI	Len: 194	Check: 6170	Weight: 1.00
Name: G_BE_DRCBL	Len: 194	Check: 6155	Weight: 1.00
Name: G_NG_92NG0	Len: 194	Check: 5616	Weight: 1.00
Name: G_SE_SE616	Len: 194	Check: 6641	Weight: 1.00
Name: H_BE_VI991	Len: 194	Check: 5850	Weight: 1.00
Name: H_BE_VI997	Len: 194	Check: 6598	Weight: 1.00
Name: H_CF_90CF0	Len: 194	Check: 4443	Weight: 1.00
Name: J_SE_SE702	Len: 194	Check: 6028	Weight: 1.00
Name: J_SE_SE788	Len: 194	Check: 5724	Weight: 1.00
Name: K_CD_EQTB1	Len: 194	Check: 6926	Weight: 1.00
Name: K_CM_MP535	Len: 194	Check: 6479	Weight: 1.00
Name: N_CM_YBF30	Len: 194	Check: 4619	Weight: 1.00
Name: O_CM_ANT70	Len: 194	Check: 412	Weight: 1.00
Name: O_CM_MVP51	Len: 194	Check: 6622	Weight: 1.00
Name: O_SN_99SE_	Len: 194	Check: 8844	Weight: 1.00
Name: O_SN_99SE_	Len: 194	Check: 9492	Weight: 1.00
Name: U_CD_83C	Len: 194	Check: 5631	Weight: 1.00

1

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00BW0762_1	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRANGWFY	RHHYESRHPK
00BW0768_2	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	VSRRANGWFY	RHHYESRHPK
00BW0874_2	MENRWQVLIV	WQVDRMKIRA	WNSLVKHHMY	ISRKASGWFY	RHHYESRHPK
00BW1471_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRAKGWVY	RHHYESRHPK
00BW1616_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRRASGWFY	RHHYESRHPK
00BW1686_8	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWSY	RHHYESRHPK
00BW1759_3	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAKGWLY	RHHYENRHPK

00BW1773_2	MENRWQVLIV	WQVDRMKIKT	WNSLVKHHMY	VSKRAKGWYF	RHHYESSHPR
00BW1783_5	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	ISKKARGWYF	RHHYESRHPK
00BW1795_6	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSRRKANGWYF	RHHYESRHPK
00BW1811_3	MENRWQVLIV	WQVDRMKIKT	WNSLVKHHMY	ISKKAKGWYF	RHHYESRNP
00BW1859_5	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRKAGWYF	RHHFESRHPK
00BW1880_2	MENRWQVLIV	WQIDRMKIRT	WNSLVKHHMY	ISRRASGWYF	RHHYESRNP
00BW1921_1	MENRWQVLIV	WQIDRMKIRT	WNSLVKHHMY	ISRRANGWYF	RHHYESRHPK
00BW2036_1	MENRWQALIV	WQVDRMRIRT	WNSLVKHHMH	VSKRAKGWYF	RHHFESRHPK
00BW2063_6	MENRWQGLIV	WQVDRMRIRT	WNSLVKHHMY	ISRRASGWYF	RHHYDSRHPK
00BW2087_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRAGWYF	RHHYESRNP
00BW2127_2	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	TSKKATGWYF	RHHYESRHPK
00BW2128_3	MENRWQVLIV	WQVDRMRIRT	WNSIVKHHMY	VSRRRTNGWYF	RHHYESRNP
00BW2276_7	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRTMGWYF	RHHFQSRHPK
00BW3819_3	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMH	ISKRAKGWYF	RHHFESRHPK
00BW3842_8	MENRWQALIV	WQVDRMRIRT	WNSLVKHHMY	ISRRASGWYF	RHHFESRHPK
00BW3871_3	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	ISRRASGWYF	RHHYESRHPK
00BW3876_9	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	VSRRKAGWYF	RHHYQSRHPK
00BW3886_8	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRANGWYF	RHHYQSRHPK
00BW3891_6	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	VSKKANGWYF	RHHYESRHP
00BW3970_2	MENRWQVLIV	WQIDRMKIRT	WNSLVKHHMY	VSRRASGWYF	RHHFESRHPK
00BW5031_1	MDNRWQGLIV	WQVDRMRIRT	WNSLVKHHMY	VSRRANGWYF	RHHHESRHPK
96BW01B21	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	VSRRASGWYF	RHHFESRHPK
96BW0407	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	VSKKAKGWYF	RHHYESRHP
96BW0502	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMH	ISKRAKGWYF	RHHYESRHPK
96BW06_J4	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISKRANGWYF	RHHYESRHPK
96BW11_06	MENRWQALIV	WQVDRMRIRT	WNSLVKHHMY	VSRRANGWYF	RHHYESRHPK
96BW1210	MENRWQGLIV	WQVDRMRIRT	WNSLVKHHMY	VSKRADGWYF	RHHYESRHPK
96BW15B03	MENRWQALIV	WQVDRMRIRT	WNSLVKHHMY	VSKRTNGWYF	RHHFESRHPK
96BW16_26	MENRWQVLIV	WQVDRMKIKT	WNSLVKHHMY	ISRRANGWYF	GHHYESRNP
96BW17A09	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRKAGWYF	RHHYESRHPK
96BWM01_5	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAAGWYF	RHHYESRHPK
96BWM03_2	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAAGWYF	RHHYESRHPK
98BWM012_2	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	TSGRASGWYF	RHHYESRHPK
98BWM013_4	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRAKGWYF	RHHYESRHPK
98BWM014_a	MENRWQGLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRASGWYF	RHHFESRHPK
98BWM014_1	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	ISRRKAGWYF	RHHYESRNP
98BWM018_d	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	VSKRAKGWYF	RHHYESRHPK
98BWM036_a	MENRWQVLIV	WQVDRMRIRA	WNSLVKHHMH	ISKRAAGWYF	RHHYESRNP
98BWM037_d	MENRWQVLIV	WQVDRMKIRT	WNSLVKHHMY	VSKRASKWYF	RHHYESRHPK
99BW3932_1	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMY	ISRRAGWYF	RHHYESRHPK
99BW4642_4	MENRWQVLIV	WQIDRMKIRT	WNSLVKHHMY	VSKRAKGWYF	RHHFESRHPK
99BW4745_8	MENRWQVLIV	WQVDRMRIRT	WNSLVKHHMH	ISRRANGWYF	RHHYESRHP
99BW4754_7	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	VSRRANGWYF	RHHYESRHPK
99BWM016_8	MENRWQGLIV	WQVDRMRIRT	WNSLVKHHMH	VSRRANGWYF	RHHYESRHPK
A2_CD_97CD	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAREWYF	RHHYESRHP
A2_CY_94CY	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISRRKAGWYF	RHHYESRNP
A2D_97KR	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKDWYF	RHHYESRNP
A2G_CD_97C	MENRWQVMIV	WQVDRMRIRK	WNSLVKHHMY	VSRRKAGWYF	RHHYESRHPK
A_BY_97BL0	XENRWQVXIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAR.EVY	RHHYESRQPR
A_KE_Q23_A	MENRWQAMIV	WQVDRMRIRT	WNSLVKHHMH	VSKKAKRWYF	RHHYESRHPK
A_SE_SE659	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKAKNWYF	RHHFESRHPK
A_SE_SE725	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSRRKAGWYF	RHHYESRNP
A_SE_SE753	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	VSKKARNWYF	RHHYESRHPK
A_SE_SE853	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKNWYF	RHHFESRHPK
A_SE_SE889	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAKGWLY	RHHFESRHPK
A_SE_UGSE8	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISKKAGWYF	RHHYESRHPK
A_UG_92UG0	MENRWQVMIV	WQVDRMRIRT	WNSLVKHHMY	ISRRKAGWYF	RHHYESRHPK
A_UG_U455	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	VSKKAGWYF	RHHYESRHSR
AC_IN_2130	MENRWQALIV	WQVDRMKIRT	WNSLVKHHMY	VSRRKAGWYF	RHHYDSRHPK
AC_RW_92RW	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	ASRRKAGWYF	RHHYESRHPK

CRF02_AG_S	MENRWQVMIV	WQVDRMIRI	WNSLVKHHMY	VSKKAHRWFY	RHHYESRHPK
CRF03_AB_R	MENRWQVMIV	WQVDRMIRI	WNSLVKHHIY	ISKKARGWVY	KHHYESRNPR
CRF03_AB_R	MENRWQVMIV	WQVDRMIRI	WNSLVKHHIY	ISKKARGWVY	KHHYESRNPR
CRF04_cpx_	MANRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	VSKKAKGF.Y	RHHYESRHPK
CRF04_cpx_	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	ISKKAKGWSY	RHHYESRHPK
CRF04_cpx_	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMH	ISKKAKGWSY	KHHYESRNPR
CRF05_DF_B	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	VSKKANRWCY	RHHFESRNPR
CRF05_DF_B	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	VSKKTKAWFY	RHHYESRHPK
CRF06_cpx_	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKRWNY	RHHYDSNHPK
CRF06_cpx_	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKRWTY	RHHYDSNHPK
CRF06_cpx_	MENRWQVMIV	WQVDRMRINA	WKS LVKYHMH	VSKKAKGWLY	RHHYDSNHPK
CRF06_cpx_	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKARKWAY	RHHYDSHHPK
CRF11_cpx_	MENRWQVMIV	WQVDRMIRI	WNSLVKHHMY	VSKKARRWMY	RHHYESRHPK
CRF11_cpx_	MENRWQVMIV	WQVDRMIRI	WNSLVKHHMY	VSKKAKGWLY	RHHYESRHPK
D_CD_84ZR0	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKGWFY	RHHYDSHPK
D_CD_ELI_K	MENRWQVMIV	WQVDRMRIKT	WKS LVKHHMY	VSKKANRWFY	RHHYESHPK
D_CD_NDK_M	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMY	VSKKANRWFY	RHHYDSHHPK
D_UG_94UG1	MENRWQVMIV	WQVDRMIRI	WKS LVKHHMY	ISKKAKGWLY	RHHYDCPNPK
F1_BE_VI85	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMY	VSKKAKGWSY	RHHFQSRHPK
F1_BR_93BR	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKAKGWFY	RHHFESRHPK
F1_FI_FIN9	MENRWQVTIV	WQVDRMRINT	WKS LVKYHMH	VSKKAKRWFY	RHHFESRHPK
F1_FR_MP41	MENRWQVMIV	WQVDRMRIST	WKS LVKYHMH	VSKKAKNWFY	RHHFQSRHPK
F2_CM_MP25	MENRWQVMIV	WQVDRMKIRT	WNSLVKHHMY	ISKRAAGWFY	RHHYESRHPK
F2KU_BE_VI	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	VSRKTGWSY	RHHYESINPR
G_BE_DRCBL	MENRWQVMIV	WQVDRMRINT	WNSLVKHHMY	ISKKAKGWFY	RHHYESRHPK
G_NG_92NG0	MENRWQVVIV	WQVDRMRINT	WNSLVKHHMY	VSKKAKGWFY	RHHYESRHPK
G_SE_SE616	MENRWQVMIV	WQVDRMRINT	WNSLVKHHMY	VSKKARGWVY	RPHYASRHPK
H_BE_VI991	MENRWQVMIV	WQVDRMRINT	WNSLVKHHMY	VSKKAKKWVY	RHHYESTNPK
H_BE_VI997	MENRWQVMIV	WQVDRMRINK	WKS LVKYHMY	ISKKANRWVY	RHHYDSHPK
H_CF_90CF0	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISRKARGWVY	RHHFESTHPR
J_SE_SE702	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	VSKKARQWLY	RHHYDSRHPK
J_SE_SE788	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	VSKKARKWLY	RHHYDSNHPK
K_CD_EQTB1	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMY	VSKKANRWRY	RHHYDSNHPK
K_CM_MP535	MENRWQVMIV	WQVDRMRINT	WKS LVKYHMH	ISKKANRWYY	RHHYESRHPK
N_CM_YBF30	MENRWQVMIV	WQVDRMKIRK	WNSLVKHHMY	VSKKAKGWY	RHHYETHHPK
O_CM_ANT70	MENRWQVLIV	WQVDRQKVKA	WNSLVKYHMY	RSRK TENWVY	RHHYESRNPR
O_CM_MVP51	MENRWQVLIV	WQVDRQKVKA	WNSLVKYHMY	MSKKAANWRY	RHHYESRNPK
O_SN_99SE_	MENRWQVLIV	WQVDRQKVKT	WNSLVKYHMY	RSGKTRDWY	RHHFESRNPR
O_SN_99SE_	MENRWQVLIV	WQVDRQKVKT	WNSLVKYHMY	RSGKTRDWY	RHHFESKNPR
U_CD_83C	MENRWQVMIV	WQVDRMRIKT	WNSLVKHHMY	ISKKAKGWVY	KHHYESTNPR

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00BW0762_1	LSSEVHIPLG	D.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	KLRRYSTQVD
00BW0768_2	VSSEVHIPLG	D.ARLVIITY	WGLHTGERDW	HLGHGVSIEW	RLRRYSTQVD
00BW0874_2	ISSEVHIPLG	D.ARLVIKTY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW1471_2	ISSEVHIPLG	D.AKLVIKTY	WGLHTGEREW	HLGHGVSIEW	RLKSPSTQVD
00BW1616_2	ISSEVHIPLG	D.ARLIIKTY	WGLQTGEREW	HLGHGVSIEW	RLRKYSTQVD
00BW1686_8	ISSEVHIPLG	E.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW1759_3	ISSEVHIPLG	D.ARLVITTY	WGLNTGERDW	HLGHGVSIEW	RLGRYSTQVD
00BW1773_2	VSSEIHIPLG	E.ARLVIKTY	WGLQTGEREW	HLGHGVSIEW	RWKRYSTQVE
00BW1783_5	ISSEVHIPLG	D.ARLVIKTY	WGLHTGEREW	HLGHGVSIEW	RLRKYSTQID
00BW1795_6	ISSEVHIPLG	E.ARLVIITY	WGLQTGEREW	HLGHGVSIEW	RLRRYSTQVD
00BW1811_3	ISSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRKYSTQVE
00BW1859_5	ISSEVHIPLG	E.ARLVVKTY	WGLQTGEREW	HLGHGVSIEW	RLRGYSTQVD
00BW1880_2	ISSEVHIPLG	E.ARLVIKTY	WGLHTGERDW	HLGHGVSIEW	KLKRYSTQVD
00BW1921_1	VSSEVHIPLG	E.ARLVITTY	WGLQTGEREW	HLGHGVSIEW	RLRRYKTQVD
00BW2036_1	VSSEVHIPLG	E.ARLVVITY	WGLQTGEREW	HLGQGVSI EW	RLRRYSTQVD
00BW2063_6	ISSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSIEW	RLRKYSTQVD
00BW2087_2	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERAW	HLGHGVSIEW	RMKRYSTQVD
00BW2127_2	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGASIEW	RLRRYSTQVW

00BW2128_3	VSSGVHIPLG	D.ARLVIKTY	WGLQTGEREW	HLGHGVSI EW	RLRKYSTQVE
00BW2276_7	VSSEVHIPLG	D.ARLVITTY	WGLQTGEREW	HLGHGVSI EW	RLKRYSTQVD
00BW3819_3	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLGKYNTQVE
00BW3842_8	VSSEVHIPLG	E.ARLVIITY	WGLQTGEREW	HLGHGVSI EW	RLRRYSTQVD
00BW3871_3	VGSEVHIPLG	E.ARLVIRTY	WGLQTGEREW	HLGHGVSI EW	RLRKYSTQVD
00BW3876_9	VSSEVHIPLG	E.DKLVIITY	WGLQTGEREW	HLGHGVSI EW	RLKKYSTQVD
00BW3886_8	VSSEVHIPLG	E.ARLVITTY	WGLQTGEREW	HLGHGVSI EW	RLKRYSTQVD
00BW3891_6	ISSEVHIPLG	E.ARLIKTY	WGLQTGERDW	HLGHGASIEW	RLRRYSTQVD
00BW3970_2	ISSEVHIPLG	E.ARLIKTY	G.LQTGECDW	HLGHGCSIEW	RLRKYSTQVD
00BW5031_1	VSSEVHIPLG	D.ARLVIKTY	WGLHTGERDW	HLGHGVSI EW	RLRRYSTQVD
96BW01B21	VSSEVHIPLG	E.ARLVIKTY	WGLQTGEREW	HLGHGVSI EW	RLRRYSTQVD
96BW0407	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRGYSTQVD
96BW0502	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRKYSTQVE
96BW06_J4	VSSEVHIPLG	D.ARLVITTY	WGLQTGEREW	HLGHGVSI EW	RLRRYSTQVD
96BW11_06	VSSEVHISLG	E.ARLVIKTY	WGLHTGERDW	HLGHGVSI EW	KLRGYSTQVD
96BW1210	VSSEVHIPLG	D.ARLVIITY	WGLQTGEREW	HLGHGVSI EW	RLRSYSTQVD
96BW15B03	VSSEVHIPLG	E.ARLVIITY	WGLQTGEREW	HLGHGVSI EW	RLRRYSTQVD
96BW16_26	VSSEVHIPLG	D.AKLVIKTY	WGLQTGERDW	HLGHGVSI EW	RWGNYSTQVE
96BW17A09	ISSEVHIPLG	D.AKLVIITY	WGLHTGECDW	HLGHGVSI EW	RLKRFSTQVD
96BWM01_5	ISSEVHIPLG	D.ARLVIKTY	WGLNTGERDW	HLGHGVSI EW	RLRKYSTQVD
96BWM03_2	VSSEIHIPLG	D.ARLVIRTY	WGLQTGEKEW	QLGHGVSI EW	RLRSFSTQVD
98BWMC12_2	VSSEVHIPLG	K.ARLVITTY	WGLQIGERDW	HLGHGVSI EW	RLRKYSTQVD
98BWMC13_4	ISSEVHIPLG	D.ARLVIKTY	WGLNTGERDW	HLGHGVSI EW	RLRKYSTQVD
98BWMC14_a	VSSEVHIPLG	E.AKLVIITY	WGLQPGEREW	HLGHGASIEW	RLRRYSTQVD
98BWM014_1	ISSEIHIPLG	E.ARLVIKTY	WGLNTGERDW	HLGHGVSI EW	RMRGYSTQVD
98BWM018_d	ISSEVHIPLG	D.AKLVIKTY	WGLQTGEREW	HLGHGTSIEW	ILGGYSTQVD
98BWM036_a	ISSEVHIPLG	D.ARLVIRTY	WGLQTGERDW	HLGHGVSI EW	RLRRYSTQVD
98BWM037_d	VSSEVHIPLG	D.ARLIKTY	WGLQTGERDW	HLGHGCSIEW	RLRRYSTQVD
99BW3932_1	VSSEVHIPLG	E.ARLVIKTY	WGLQTGECDW	HLGHGVSI EW	RLKRYSTQVD
99BW4642_4	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEREW	HLGHGVSI EW	RLRRYSTQVD
99BW4745_8	VSSEVHIPLG	E.ARLVITTY	WGLLPGEREW	HLGHGVSI EW	RLRRYSTQVD
99BW4754_7	ISSEVHIPLR	D.ARLVIKTY	WGLHTGERDW	HLGHGVSI EW	RLGRYSTQVD
99BWMC16_8	VSSEVHIPLG	D.ARLVITTY	WGLHTGEREW	HLGHGVSI EW	RLRRYSTQVD
A2_CD_97CD	VSSEVHIPLK	E.ARLVIRTY	WGLHPGECDW	HLGHGVSI EW	RQGRYSTQID
A2_CY_94CY	ISSEVHIPLG	E.ARLVIRTY	WGLHIGEKDW	HLGHGVSI EW	RQNRYSTQID
A2D_97KR	VSSEVHIPLG	G.AKLVIKTY	WGLHPGECDW	HLGHGVSI EW	RQERYSTQID
A2G_CD_97C	VSSEVHIPLG	E.ATLVIRTY	WGLQTGECDW	QLGHGVSI EW	RQKRYSTQID
A_BY_97BL0	VSSEVHIPLG	D.ARLVVKTY	XGLHAXEKDW	QLGHXVSI EW	ROEXYSTQID
A_KE_Q23_A	VSSEVHIPLG	D.ATLVVIRTY	WGLHTGECDW	HLGHGVSI EW	RLKRYSTQIT
A_SE_SE659	VSSEVHIPLG	D.AKLVVIRTY	WGLHTGEKEW	HLGHGVSI EW	RLNRYSTQID
A_SE_SE725	TSSEVHIPLG	D.ARLVVIRTY	WGLHTGECDW	QLGHGVSI EW	RLRRYSTQID
A_SE_SE753	VSSEVHIPLG	D.ARLVVIRTY	WGLQTGECDW	HLGHGVSI EW	RLKRYSTQID
A_SE_SE853	VSSEVHIPLG	E.AKLVVIRTY	WGLQTGECDW	QLGHGVSI EW	RLRRYSTQID
A_SE_SE889	VSSEVHIPLG	E.ARLVVIRTY	WGLQTGECDW	HLGHGVSI EW	RLRRYSTQID
A_SE_UGSE8	VSSEVHIPLG	D.ARLVIRTY	WGLHPGERDW	QLGHGVSI EW	RLRRYSTQID
A_UG_92UG0	VSSEVHIPIG	D.ARLVVIRTY	WGLQTGECDW	HLGHGVSI EW	RLKRYSTQID
A_UG_U455_	VSSEVHIPLG	E.ARLVVIRTY	WGLHTGECDW	HLGHGVSI EW	RLKRYSTQVD
AC_IN_2130	VSSEVHIPLG	E.AKLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRRYSTQVE
AC_RW_92RW	ISSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRRYSTQVD
AC_SE_SE94	TSSEVHIPLG	E.ARLVIITY	WGLQTGERDW	HLGHGVSI EW	RLCRYSTQVD
ACD_SE_SE8	ISSEVHIPLG	D.AKLVVIRTY	WGLHTGECDW	HLGHGVSI EW	RLRKYSTQID
ACG_BE_VI1	VSSEVHIPLG	D.ARLVVIRTY	WGLHTGEKAW	QLGHGVSI EW	RQRRYSTQID
AD_SE_SE69	VSSEVHIPLG	E.ARLVVKTY	WGLHTGERDW	HLGHGVSI EW	RKRRYSTQVD
AD_SE_SE71	VSSEVHIPLG	D.AKLVVIRTY	WGLHTGECDW	HLGHGVSI EW	RLRRYSTQID
ADHK_NO_97	VSSEVHIPLG	D.ARLVVIRTY	WGLQTGEKAW	HLGHGVSI EW	RQKRYSTQID
ADK_CD_MAL	VSSEVHIPLG	D.ARLVVIRTY	WGLQTGECDW	HLGHGVSI EW	RQKRYSTQID
AG_BE_VI11	VSSEVHIPLG	D.ARLVVIRTY	WGLHTGECDW	HLGHGVSI EW	RQRRYSTQID
AG_NG_92NG	VSSEVHIPLG	E.ARLVVIRTY	WGLHTGERDW	HLGHGVSI EW	RQRRYSTQID
AGHU_GA_VI	VSSEVHIPLG	D.ARLVIKTY	WGLHTGERDW	HLGHGVSI EW	RKGRYSTQVD
AGU_CD_Z32	ISSEVHIPLG	E.AKLVVITTY	WGLHTGEREW	HLGHGVSI EW	RLRRYSTQVD

AJ_BW_BW21	ISSEVHIPLG	S.AELVVTTY	WGLNTGEREW	HLGQGLSIEW	RLKRYRTQVD
B_AU_VH_AF	ISSEVHIPLG	E.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_CN_RL42_	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_DE_D31_U	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	QLGHGVSIEW	RKKRYSTQVD
B_DE_HAN_U	VSSEVHIPLG	E.AKLVITTY	WGLHTGERDW	HLGQGASIEW	RKKRYSTQVD
B_FR_HXB2_	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_GA_OYI_	ISSEVHIPLG	D.ATLVTTY	WGLHTGEREW	HLGQGASIEW	RKKRYSTQVD
B_GB_CAM1	ISSEVHIPLG	E.ARLVTTY	WGLHTGERDW	HLGQGVSI EW	RTKGYNTQVD
B_GB_GB8_A	ISSEVHIPLG	E.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYRTQVD
B_GB_MANC_	VSSEVHIPLG	D.AKLVIKTY	WGLHTGERDW	HLGQGASIEW	RKKGYSIQVD
B_KR_WK_AF	ISSEVHIPLG	D.AKLVITTY	WGLHTGEREW	HLGQGVSI EW	RKKRYNTQVD
B_NL_3202A	ISSEVHIPVG	E.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_TW_TWCYS	ISSEVHIPLG	D.ATLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_US_BC_L0	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGHGVSV EW	RKKRYSTQVD
B_US_DH123	ISSEVHIPLG	D.ASLVTTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_US_JRCSP	VSSEVQIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSM EW	RTRRYSTQVD
B_US_MNCG_	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_US_P896_	ISSEVHIPLG	D.AKLVVTTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_US_RF_M1	ISSEVHIPPG	D.ERLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
B_US_SF2_K	VSSEVHIPLG	D.AKLVITTY	WGLHTGEREW	HLGQGVAI EW	RKKKYSTQVD
B_US_WBAU1	ISSEVHIPLG	E.GKLVITTY	WGLHTGERDW	HLGQGVSI EW	RKQRYSTQVD
B_US_WR27_	ISSEVHIPLG	D.AMLVITTY	WGLHTGERDW	HLGQGVSI EW	RKQNYRTQVT
B_US_YU2_M	ISSEVHIPLG	D.AKLVITTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
BF1_BR_93B	VSSEVHIPLG	E.AKLVITTY	WGLHTGERDW	HLGQGVSI EW	RQGRYRTQID
C_BR_92BR0	ISSEVHIPLG	E.ARLVIITY	WGLQTGERDW	HLGHGVSI EW	RLRRYSTRVD
C_BW_96BW0	VSSEVHIPLG	D.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRRYSTQVD
C_BW_96BW1	VSSEVHIPLG	E.ARLVIKTY	WGLHTGERDW	HLGHGVSI EW	TVRGYST.VD
C_BW_96BW1	VSSEVHIPLG	D.ARLVIITY	WGLQTGEREW	HLGHGVSI EW	RLRSYSTQVD
C_BW_96BW1	VSSEVHIPLG	E.ARLVIITY	WGLQT.EREW	HLGHGVSI EW	RLRRYSTQVD
C_ET_ETH22	VSSEVHIPLG	E.ARLIIKTY	WGLQTGERDW	HLGHGVSI EW	RLRSYNTQVD
C_IN_93IN1	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRRYNTQIE
C_IN_93IN9	VSSEVHIPLG	E.ATLVIKTY	WGLQTGERDW	HLGHEVSI EW	RLRRYNTQIE
C_IN_93IN9	VSSEVHIPLG	E.ARLVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRRYSTQVE
C_IN_94IN1	VSSEVHIPLG	E.AILVIKTY	WGLQTGERDW	HLGHGVSI EW	RLRRYNTQIE
C_IN_95IN2	VSSEVHIPLG	E.ARLVITTY	WGLQTGERDW	HLGHGVSI EW	RLRKYSTQVE
CRF01_AE_C	VSSEVHIPIG	D.ARLVIRTY	WGLHTGEKDW	HLGHGVSI EW	RQRKYSTQVD
CRF01_AE_C	VSSEVHIPLG	D.ARLIIRTY	WGLHTGEKDW	HLGHGVSI EW	RQR.KSTQID
CRF01_AE_C	VSSEVHIPLG	E.ARLVIRTY	WGLHTGEKDW	HLGHGVSI EW	RQEKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHGVSI EW	RQRNYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHEVSI EW	RQRTYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	QLGHGVSI EW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.AKLIIIRTY	WGLQTGEKDW	QLGHGVSI EW	RQRTYSTQID
CRF01_AE_T	VSSEVHIPLG	E.ARLVIRTY	WGLQTGEKDW	HLGHGVSI EW	RQRKYSTQID
CRF01_AE_T	VSSEVHIPLG	E.AKLVIKTY	WGLQTGEKDW	QLGHGVSI EW	RQRKYSTQID
CRF02_AG_F	VSSEVHIPLG	D.ARLIVRTY	WGLHAGERDW	HLGHGVSI EW	KQRKYSTQID
CRF02_AG_F	VSSEVHIPLG	D.ARLIVRTY	WGLHAGERDW	YLGHGVSI EW	KQRKYSTQID
CRF02_AG_G	VSSEVHIPLG	D.ARLIVRTY	WGLHTGERDW	HLGHGVSI EW	RQKRYSTQID
CRF02_AG_N	VSSEVHIPLG	D.ARLVVRTY	WGLHTGERDW	HLGHGVSI EW	KQKRYSTQID
CRF02_AG_S	VSSEVHIPLG	D.ARLVVRTY	WGLHTGERDW	HLGHGVSI EW	KQKRYSTQID
CRF02_AG_S	VSSEVHIPLG	D.ATLIVRTY	WGLQPGERDW	HLGHGVSI VW	QQKRYSTQID
CRF03_AB_R	ISSEVHIPLG	D.AKLVIKTY	WGLHTGERDW	HLGQGASIEW	RKERYSTQVD
CRF03_AB_R	ISSEVHIPLG	D.AKLVIKTY	WGLHTGERDW	HLGQGASIEW	RKERYSTQVD
CRF04_cpx_	VSSEVHIPLG	E.ARLVVRTY	WGLQPGEQDW	HLGHGVSI EW	RLRRYSTQVD
CRF04_cpx_	VSSEVQIPLG	D.ARLVIRTY	WGLQPGEKDW	HLGHGVSM EW	RLRRYSTQVD
CRF04_cpx_	ASSEVHIPLG	E.AKLVVRTY	WGLQPGKKDW	HLGHGVSI XW	RLRSYSTQVD
CRF05_DF_B	ISSEVHIPLG	D.AKLVVTTY	WGLHTGERDW	HLGQGVSI EW	RKKRYSTQVD
CRF05_DF_B	ISSEVHIPLG	E.AKLVIITY	WGLHTGEREW	HLGQGVSI EW	RKGRYSTQID
CRF06_cpx_	ISSEVHIPLG	S.AELVITTY	WGLNTGERKW	HLGQGVSI EW	RLRRYRTQVD
CRF06_cpx_	VSSEVHIPLG	C.AELVITTY	WGLNTGERKW	HLGQGVSI EW	RLRRYRTQVD
CRF06_cpx_	ISSEVHIPLG	C.AELVVTTY	WGLNTGEREW	HLGQGVSI EW	RLKKYRTQVD

CRF06_cpx_	ISSEVHIPLG	K.AELVVTTY	WGLNTGERKW	HLGQGVSI EW	RLKRYRTQVD
CRF11_cpx_	ISSEVHIPLG	D.ADLVVTTY	WGLHTGEREW	HLGQGVSI EW	RMKRYRTQVD
CRF11_cpx_	VSSEVHIPLG	E.DMLVVTTY	WGLHTGEREW	HLGQGVSI EW	RRKRYRTQVD
D_CD_84ZR0	ISSEVHIPLG	D.ARLVVTTY	WGLHTGEREW	HLGQGVSI EW	RKRRYSTQVD
D_CD_ELI_K	ISSEVHIPLG	E.ARLVIKTY	WGLHTGEREW	HLGQGVSI EW	RKRRYSTQVD
D_CD_NDK_M	ISSEVHIPLG	E.ARLVVTTY	WGLHTGEREW	HLGQGVSI EW	RKRRYSTQVD
D_UG_94UG1	ISSEVHIPLG	E.ARLVVKTY	WGLHTGEREW	HLGQGVSI EW	RKGRYNTQID
F1_BE_VI85	VSSEVHIPLG	E.VKLVITTY	WGLHPGEREW	HLGQGVSI EW	RQGKYRTQID
F1_BR_93BR	ISSEVHIPLG	T.AELVITTY	WGLLPGEREW	HLGQGVSI EW	RQGRYRTQID
F1_FI_FIN9	ISSEVHIPLG	E.AELVITTY	WGLNTGERDW	HLGQGVSI EW	RQGRYRTQID
F1_FR_MP41	ISSEVHIPLG	E.AKLVVTTY	WGLHTGERDW	HLGQGVSI EW	RQGRYRTQID
F2_CM_MP25	VSSEVHIPLG	EDSKLVIITTY	WGLHTGERDW	HLGQGVSI EW	RQKRYRTQVD
F2KU_BE_VI	VSSEVHIPLG	E.AKLVVTTY	WGLNTGERDW	HLGQGVSI EW	RLKKYSTQID
G_BE_DRCBL	VSSEVHIPLG	D.AKLVVRTY	WGLHTGDK EW	HLGHGVSI EW	RQGRYSTQVD
G_NG_92NG0	VSSEVHIPLG	D.ATLVVTTY	WGLHAGEKDW	QLGHGVSI EW	RQKRYSTQID
G_SE_SE616	VSSEVHIPLG	D.ATLVVTTY	WGLHTGKDW	QLGHGVSI EW	RQRRYRTQVE
H_BE_VI991	TSSEVHIPVG	D.ARLVITTY	WGLHTGERDW	HLGHGVSI EW	RQERYSTQID
H_BE_VI997	ISSEVHIPLG	D.ARLVITTY	WGLHTGERDW	HLGQGVSI EW	RQKRYSTQVD
H_CF_90CF0	ISSEVHIPLG	E.ARLVITTY	WGLNTGEREW	HLGQGVSI EW	RLKRYSTQVE
J_SE_SE702	ISSEVHIPLG	E.ARLVVTTY	WGLQTGERDW	HLGQGVSI EW	RRKRYRTQVD
J_SE_SE788	ISSEVHIPLG	E.AILVITTY	WGLQTGERDW	HLGQGVSI EW	RQRRYRTQVD
K_CD_EQTB1	ISSEVHIPLG	D.AELVVTTY	WGLHTGEREW	HLGQGVSI EW	RLKKYRTQVD
K_CM_MP535	ISSEVHIPLG	D.AELVVTTY	WGLLTGERDW	HLGQGVSI EW	RLKRYRTQVE
N_CM_YBF30	ISSEVHIPVG	Q.ARLVTVTY	WGLTTGEQSW	HLGHGVSI EW	RLRKYKTQVD
O_CM_ANT70	VSSSVYIPVG	V.AHVVVTTY	WGLMPGERDE	HLGHGVSI EW	RYKKYKTQID
O_CM_MVP51	VSSAVYIPVA	E.ADIVVTY	WGLMPGEREE	HLGHGVSI EW	QYKEYKTQID
O_SN_99SE	VSSGVYIPVG	G.PWIVVTY	WGLMPGERDE	HLGHGVSI EW	RYKKYKTQID
O_SN_99SE	VSSGVYIPVG	G.PWIVVTY	WGLMPGERDE	HLGHGVSI DW	RYRKYTTQID
U_CD_83C	ISSEVHIPLG	N.ARIVVTAY	WGLHTGERDW	HLGQGVSI EW	RQGRYSTQID

101

150

00BW0762_1	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV	IPRCDYQAGH	NKVGSLQYLA
00BW0768_2	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	IPRCDYQAGH	TKVGSLQYLA
00BW0874_2	PGLADQLIHI	HYFDCFADSA	IRKAILGHIV	TPRCDYQAGH	NKVGSLQYLA
00BW1471_2	PGLADQLIHM	HYFDCFAGSA	IRKAILGQIV	SPRCDYQAGH	SKVGSLQYLA
00BW1616_2	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV	NPRCDYQAGH	NKVGSLQYLA
00BW1686_8	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW1759_3	PGLADQLIHM	HYFDCFADSA	IRKALLGHIV	IHRCDYQAGH	NKVGSLQYLA
00BW1773_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW1783_5	PGLADQLIHM	HYFDCFADSA	IRKALLGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW1795_6	PGLADQLIHT	HYFDCFADSA	IRKAILGHRV	SPRCDYQAGH	NKVGSLQYLA
00BW1811_3	PGLADQLIHI	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW1859_5	PGLADQLIHM	HYFDCFADSA	IRKAILGHRV	IHRCDYQAGH	NKVGSLQYLA
00BW1880_2	PGLADL_IHM	HYFDCFADSA	IRKAILGQVV	IPRCDYQAGH	NKVGSLQYLA
00BW1921_1	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW2036_1	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW2063_6	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW2087_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	SPRCDYQAGH	NKVGSLQYLA
00BW2127_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCVYQAGH	NKVGSIQYLA
00BW2128_3	PGLADQLIHM	HYFDCFADSA	IRRAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW2276_7	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	FPRCDYPAGH	NKVGSLQYLA
00BW3819_3	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	FPRCDYQAGH	NKVGSLQYLA
00BW3842_8	PGLADQLIHI	HYFDCFADSA	IRKAILGHIV	ISRCDYQAGH	NKVGSLQYLA
00BW3871_3	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW3876_9	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLT
00BW3886_8	PGLADQLIHM	HYFDCFADSA	LRKAILGHIV	FPRCDYQAGH	NKVGSLQYLA
00BW3891_6	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
00BW3970_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NQVGSLQYLA
00BW5031_1	PGLADQLIHM	HYFDCFADSA	IRKAILGRIV	IPRCDYQAGH	NQVGSLQYLA
96BW01B21	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA

96BW0407	PGLADQLIHM	HYFDCFADSA	IRKAILGQIV	SPRCEYQAGH	NKVGSLQYLA
96BW0502	PGLADQLIHM	HYFDCFADSA	IRKAILGEIV	IPRCDYQAGH	NQVGSLQYLA
96BW06_J4	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV	NPRCDYQAGH	NKVGSLQYLA
96BW11_06	PGLADQLIHM	HYFDCFTDSA	IRKALLGQVV	IPRCDYQAGH	NKVGSLQYLA
96BW1210	PGLADQLIHM	HYFDCFAGSA	IRQAILGHIV	IPRCDYQAGH	KKVGSLQYLA
96BW15B03	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV	IPRCNYQAGH	NKVGSLQYLA
96BW16_26	PGLADQLIHM	HYFDCFTDSA	IRKAILGNKI	IHRCNYPAGH	NKVGSLQYLA
96BW17A09	PGLADQLIHT	HYFDCFADSA	IRKAILGEIV	SPRCDYPARH	SVVGSLQYLA
96BWM01_5	PGLADQLIHM	YYFDCFADSA	IRRAILGYIV	IPRCDYQAGH	NKVGSLQYLA
96BWM03_2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	FPRCDYQAGH	NKVGSLQYLA
98BWM012_2	PGLADQLIHM	HYFDCFTDSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
98BWM013_4	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
98BWM014_a	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
98BWM014_1	PGLADQLIHM	HYFDCFADSA	IRKAILGNLV	IPRCDYQAGH	NKVGSLQYLA
98BWM018_d	PGLADQLIHM	HYFDCFADSA	IRKAILGDRV	SPRCDYQAGH	NKVGSLQYLA
98BWM036_a	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	SKVGSLQYLA
98BWM037_d	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	IPRCDYQAGH	NKVGSLQYLA
99BW3932_1	PSMADQLIHM	HYFDCFADSA	IRKAILCHIV	IPRCDYQAGH	NKVGFLQYLA
99BW4642_4	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
99BW4745_8	PGMADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLKYLA
99BW4754_7	PGLADQLIHM	HYFDCFTDSA	IRKAILGHIV	IHRCEYPAGH	NKVGSLQYLA
99BWM016_8	PSLADQLIHM	HYFDCADSA	IRQAILGHIV	IPRCNYQAGH	NKVGSLQYLA
A2_CD_97CD	PDLADHLIHL	YYFDCFSESA	IRRAILGEIV	RPRCEYQAGH	NKVGSLQYLA
A2_CY_94CY	PDLADHLIHL	YYFDCFSESA	IRKAILGEIV	SPRCEYQAGH	NKVGSLQYLA
A2D_97KR	PDLAGHLIHL	HYFDCFSDSA	IRKAILGKIV	RPRCEYQAGH	NKVGSLQYLA
A2G_CD_97C	PELADQLIHL	HYFDCFSESA	IRKAILGQVV	RPRCQYQAGH	TKVGSLQYLA
A_BY_97BL0	PDLADQLIHL	YYFDCFSESA	IRKAILGVHIV	SPRCNYQAGH	NKVGSLQYLA
A_KE_Q23_A	PDLADQLIHM	HYFDCFSDSA	IRKAILGVQVV	SPKCEYQAGH	NKVGSLQYLA
A_SE_SE659	PDQADQLIHL	HYFDCFSDSA	IRKALLGQVV	SPRCEYQAGH	KKVGSLQYLA
A_SE_SE725	PDLADQQLIHL	HYFDCFSDSA	IRKAILGHVV	SPICEYHTGH	NKVGSLQYLA
A_SE_SE753	PDLADQLIHL	YYLDCFSDSA	IRKALLGQVV	SPSCEYHTGH	NQVGSLQYLA
A_SE_SE853	PDLADQLIHM	HYXNCFSDSA	IRKAILGQVV	SPSCEYQAGH	NKVGSLQYLA
A_SE_SE889	PDLADQLIHL	HYFKCFSDSA	IRKAILGEIV	SPRCEYQAGH	NKVGSLQYLA
A_SE_UGSE8	PDLADQLIHL	HYFNCFSDSA	IRKAILGRVV	SPSCEYQAGH	NKVGSLQYLA
A_UG_92UG0	PDLADQLIHL	HYFNCFSDSA	IRKAILGQVV	SPRCDYQAGH	NKVGSLQYLA
A_UG_U455_	PDLADHLIHL	HYFDCFSESA	IRRAILGQIV	RPRCEYQAGH	NKVGSLQYLA
AC_IN_2130	PGLADQLIHM	HYFDCFADSA	IRQAILGHIV	IPRCDYQAGH	.KVGSLQYLA
AC_RW_92RW	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	SPRCDYQAGH	NKVGSLQYLA
AC_SE_SE94	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	SPRCDYQAGH	NKVGSLQYLA
ACD_SE_SE8	PDPADQLIHL	HYFDCFSDSA	IRKAILGQVV	SPRCDYTAGH	NKVGSLQYLA
ACG_BE_VI1	PDLADQLIHL	YYFDCFSDSA	IRKAILGQVV	RPRCEYQAGH	NKVGSLQYLA
AD_SE_SE69	PGLADQLIHL	YYFDCFSDSA	IRKAILGQVV	RPRCEYQAGH	NKVGSLQYLA
AD_SE_SE71	PDQADQLIHL	HYFDCFSDSA	IRKAILGHIV	TTRCNQYQAGH	NKVGSLQYLA
ADHK_NO_97	PDLADHLIHL	HYFDCFSDSA	IRKAILGQVV	RPRCEYQAGH	NKVGSLQYLA
ADK_CD_MAL	PDLADQLIHL	HYFDCFSDSA	IRQAILGHIV	SPRCDYQAGH	NKVGSLQYLA
AG_BE_VI11	PDLADQLIHL	NYFDCFSDSA	IRKAILGQVV	RPRCEYQAGH	NKVGSLQYLA
AG_NG_92NG	PDLADQLIHL	HYFNCFSDSA	VRKAILGEVV	RPRCEYQAGH	NQVGSLQYLA
AGHU_GA_VI	PGLADQLIHM	HYFDCFSDSA	IRKAILGQVV	RPRCEYSAGH	NQVGSLQYLA
AGU_CD_Z32	PGLADQLIHM	HYFDCFSESA	IRKAILGHRV	SPRCEYQAGH	NKVGSLQYLA
AJ_BW_BW21	PGLADQLIHM	HYFNCFSDSA	IRKAILGHIV	SPICEYQAGH	NKVGSLQYLA
B_AU_VH_AF	PGLADQLIHM	YYFDCFSESA	IRNAILERIV	SPSCEHQAGH	NKVGSLQYLA
B_CN_RL42_	PGLADQLIHL	YYFDCFSESA	IRNAILGRVV	SPSCDYQAGH	NKVGSLQYLA
B_DE_D31_U	PGLADQLIHL	YYFDCFSESA	IRNAILGRIG	SPSCEYRAGH	NKVGSLQYLA
B_DE_HAN_U	PNLADQLIHL	YYFDCFSESA	IRNAILGRIV	SPRCEYQAGH	SKVGSLQYLA
B_FR_HXB2_	PELADQLIHL	YYFDCFSDSA	IRKALLGHIV	SPRCEYQAGH	NKVGSLQYLA
B_GA_OYI_	PGLADQLIHT	YYFDCFSESA	IRNAILGNIV	SPRCEYPAGH	NKVGSLQYLA
B_GB_CAM1_	PDLADQLIHL	YYFDCFSESA	IRKAILGRLV	SPRCEYQAGH	NKVGSLQYLA
B_GB_GB8_A	PGLADQLIHQ	YYFDCFSESA	IRNALLGRTV	SPSCKYQAGH	NKVGSLQYLA
B_GB_MANC_	PGLADQLIHL	YYFDCFSESA	IRNAILGHIV	SPRCEYQAGH	NKVGSLQYLA
B_KR_WK_AF	PDLADKLHL	HYFDCFSDSA	IRHAILGHRV	RPKCEYQAGH	NKVGSLQYLA

B_NL_3202A	PGLADQLIHL	YYFDCFSESA	IRNAILGHVV	SPRCEYQAGH	NKVGSLQYLA
B_TW_TWCYS	PDQADQLIHL	YYFDCFSESA	IRKAIVGCRV	SPRCEYQAGH	NKVGSLQYLA
B_US_BC_L0	PDLADQLIHL	YYFDCFSESA	IRNAILGHIV	SPRCEYQAGH	NKVGSLQYLA
B_US_DH123	PDLADQLIHL	YYFDCFSESA	IRNAILGHRV	SPRCEYQAGH	NKVGSLQYLA
B_US_JRCSF	PDLADQLIHL	YYFDCFSESA	IRNAILGHIV	SPRCEYQAGH	SKVGSLQYLA
B_US_MNCG_	PDLADHLIHL	HYFDCFSDSA	IRKAILGHRV	SPICEFQAGH	NKVGSLQYLA
B_US_P896	PGLADRLIHL	YYFDCFSDSA	IRKSILGHIV	SPSCEYQAGH	NKVGSLQYLA
B_US_RF_M1	PDLADQLIHL	YYFDCFSESA	IRKPSLGHIV	SPRCEYQAGH	NKVGSLQYLA
B_US_SF2_K	PGLADQLIHL	HYFDCFSESA	IKNAILGYRV	SPRCEYQAGH	NKVGSLQYLA
B_US_WEAU1	PDLADQLIHL	YHFDCFSESA	IRNAILGHLV	IPRCEYQAGH	NKVGSLQYLA
B_US_WR27_	PDLADQLIHR	YYFDCFSEPA	IRNTIVGRIV	SPRCEYQTGH	NKVGSLQYLA
B_US_YU2_M	PDLADQLIHL	YYFDCFSESA	IRKAILGYRV	SPRCEYQAGH	NKVGSLQYLA
BF1_BR_93B	PGLADQLIHL	YYFDCFSESA	IRKAILGHRI	SPRCDYQAGH	NKVGSLQYLA
C_BR_92BR0	PGLADQLIHM	HYFDCFADSA	IRKAILGHRV	SSRCDYQAGH	NKVGSLQYLA
C_BW_96BW0	PGLADQLIHM	HYFDCFADSA	IRKAILGQIV	SPRCEYQAGH	NKVGSLQYLA
C_BW_96BW1	PGLADQLIHM	HYFDCFADSA	IRKALLGQVV	IPRCDYQAGH	NKVGSLQYLA
C_BW_96BW1	PGLADQLIHM	HYFDCFAGSA	IRQAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_BW_96BW1	PGLADQLIHM	YYFDCFSESA	IRKAILGHIV	IPRCNYQAGH	NKVGSLQYLA
C_ET_ETH22	PGLADHLIHM	HYFDCFSESA	IRKAILGYRV	SPRCDYQAGH	NKVGSLQYLA
C_IN_93IN1	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_IN_93IN9	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_IN_93IN9	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
C_IN_94IN1	PGLADQLIHM	HYFDCFADSA	IRKAILGRIV	IPRCDYQAGH	NKIGSLQYLA
C_IN_95IN2	PGLADQLIHM	HYFDCFADSA	IRKAILGHIV	IPRCDYQAGH	NKVGSLQYLA
CRF01_AE_C	PDLADRLIHL	QYFDCFSDSA	IRKAMLGQVV	RPRCEYPTGH	NKVGSLQYLA
CRF01_AE_C	PDLADQLIHL	QYFDCFSDSA	IRKALLGQIV	RPRCEYPAGH	NKVGSLQYLA
CRF01_AE_C	PDLADRLIHL	QYFDCFSESA	IRKAILGQVV	RPRCDYPEGH	NKVGSLQYLA
CRF01_AE_T	PDLADRLIHL	QYFDCFSDSA	IRRAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	QYFDCFSDSA	IRKAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	QYFDCFSDST	IRRAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	HYFDCFSDSA	IRRAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADKLIHL	QYFDCFSDSA	IRKAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF01_AE_T	PDLADQLIHL	QYFDCFSDSA	IRKAILGQVV	RRRCEYPSGH	NKVGSLQYLA
CRF02_AG_F	PDLADQLIHL	HYFDCFSESA	IRKAILGEVV	RPRCEYQAGH	KQVGSLOQYLA
CRF02_AG_F	PDLADQLIHL	HYFDCFADSA	IRKAILGQVV	SPRCEYQAGH	NQVGSLOQYLA
CRF02_AG_G	PDLADQLIHL	HYFDCFSESA	IRKAILGEVV	RPRCEYQAGH	NKVGSLQYLA
CRF02_AG_N	PDLADQLIHL	YYFNCFSDSA	IRKAILGEIV	RPRCEYQAGH	NKVGSLQYLA
CRF02_AG_S	PDLADQLIHL	HYFDCFSDSA	IRKAILGQIV	RPRCEYQAGH	TKVGSLOQYLA
CRF02_AG_S	PDLADQLIHL	HYFDCFSESA	IRKALLGQVV	RPKCEYQAGH	NKVGSLQYLA
CRF03_AB_R	PNLADQLIHL	YYFDCFSESA	IRNAILGHRV	SPSCEYRAGH	NKVGSLQYLA
CRF03_AB_R	PNLADQLIHL	YYFDCFSDSA	IRNAILGHRV	SPSCEYRAGH	NKVGSLQYLA
CRF04_cpx_	PDLADQLIHM	HYFDCFSESA	IRKAILGHRV	SPRCEYQAGH	NKVGSLQYLA
CRF04_cpx_	PDLADQLIHM	HYFDCFSESA	IRQAILGYRV	SPRCEYQAGH	NEVGSLOQYLA
CRF04_cpx_	PDLADQLIHL	HYFDCFSESA	IRKAILGHRV	SPRCEYQAGH	NKPGSLQYLA
CRF05_DF_B	PSLADQLIHL	YYFDCFSESA	IRNAILGRIV	SPRCEYQAGH	NKVGSLQYLA
CRF05_DF_B	PGLADQLIHM	YYFDCFSESA	IRKAILGYRV	SPRCEYQAGH	NKVGSLQYLA
CRF06_cpx_	PSMADQLIHL	HYFDCFSESA	IRKALLGHRV	SPRCDYQAGH	NKVGSLQYLA
CRF06_cpx_	PGLADQLIHM	HYFDCFSESA	IRKAILGQIV	SPQCDYQAGH	NKVGSLQYLA
CRF06_cpx_	PSLADQLIHM	HYFDCFSESA	IRKAILGHVV	SPKCDYQAGH	NKVGSLQYLA
CRF06_cpx_	PSLADQLIHM	HYFDCFSESA	IREAILGHIV	SPRCDYQAGH	NKVGSLQYLA
CRF11_cpx_	PGLADQLIHL	HYFDCFSESA	IREAILGHRV	SPRCEYQAGH	NQVGSLOQYLA
CRF11_cpx_	PELADQLIHM	HYFDCFSESA	IRKAILGHRV	SPRCEYPAGR	NKVGSLQYLA
D_CD_84ZR0	PGLADQLIHM	YYFDCFADSA	IRKAILGHIV	SPRCEYQAGH	NKVGSLQYLA
D_CD_ELI_K	PGLADQLIHM	YYFDCFSESA	IRKAILGDIV	SPRCEYQAGH	NKVGSLQYLA
D_CD_NDK_M	PGLADQLIHM	YYFDCFSESA	IRKAILGHIV	SPSCEYQAGH	NKVGSLQYLA
D_UG_94UG1	PGLADQLIHL	YHFDCFSESA	IRKAILGQVV	YPRCNYQAGH	NKVGSLQYLA
F1_BE_VI85	PGLADQLIHL	YYFDCFSESA	IRKAILGHRI	SPRCDYQAGH	NKVGSLQYLA
F1_BR_93BR	PGLADQLIHL	YYFDCFSESA	IRKAILGHKI	SPRCDYQAGH	NKVGSLQYLA
F1_FI_FIN9	PGLADQLIHL	YYFDCFSESA	IRKAILGHRI	SPRCDYQAGH	NKVGSLQYLA
F1_FR_MP41	PDLADQLIHL	YYFDCFSESA	IRKAILGHRI	SPRCDYQAGH	NKVGSLQYLA

F2_CM_MP25	PGLADQLIHL	HYFDCFSDSA	IRKAILGQRV	SPRCNYQAGH	NKVGSLQYLA
F2KU_BE_VI	PGLADQLIHM	HYFDCFTDSA	IRKALIGLRV	SPRCEYQAGH	NKVGSLQYLA
G_BE_DRCBL	PDADHLIHL	HYFNCFSESA	IRKAILGQTV	RPSCEYPAGH	NKVGSLQYLA
G_NG_92NG0	PNTADHLIHL	YYFDCFSESA	IRKAILGEIV	SPRCEYPAGH	NKVGSLQYLA
G_SE_SE616	PDADHLIHL	HYFDCFSDSA	IRKAILGQIV	SPRCEYQAGH	NQVGSLQYLA
H_BE_VI991	PDADQLIHL	HYFDCFSDSA	IRKAILGHRV	SPICDYQAGH	RKVGSLQYLA
H_BE_VI997	PGLADQLIHT	HYFDCFSESA	IRGAILGRVV	SPRCEYQAGH	NQVGSLQYLA
H_CF_90CF0	PGLADQLIHM	HYFDCFSESA	IRKAILGRVV	RPRCNYPAGH	KQVGTLQYLA
J_SE_SE702	PGLADQLIHM	HYFDCFSDSA	IRKAILGQIV	SPRCDYQAGH	NKVGSLQYLA
J_SE_SE788	PGLADQLIHM	CYFDCFSDSA	IRKAILGQIV	SPRCDYQAGH	NKVGSLQYLA
K_CD_EQTB1	PGLADQLIHI	YYFDCFSESA	IRKALLGHRV	SPRCEYQAGH	TQVGSLQYLA
K_CM_MP535	PDADQLIHI	YYFDCFSESA	VRKAILGHRV	SPRCECQAGH	NKVGSLQYLA
N_CM_YBF30	PEMADKLIHL	HYFDCFTASA	IRQAVLGRP	LPRCEYPAGH	KQVGTLQYLA
O_CM_ANT70	PETADRMHL	HYFTCFCTASA	VRKAILGQRV	LTKCEYPTGH	SQVGTLQLLA
O_CM_MVP51	PETADRMHL	HYFTCFCTASA	IRKAILGQRV	LTKCEYLAGH	SQVGTLQFLA
O_SN_99SE_	PETADRMHI	YYFACFTESA	IRKAILGQRV	LTRCEYPAGH	SQVGTLQLLA
O_SN_99SE_	PETADRMHT	YYFACFTESA	IRKAILGQRV	LTRCEYSAGH	SQVGTLQLLA
U_CD_83C	PDADQLIHL	HYFDCFSDSA	IRKAILGHIV	SPRCEYQTGH	NKVGSLQYLA

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00BW0762_1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW0768_2	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQR	TKGRRGNHTM	NGH.
00BW0874_2	LTALIKPHKR	KPPLPSVRKL	VEDRWNPQK	TKGRRGNHTM	NGH.
00BW1471_2	LTALIKPKRI	KPPLPSLQKL	VEDKWNPNQK	TRGHRGSHTM	NGH.
00BW1616_2	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW1686_8	LTALIKPKKI	KPPLPSIRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW1759_3	LTALIKPRKI	KPPLPSVRKL	VEDKWNPNQK	TRGRRGNHTM	NGH.
00BW1773_2	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW1783_5	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRDRRGNHTM	NGH.
00BW1795_6	LTALIKPKKR	KPPLPSVKKL	VEDRWNPQK	TRGRRGSHTM	NEH.
00BW1811_3	LTALIKPQRR	KPPLPSVSKL	VEDRWNPQK	TRGRRGCHTM	NGH.
00BW1859_5	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW1880_2	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW1921_1	LTALIKPKKI	KPPLPSVQKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW2036_1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRKGNHTM	NGH.
00BW2063_6	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGHRGNHTM	NGH.
00BW2087_2	LTALVKKKI	KPPLPSVKKL	VEDRWNPQK	TRGRRGNHTM	NGR.
00BW2127_2	LTALIKPKQI	KPPLPSVQKL	VEDRWNPQK	TRGRRGDHTM	NGH.
00BW2128_3	LTALIKPKKI	KPPLPSVKKL	VEDRWNPQK	TRGRRGNHTM	SGH.
00BW2276_7	LTALIKPKRR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW3819_3	LTAIK.PKKR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
00BW3842_8	LTALIKPKKR	KPPLPSVRKL	VEDRWNSQK	TRDRRGNHTM	NGH.
00BW3871_3	LTALIKPKKI	KPPLPSIRKL	VEDRWNSQK	TRGRRGNHTM	NGH.
00BW3876_9	LTALIKPKKI	KPPLPSVRKL	AEDRWNPQK	TRGRRGNHTM	SGH.
00BW3886_8	LTALIKPKKR	KPPLPSVRKL	VEDRWNSQK	TRDHRGNHTM	SGH.
00BW3891_6	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGHRGNHTM	NGH.
00BW3970_2	LTTLIKPKRR	KPPLPSVRKL	AEDRWNPQK	TRDRRGNHTM	NGH.
00BW5031_1	LTALIKPKRP	KPPLPSVRKL	AEDRWNPQK	TRGRRGNHTM	NGH.
96BW01B21	LTALIKPKKR	KPPLPSVKKL	VEDRWNPQK	TRGRRGSHTM	NGH.
96BW0407	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
96BW0502	LTALIKPKQR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
96BW06_J4	LTALIKPKKR	KPPLPSISKL	VEDRWNPQK	TRGRRGNHTM	NGH.
96BW11_06	LTALVKKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
96BW1210	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRKGNHTM	NGH.
96BW15B03	LTALIKPKQI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNRTM	NGH.
96BW16_26	LTALIKPKKI	KPPLPSVKNL	VEDRWNPQK	TRGRRGNHTL	NGH.
96BW17A09	LTAIVKPKKI	KPPLPSVQKL	VEDRWNPQK	TRGHRGSHTM	NGH.
96BWMO1_5	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRRESHTM	NGH.
96BWMO3_2	LTALIKPKRI	KPPLPSVRKL	VEDRWNPQK	TKGRRGNHTM	NGH.
98BWMC12_2	LTALIKPQKR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.

98BWMC13_4	LTALIKPKKR	KPPLPSVKKL	VEDRWNPQK	TRGRRGSHIM	NGH.
98BWMC14_a	LTALIKTKKR	KPPLPSVSKL	VEDRWNPQK	TRGRRENHTM	NGH.
98BWM014_1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGHRGNHTM	NGH.
98BWM018_d	LTALIKPKKI	KPPLPSVKKL	VEDRWNPQK	TRDRRGNHTM	NGH.
98BWM036_a	LTALIKPKRR	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
98BWM037_d	LTALIKPKRR	KPPLPSVRKL	TEDRWNPQK	TRDHRGNHTM	NGH.
99BW3932_1	LTALIKPKKI	KPPLPSVQKL	VEDRWNPQK	TRGRRGNHTM	NGH.
99BW4642_4	LTALIKPKKI	KPPLPSIRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
99BW4745_8	LTALLKTKRR	KPPLPSVRKL	VEDRWNPQK	TRGHRGNHTM	NGH.
99BW4754_7	LTALIKPKRI	KPPLPSVRKL	VEDRWNPQK	TRGHRGNHTM	NGH.
99BWMC16_8	LTALIKPKVI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
A2_CD_97CD	LRALVASTRT	KPPLPSVRKL	VEDRWNPQK	TRGHRGSHTM	NGC.
A2_CY_94CY	LKAVVASTRT	KPPLPSVRKL	VEDRWNPQK	TKGHRGSHTM	NGC.
A2D_97KR	LKALVGETRT	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
A2G_CD_97C	LRALVPTKI	KPPLPSVKKL	TEDRWNPQK	TRGHRENPTM	SGY.
A_BY_97BL0	LKALVTPTRE	RPPLPSVRXL	TEDRXNKPQK	TRGRRXNHTM	NXC.
A_KE_Q23_A	LKALVTPKKT	KPPLPSVRIL	TEDRWNPQK	TRGLRESHTM	NGC.
A_SE_SE659	LRALVAPRKT	KPPLPSVRIL	AEDRWNPQK	TRDPRESHTM	NGC.
A_SE_SE725	LKALVTPTRT	KPPLPSVRKL	AEDRWSKPQK	TRGHRGSHTM	NGC.
A_SE_SE753	LKALVTPKKT	RPPLPSVRIL	AEDRWNSRK	TRGPRGSHTM	NGC.
A_SE_SE853	LKALVTPKKI	KPPLPSVKKL	TEDRWNPQK	TRGHRGNHTM	HGY.
A_SE_SE889	LKALVTPKKI	RPPLPSVRKL	AEDRWNPQK	TKGHRGSHTM	NGH.
A_SE_UGSE8	LKALVTPKRT	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGC.
A_UG_92UG0	LKALVTPSRM	KPPLPSVKKL	AEDRWNPQK	TRGRRESHTM	NGC.
A_UG_U455	LKALVTPTRA	KPPLPSVKKL	TEDRWNPQK	TRGHRGSRTL	NRH.
AC_IN_2130	LTALIKPKKR	KPPLPSIRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
AC_RW_92RW	LTALIKPKKI	KPPLPSVSKL	VEDKWNKPQK	TRGRRGNHTM	NGH.
AC_SE_SE94	LTALIKPKKI	KPPLPSVRKL	VEDKWNKPQK	TRGRRGNHTM	NGH.
ACD_SE_SE8	LKALVTPTRV	KPPLPSVRKL	AEDRWSKSQK	TRGLRGSHTM	NGC.
ACG_BE_VI1	LKALVTPQI	RPPLPSVRKL	TEDRWNPQK	TRGHRGNHTM	NGH.
AD_SE_SE69	LTALITPKKE	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
AD_SE_SE71	LKALVTPTKT	KPPLPSVRIL	TEDRWNPQK	TRGLRESHTM	NGC.
ADHK_NO_97	LTALVAPKKI	KPPLPSIKKL	AEDRWNPQK	TRGHRGSHTM	NGC.
ADK_CD_MAL	LTALIAPKKT	RPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
AG_BE_VI11	LKALVTPTRI	RPPLPSVRKL	TEDRWNPQK	TRGHRGSHTM	NGQW
AG_NG_92NG	LKALVTPQT	KPPLPSVKKL	TEDRWNPQK	TRGHRGSHTM	NGH.
AGHU_GA_VI	LKALVTPTRE	RPPLPSVQKL	TEDRWNPQK	TKDHRGSHTM	NGC.
AGU_CD_Z32	LTALITPKKT	KPPLPSVKKL	VEDRWNPQK	TRGHRENQTM	NEH.
AJ_BW_BW21	LKAILKTEKR	KPPLPSVQKL	VEDRWNPQK	TRGHRESHTM	NGH.
B_AU_VH_AF	LAALITPRQT	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	SGH.
B_CN_RL42	LTALITPKNR	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	SGH.
B_DE_D31_U	LAALITPKKI	KPPLPSVAKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_DE_HAN_U	LAALITPKKI	KPPLPIVTKL	TEDRWNPQK	TKGHRGSHTM	HGH.
B_FR_HXB2	LAALITPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GA_OYI	LAALIKPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GB_CAM1	LTALIAPKKI	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GB_GB8_A	LTALITPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_GB_MANC	LAALITPKKT	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_KR_WK_AF	LTALITPKKI	KPPLPSVRKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_NL_3202A	LAALIKPKKI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_TW_TWCYS	LTALVQPKKI	KPPLPSVVKL	TEDRWNPQK	TKGHRGSHTM	HGH.
B_US_BC_L0	LAALITPKRI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_DH123	LAALVTPRKI	KPPLPSVAKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_JRCSE	LTALIKPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_MNCG	LTALITPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTI	NGH.
B_US_P896	LAALITPRRI	KPPLPSVTKL	TEDRWNPQK	TKGHRGSHTM	TGH.
B_US_RF_M1	LAALITPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_SF2_K	LAALITPKKT	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_WEAU1	LTALITPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.
B_US_WR27	LTALIKPKKI	KPPLPSVKKL	TEDRWNPQK	TKGHRGSHTM	NGH.

B_US_YU2_M	LTALITPKKT	KPPLPSVKKL	TEDRWNPQK	TKGHRGSRTM	NGH.
BF1_BR_93B	LTALIKPKKR	KPPLPSVKKL	TEDRWNPQK	TKDHRGSHTM	NGH.
C_BR_92BR0	LTALIKPKKI	KPPLPSVKKL	VEDRWNPQK	TRDRRGNHTM	NGH.
C_BW_96BW0	LTALIKPKKR	KPPLPSVRKL	VEDRWNEPQK	TRGRRGNHTM	NGH.
C_BW_96BW1	LTALIKPKKI	KPPLPSVRKL	VEDRWNPQK	TRGRRGNHTM	NGH.
C_BW_96BW1	LTALIKPKKR	KPPLPSVRKL	VEDRWNPQK	TRGRKGNHTM	NGH.
C_BW_96BW1	LTALIKPKQI	KPPLPSVRKL	VEDRRNPQK	TRGRRGNRTM	NGH.
C_ET_ETH22	LTALIKPKKA	KPPLPSVSKL	VEDKWNKPQK	TRGRRGNHTM	NGH.
C_IN_93IN1	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRRGNHTM	NGH.
C_IN_93IN9	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRRGNHTM	NGH.
C_IN_93IN9	LTALIKPKKI	KPPLPSVRKL	VEDRWNNPLK	TRGRRGNHTM	NGH.
C_IN_94IN1	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRRGNHTM	NGH.
C_IN_95IN2	LTALIKPKKI	KPPLPSIKKL	VEDRWNNPQK	IRGRKGNHIM	HGH.
CRF01_AE_C	LKALATPKKT	RPPLPSVRKL	TEDRWNPQK	TRGHRENPTM	NGH.
CRF01_AE_C	LKALTCTKKT	KPPLPSVRKL	TEDRWNPQK	TKGHRRESPTM	NGH.
CRF01_AE_C	LKALATPKKI	RPPLPSVRKL	TEDRWNPQK	TRGHRENPTM	SGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSVKKL	TEDRWNPQK	IWGHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	KPPLPSVKKL	TEDRWNPQK	IRDHREYRTM	NGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSVKKL	TEDRWNPQK	IKGHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSVKKL	TEDRWKHQ.	KGDHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	RPPLPSV.EI	TEDRWNPQ.	KRGHRENPTM	NGH.
CRF01_AE_T	LKALTTPKRI	KPPLPSVRKL	TEDRWNEPQK	IRGHREYPTM	NGH.
CRF02_AG_F	LKALVTPAKT	KPPLPSVKKL	AEDRWNPQK	TRGHRGNRSM	NGH.
CRF02_AG_F	LKALVTPVKT	KPPLPSVKKL	AEDRWNPQK	TRGHRGNRSM	NGQ.
CRF02_AG_G	LKALVTPTRK	KPPLPSVRKL	AEDRWNEPQK	TRGHRGSRPM	NGR.
CRF02_AG_N	LNALVAPTKT	KPPLPSVRKL	AEDRWKEPQK	TRGHRGSRPM	NGH.
CRF02_AG_S	LKALVTPTRT	KPPLPSVKKL	AEDRWNEPQK	TRGHRGSRSM	NGH.
CRF02_AG_S	LKALVTPTRR	KPPLPSVKKL	AEDRWNEPQK	TRGHRGNRSM	NGH.
CRF03_AB_R	LAALRTPKKI	KPPLPSVTKL	TEDRWNPQR	TKDHRGSHTM	SGH.
CRF03_AB_R	LAALRTPKKI	KPPLPSVTKL	TEDRWNPQR	TKDHRGSHTM	SGH.
CRF04_cpx_	LAALISPCKT	KPPLPSVKKL	VEDRWNPQK	TRGRRENQIM	NGH.
CRF04_cpx_	LAALISPCKT	KPPLPSVKKL	VEDRWNPQK	TRGRRENQIM	NGH.
CRF04_cpx_	LAALISPCKT	KPPLPSVKKL	VEDRWNSQK	TKGRRESHIM	NGH.
CRF05_DF_B	LTALITPKKT	KPPLPSVRKL	TEDRWNPQK	TKGRRGNHTM	NGY.
CRF05_DF_B	LTALITPQKI	KPPLPSVRKL	TEDRWNPQR	TKGHRGCHTM	NGY.
CRF06_cpx_	LTALIKPEKR	KPPLPSVQKL	VEDRWNPQK	TRGHRESHTM	NGH.
CRF06_cpx_	LTALIKPKKR	KPPLPSVQKL	VEDRWNPQK	TRDHRESHTM	NGH.
CRF06_cpx_	LTALIKPKRR	KPPLPSVQKL	VEDRWNPQK	TRDHRECHTM	NGH.
CRF06_cpx_	LKALVTKRR	KPPLPSVQKL	VEDRWNPQK	TKDHRESHIM	DGH.
CRF11_cpx_	LKALVTPTRA	KPPLPSVRKL	AEDRWNPQK	TRGHRGNHTA	NGC.
CRF11_cpx_	LKALVTPKRT	KPPLPSVRKL	TEDRWNPQK	TRGRRGNHTV	NGC.
D_CD_84ZR0	LTALIAPKKR	KPPLPSVKKL	TEDRWNPQR	TKGRRGSHTM	NGH.
D_CD_ELI_K	LTALIAPQKI	KPPLPSVRKL	TEDRWNPQQ	TRGHRGSHTM	NGH.
D_CD_NDK_M	LAALIAPKKI	KPPLPSVRKL	TEDRWNPQK	TKGRRGSHTM	NGH.
D_UG_94UG1	LTALVTPRKI	KPPLPSVGKL	TEDRWNPQR	TKGHRGSHTM	NGH.
F1_BE_VI85	LTALIAPEKT	KPPLPSVQKL	VEDRWNPQB	TRGHRGSHTM	NGH.
F1_BR_93BR	LTALIAPKKT	KPPLPSVQKL	VEDRWNPQK	TRGHRESHTM	NGH.
F1_FI_FIN9	LTALVSPKKA	KPPLPSVKKL	VEDRWNPQR	IRGHRGSHTM	NGH.
F1_FR_MP41	LTALIAPKKT	KPPLPSVKKL	VEDRWNPQB	TRGHRGSHTM	NGH.
F2_CM_MP25	LTALITPKKI	KPPLPSVRKL	VEDRWNNPQK	TRGHRGSHTM	NGH.
F2KU_BE_VI	LTALVAPKKT	KPPLPSVRKL	VEDRWNPQK	TRDHRGSHTM	NGH.
G_BE_DRCBL	LKVLVAPTRR	RPPLPSVRKL	TEDRWNEPQK	TRGHRENPTM	NGH.
G_NG_92NG0	SKALVTPTRK	RPPLPSVGKL	AEDRWNPQK	TRDHRENPTM	NGH.
G_SE_SE616	LKVLVTSKRS	RPPLPSVTEL	AEDRWNPQK	TRGHRENPTM	NGH.
H_BE_VI991	LTALISPCKT	KPPLPSVRKL	VEDRWNPQK	TRGHRGSHTM	NGH.
H_BE_VI997	LTALVAPKKT	KPPLPSVKKL	VEDGWNKPQK	TRGHRGSHTM	NRH.
H_CF_90CF0	LTALVAPKKI	KPPLPSVRKL	VEDRWNPQK	TRGHRGSHTM	NGH.
J_SE_SE702	LTALIKPKRR	KPPLPSVQKL	VEDRWNPQK	TRDHRESHTM	NGH.
J_SE_SE788	LTALIRPKRR	KPPLPSVQKL	VEDRWNPQK	TTGHRESHTM	NGH.
K_CD_EQTB1	LTALIAPKKT	KPPVPSVQKL	VEDRWNPQK	TRGHRGSHTM	SGQ.

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K_CM_MP535	LTALVAPRRP	KPPVPSVKKL	VEDRWNPQK	TRGHRGSQTM	NGH.
N_CM_YBF30	LTAWVGAKKR	KPPLPSVTKL	TEDRWNEHQK	MQGHRGNPIM	NGH.
O_CM_ANT70	LRAVVKARSR	KPPLPSVQKL	TEDRWNKHLR	IRDQLKSPSM	NGH.
O_CM_MVP51	LKAVVKVKRN	KPPLPSVQRL	TEDRWNPWK	IRDQLGSHSM	NGH.
O_SN_99SE	LRVVVKEKRN	KPPLPSVQKL	TEDRWSRHLR	IRDQLESHSM	NGH.
O_SN_99SE	LRVVVKEKRH	KPPLPSVQKL	TEDRWSRHLR	IRDQLGSHSM	NGH.
U_CD___83C	LTTLVAPTKR	KPPLPSVRKL	VEDRWNPQK	TKGHKGSHTM	HGH.

Table 18. HIV Vpr Sequence Alignment
 GCG Multiple Sequence File.
 Written by Omega 1.1

Name: 00BW0762_1	Len: 100	Check: 8179	Weight: 1.00
Name: 00BW0768_2	Len: 100	Check: 8119	Weight: 1.00
Name: 00BW0874_2	Len: 100	Check: 7661	Weight: 1.00
Name: 00BW1471_2	Len: 100	Check: 6614	Weight: 1.00
Name: 00BW1616_2	Len: 100	Check: 6361	Weight: 1.00
Name: 00BW1686_8	Len: 100	Check: 6014	Weight: 1.00
Name: 00BW1759_3	Len: 100	Check: 6894	Weight: 1.00
Name: 00BW1773_2	Len: 100	Check: 7772	Weight: 1.00
Name: 00BW1783_5	Len: 100	Check: 7149	Weight: 1.00
Name: 00BW1795_6	Len: 100	Check: 7614	Weight: 1.00
Name: 00BW1811_3	Len: 100	Check: 7968	Weight: 1.00
Name: 00BW1859_5	Len: 100	Check: 6222	Weight: 1.00
Name: 00BW1880_2	Len: 100	Check: 6941	Weight: 1.00
Name: 00BW1921_1	Len: 100	Check: 8183	Weight: 1.00
Name: 00BW2036_1	Len: 100	Check: 8175	Weight: 1.00
Name: 00BW2063_6	Len: 100	Check: 8705	Weight: 1.00
Name: 00BW2087_2	Len: 100	Check: 7388	Weight: 1.00
Name: 00BW2127_2	Len: 100	Check: 8282	Weight: 1.00
Name: 00BW2128_3	Len: 100	Check: 1723	Weight: 1.00
Name: 00BW2276_7	Len: 100	Check: 6468	Weight: 1.00
Name: 00BW3819_3	Len: 100	Check: 5670	Weight: 1.00
Name: 00BW3842_8	Len: 100	Check: 7788	Weight: 1.00
Name: 00BW3871_3	Len: 100	Check: 8574	Weight: 1.00
Name: 00BW3876_9	Len: 100	Check: 7285	Weight: 1.00
Name: 00BW3886_8	Len: 100	Check: 6446	Weight: 1.00
Name: 00BW3891_6	Len: 100	Check: 8629	Weight: 1.00
Name: 00BW3970_2	Len: 100	Check: 7113	Weight: 1.00
Name: 00BW5031_1	Len: 100	Check: 5511	Weight: 1.00
Name: 96BW01B21	Len: 100	Check: 7551	Weight: 1.00
Name: 96BW0407	Len: 100	Check: 8226	Weight: 1.00
Name: 96BW0502	Len: 100	Check: 8242	Weight: 1.00
Name: 96BW06_J4	Len: 100	Check: 7544	Weight: 1.00
Name: 96BW11_06	Len: 100	Check: 7942	Weight: 1.00
Name: 96BW1210	Len: 100	Check: 8580	Weight: 1.00
Name: 96BW15B03	Len: 100	Check: 7308	Weight: 1.00
Name: 96BW16_26	Len: 100	Check: 7009	Weight: 1.00
Name: 96BW17A09	Len: 100	Check: 6492	Weight: 1.00
Name: 96BWM01_5	Len: 100	Check: 5837	Weight: 1.00
Name: 96BWM03_2	Len: 100	Check: 5277	Weight: 1.00
Name: 98BWMC12_2	Len: 100	Check: 7807	Weight: 1.00
Name: 98BWMC13_4	Len: 100	Check: 9051	Weight: 1.00
Name: 98BWMC14_a	Len: 100	Check: 7867	Weight: 1.00
Name: 98BWM014_1	Len: 100	Check: 7266	Weight: 1.00
Name: 98BWM018_d	Len: 100	Check: 7638	Weight: 1.00
Name: 98BWM036_a	Len: 100	Check: 7495	Weight: 1.00
Name: 98BWM037_d	Len: 100	Check: 6640	Weight: 1.00
Name: 99BW3932_1	Len: 100	Check: 6974	Weight: 1.00
Name: 99BW4642_4	Len: 100	Check: 6081	Weight: 1.00
Name: 99BW4745_8	Len: 100	Check: 8860	Weight: 1.00
Name: 99BW4754_7	Len: 100	Check: 6856	Weight: 1.00
Name: 99BWMC16_8	Len: 100	Check: 8223	Weight: 1.00

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00BW0762_1	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYNTY
00BW0768_2	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLGEYIYETY
00BW0874_2	MEQPPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
00BW1471_2	MEQPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYETY
00BW1616_2	MEQPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQYIYENY
00BW1686_8	MEQAPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SIGQYIYETY
00BW1759_3	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQHIYETY
00BW1773_2	MEQPPEDQGP	QREPYNEWTL	ELLEELIQEA	VRHFPRPWLH	SLGQYIYETY
00BW1783_5	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SMGQHIYNTY
00BW1795_6	MEQAPEDQGP	QREPYN.ETL	ELLEELKQEA	VRHFPRPWLH	NLQYIYNTY
00BW1811_3	MEQPPEDQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	GLGQYVYETY
00BW1859_5	MEQPPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
00BW1880_2	MEQAPEDQGP	QRELYNEWTL	ELLEELKQEA	ARHFSSSWLH	GLGQHIYNTY
00BW1921_1	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	NLQYIYQTY
00BW2036_1	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLQ	SLGQYIYETY
00BW2063_6	MEQPPEDQGP	QREPYNEWTL	GLLEELKQEA	VRHFPRPWLH	NLQYIYNTY
00BW2087_2	MEQAPEDQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	NLQYIYETY
00BW2127_2	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLQYIYETY
00BW2128_3	MEQPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYETY
00BW2276_7	MEQTPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQYIYDITY
00BW3819_3	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLQYIYETY
00BW3842_8	MEQVPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLQ	GLGHYIYETY
00BW3871_3	MEQVPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLQYIYETY
00BW3876_9	MEQSPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GIGQYIYETY
00BW3886_8	MEQFPEDQGP	QREPYNEWTL	ELLEELKQEA	VKHFPWPWLH	NLQYIYETY
00BW3891_6	MEQPPEDQGP	QREPYNEWTL	EVLEELKQEA	VRHFPRPWLH	SLGQYVYETY
00BW3970_2	MEQPPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQHIYETY
00BW5031_1	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYETY
96BW01B21	MERPPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYETY
96BW0407	MERAPEDQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYETY
96BW0502	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	GLGQYVYETY
96BW06_J4	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
96BW11_06	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYNTY
96BW1210	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQYIYETY
96BW15B03	TEQAPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
96BW16_26	MEQPPEDQGP	QREPYTEWAL	ELLEELKQEA	VRHFPRPWLH	GLGQYIYDITY
96BW17A09	MEQTPEDQGP	QREPHNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQHIYETY
96BWMO1_5	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPR. TLH	DLGQHIYNTY
96BWMO3_2	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	IRHFPIPYLQ	HLGQYIYETY
98BWMC12_2	MEQPPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	SLGQYIYETY
98BWMC13_4	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	NLQYVYNTY
98BWMC14_a	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHLPWPWLH	SLGQHIYETY
98BWMO14_1	MEQAPEDQGP	QREPYNEWTL	ALLEDLKQEA	VRHVPRPWLH	SLGQHIYETY
98BWMO18_d	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGQYIYETY
98BWMO36_a	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	NLQYIYETY
98BWMO37_d	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFLRPWLH	DLGQYIYETY
99BW3932_1	MEQAPEDQGP	QREPYNEWTL	EILEELKQEA	VRHFPRPWLH	NLQYIYATY
99BW4642_4	MEQPPEDQGP	QREPYNEWAL	EILEELKQEA	VRHFPRPWLH	NLQYIYETY
99BW4745_8	MEQPPEDQGP	QREPYNEWTL	EVLEDLKQEA	VRHFPRPWLH	SIGQYVYSTY
99BW4754_7	MEQAPENQGP	QREPYNEWAL	ELLEELKQEA	VRHFPRPWLH	DLGQHIYNTY
99BWMC16_8	MEQAPEDQGP	QREPYNEWTL	ELLEELKQEA	VRHFPRPWLH	SLGLYIYETY

	51				100
00BW0762_1	GDTWTGVEAI	IRILQQLLFI	HFRIGCQHSR	IGIMRQ....	RRTRNGASRS
00BW0768_2	GDTWTGVEAL	IRVLQQLLFI	HFRIGCSHSR	IGIVRQ....	RRARNGSSRS
00BW0874_2	GDTWTGVETI	IRTLQQLLFI	HFRIGCQHSR	IGILRQ....	KRARNGASRS
00BW1471_2	GDTWAGVEAL	LRILQQLLFI	HFRIGCQHSR	IGIIPQ....	RRARNGSRRS
00BW1616_2	GDTWAGVEAI	TRILQQLLFI	HFRIGCQHSR	IGILRQ....	RRARNGANRS
00BW1686_8	GDTWTGVEAL	MRILQQLLFI	HFRIGCQHSR	IGILQR....	R.ARNGASRS

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00BW1759_3 GDTWTGVEAI IRILQQLLFI HYRIGCQHSR IGIVRQ.... RRARNGANRS
00BW1773_2 GDTWTGVEAI IKILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGASRS
00BW1783_5 GDTWAGVEAI IRILQQLLFI HFRIGCQHSR IGILRQ.... RRTRNGASRS
00BW1795_6 GDTWTGVEAI IRTLQQLLFV HFRIGCQHSR IGIMRQ.... RRARNGTSGS
00BW1811_3 GDTWTGVEAI IRILQQLLFV HFRIGCQHSR IGILQQ.... RRARNGASRS
00BW1859_5 GDTWAGVEAL IRILQQLLFI HFRIGCQHSR IGILQQ.... RRARNGASRS
00BW1880_2 GDTWTGVEVL IRILQQLLFI HFRIGCQHSR IGIIRQ.... RRTRNGASRP
00BW1921_1 GDTWTGVEAL IRILQQLLFI HFRIGCQHSR IGITLP.... RRARNGANRS
00BW2036_1 GDTWTGVEAI IRILQQLLFI HFRSGCAHSR IGITLP.... RRARNGASRS
00BW2063_6 GDTWTGVEAI IRILQQLLFI HFRIGCQHSR IGIIRQ.... RRTRNGDSRS
00BW2087_2 GDTWTGVEAL IRILQQLLFT HYRFGCQHSR IGILQQ.... RRARNGANRS
00BW2127_2 GDTWTGVEVI IRILQQLLFI HFRIGCQHSR IGILRQ.... RRTRNGASRS
00BW2128_3 GDTWAGVESL IRLMLQLLFI HFRIGCQHSR IDX.....
00BW2276_7 GDTWAGVEAI IRILQQLLFT HFRIGCHHSR IGILRQ.... RRARNGASRS
00BW3819_3 GDTWAGVEAL LRILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGASRP
00BW3842_8 GDTWTGVETI IRILQQLLFI HFRIGCSRSR IGPMRQ.... RRARNGASRS
00BW3871_3 GDTWTGVEAL LRVLQQLLFV HFRIGCQHSR IGILQQ.... RRARNGSSRS
00BW3876_9 GDTWTGVEAI IRILQQLLFI HYRIGCAHSR IGIVRQ.... RRARNGANRS
00BW3886_8 GDTWTGVEAI IRLMLQLLFI HFRIGCQHSR IGILRQ.... RRARNGANRS
00BW3891_6 GDTWTGVEAL IRLMLQLLFI HFRIGCQHSR IGILRR.... RRARNGASRS
00BW3970_2 GDTWTGVEAL IRILQQLLFI HFRIGCQHSR IGIILQ.... RRTRNGASRS
00BW5031_1 GDTWMGVEAL IRILQ.... HFRIGCQHSR IGIILQ.... RRTRNGASRS
96BW01B21 GDTWTGVENM IRILQQLLFV HFRIGCQHSR IGILQQ.... RRARNGASRS
96BW0407 GDTWTGVEAL IRTLQQLLFI HFRIGCQHSR IGILRQ.... RRVRNGTNRS
96BW0502 GDTWTGVETL IRILQQLLFI HFRIGCQHSR IGILRQ.... RRTRNGASRS
96BW06_J4 GDTWTGVETI IRILQQLLFI HFRIGCQHSR IGILQQ.... RRARNGASRP
96BW11_06 GDTWTGVEAI IRILQQLLFI HFRIGCQHSR IGIIRQ.... RRTRNGASRP
96BW1210 GDTWTGVEVL TRILQQLLFI HFRIGCQHSR IGILRQ.... RRTRNGASRS
96BW15B03 GDTWTGVEAI IRILQQLLFI HFRIGCLHSR IGIMRQ.... RRARNGASRS
96BW16_26 GDTWTGVEIK IRILQQLLFI HFRIGCQHSR IGILQQ.... RRARNGARRS
96BW17A09 GDTWAGVEAL LRILQQLLFI HFRIGCHHSR IGITPQ.... RRARNGSSRS
96BWMO1_5 GDTWTGVEAI TRILQQLLFI HYRIGCQHSR IGIMRQ.... RRARNGASRS
96BWMO3_2 GDTWAGVLAI IRILQQLLFI HFRIGCSHSR IGIWR.... RRARNGASRS
98BWMC12_2 GDTWTGVEAI LRILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGASRS
98BWMC13_4 GDTWTGVEAI IRILQQLLFI HFRIGCQHSR IGILRQ.... RRTRNGASRS
98BWMC14_a GDTWTGVEAI IRILQQLLFI HFRIGCQHSR IGILPR.... RRARNGSSRS
98BWMO14_1 GDTWTGVEAI IRILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGANRS
98BWMO18_d GDTWTGVEVI IRILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGANRS
98BWMO36_a GDTWTGVEAL IRTLQQLLFI HFRIGCQHSR IGILRQ.... RRARNGASRS
98BWMO37_d GDTWTGVETI IRVLQQLLFI HFRIGCH.SR IGIVRQ.... RRARNGASRS
99BW3932_1 GDTWMGVEAL LRILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGASRS
99BW4642_4 GDTWAGVEAI IRVLQQLLFI HFRIGCHHSR IGIMQQ.... RRARNGASRS
99BW4745_8 GDTWTGVEAL MRILQQLLFI HFRIGCRHSR IGILRQ.... RGARNGASRS
99BW4754_7 GDTWTGVEAI IRILQQLLFI HFRIGCHHSR IGIIRQ.... RRTRNGASRP
99BWMC16_8 GDTWTGVEVI IRILQQLLFI HFRIGCQHSR IGILRQ.... RRARNGPSRS

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Table 19. HIV Vpu Sequence Alignment
 GCG Multiple Sequence File.
 Written by Omega 1.1

Name: 00BW0762_1	Len: 106	Check: 4772	Weight: 1.00
Name: 00BW0768_2	Len: 106	Check: 7115	Weight: 1.00
Name: 00BW0874_2	Len: 106	Check: 7209	Weight: 1.00
Name: 00BW1471_2	Len: 106	Check: 7341	Weight: 1.00
Name: 00BW1616_2	Len: 106	Check: 3870	Weight: 1.00
Name: 00BW1686_8	Len: 106	Check: 8787	Weight: 1.00
Name: 00BW1759_3	Len: 106	Check: 7584	Weight: 1.00
Name: 00BW1773_2	Len: 106	Check: 7507	Weight: 1.00
Name: 00BW1783_5	Len: 106	Check: 7874	Weight: 1.00
Name: 00BW1795_6	Len: 106	Check: 8721	Weight: 1.00
Name: 00BW1811_3	Len: 106	Check: 3657	Weight: 1.00
Name: 00BW1859_5	Len: 106	Check: 6137	Weight: 1.00
Name: 00BW1880_2	Len: 106	Check: 5827	Weight: 1.00
Name: 00BW1921_1	Len: 106	Check: 4605	Weight: 1.00
Name: 00BW2036_1	Len: 106	Check: 6145	Weight: 1.00
Name: 00BW2063_6	Len: 106	Check: 7187	Weight: 1.00
Name: 00BW2087_2	Len: 106	Check: 9545	Weight: 1.00
Name: 00BW2127_2	Len: 106	Check: 4898	Weight: 1.00
Name: 00BW2276_7	Len: 106	Check: 7311	Weight: 1.00
Name: 00BW3819_3	Len: 106	Check: 4879	Weight: 1.00
Name: 00BW3842_8	Len: 106	Check: 1804	Weight: 1.00
Name: 00BW3871_3	Len: 106	Check: 6650	Weight: 1.00
Name: 00BW3876_9	Len: 106	Check: 6684	Weight: 1.00
Name: 00BW3886_8	Len: 106	Check: 8701	Weight: 1.00
Name: 00BW3891_6	Len: 106	Check: 8544	Weight: 1.00
Name: 00BW3970_2	Len: 106	Check: 9375	Weight: 1.00
Name: 00BW5031_1	Len: 106	Check: 7778	Weight: 1.00
Name: 96BW01B21	Len: 106	Check: 6481	Weight: 1.00
Name: 96BW0407	Len: 106	Check: 4225	Weight: 1.00
Name: 96BW0502	Len: 106	Check: 5292	Weight: 1.00
Name: 96BW06_J4	Len: 106	Check: 5367	Weight: 1.00
Name: 96BW11_06	Len: 106	Check: 6477	Weight: 1.00
Name: 96BW1210	Len: 106	Check: 6400	Weight: 1.00
Name: 96BW15B03	Len: 106	Check: 2981	Weight: 1.00
Name: 96BW16_26	Len: 106	Check: 5352	Weight: 1.00
Name: 96BW17A09	Len: 106	Check: 6778	Weight: 1.00
Name: 96BWM01_5	Len: 106	Check: 5954	Weight: 1.00
Name: 96BWM03_2	Len: 106	Check: 6334	Weight: 1.00
Name: 98BWMC12_2	Len: 106	Check: 6905	Weight: 1.00
Name: 98BWMC13_4	Len: 106	Check: 7458	Weight: 1.00
Name: 98BWMC14_a	Len: 106	Check: 4023	Weight: 1.00
Name: 98BWM014_1	Len: 106	Check: 5708	Weight: 1.00
Name: 98BWM018_d	Len: 106	Check: 7741	Weight: 1.00
Name: 98BWM036_a	Len: 106	Check: 5445	Weight: 1.00
Name: 98BWM037_d	Len: 106	Check: 8225	Weight: 1.00
Name: 99BW3932_1	Len: 106	Check: 1112	Weight: 1.00
Name: 99BW4642_4	Len: 106	Check: 8891	Weight: 1.00
Name: 99BW4745_8	Len: 106	Check: 3424	Weight: 1.00
Name: 99BW4754_7	Len: 106	Check: 5468	Weight: 1.00
Name: 99BWMC16_8	Len: 106	Check: 6656	Weight: 1.00
Name: A2_CD_97CD	Len: 106	Check: 6086	Weight: 1.00
Name: A2_CY_94CY	Len: 106	Check: 4609	Weight: 1.00
Name: A2D_97KR	Len: 106	Check: 2120	Weight: 1.00
Name: A2G_CD_97C	Len: 106	Check: 4405	Weight: 1.00
Name: A_BY_97BL0	Len: 106	Check: 913	Weight: 1.00
Name: A_KE_Q23_A	Len: 106	Check: 3380	Weight: 1.00

Name: A_SE_SE659	Len: 106	Check: 4192	Weight: 1.00
Name: A_SE_SE725	Len: 106	Check: 3244	Weight: 1.00
Name: A_SE_SE753	Len: 106	Check: 1918	Weight: 1.00
Name: A_SE_SE853	Len: 106	Check: 5495	Weight: 1.00
Name: A_SE_SE889	Len: 106	Check: 5422	Weight: 1.00
Name: A_SE_UGSE8	Len: 106	Check: 4254	Weight: 1.00
Name: A_UG_92UG0	Len: 106	Check: 4081	Weight: 1.00
Name: A_UG_U455_	Len: 106	Check: 2987	Weight: 1.00
Name: AC_IN_2130	Len: 106	Check: 7929	Weight: 1.00
Name: AC_RW_92RW	Len: 106	Check: 5133	Weight: 1.00
Name: AC_SE_SE94	Len: 106	Check: 7394	Weight: 1.00
Name: ACD_SE_SE8	Len: 106	Check: 1852	Weight: 1.00
Name: ACG_BE_VI1	Len: 106	Check: 6357	Weight: 1.00
Name: AD_SE_SE69	Len: 106	Check: 5734	Weight: 1.00
Name: AD_SE_SE71	Len: 106	Check: 4697	Weight: 1.00
Name: ADHK_NO_97	Len: 106	Check: 6301	Weight: 1.00
Name: ADK_CD_MAL	Len: 106	Check: 4338	Weight: 1.00
Name: AG_BE_VI11	Len: 106	Check: 3500	Weight: 1.00
Name: AG_NG_92NG	Len: 106	Check: 4859	Weight: 1.00
Name: AGHU_GA_VI	Len: 106	Check: 6173	Weight: 1.00
Name: AGU_CD_Z32	Len: 106	Check: 9411	Weight: 1.00
Name: AJ_BW_BW21	Len: 106	Check: 6158	Weight: 1.00
Name: B_AU_VH_AF	Len: 106	Check: 5007	Weight: 1.00
Name: B_CN_RL42_	Len: 106	Check: 4249	Weight: 1.00
Name: B_DE_D31_U	Len: 106	Check: 4572	Weight: 1.00
Name: B_DE_HAN_U	Len: 106	Check: 6819	Weight: 1.00
Name: B_FR_HXB2_	Len: 106	Check: 5240	Weight: 1.00
Name: B_GA_OYI_M	Len: 106	Check: 5651	Weight: 1.00
Name: B_GB_CAM1_	Len: 106	Check: 5359	Weight: 1.00
Name: B_GB_GB8_A	Len: 106	Check: 1955	Weight: 1.00
Name: B_GB_MANC_	Len: 106	Check: 6521	Weight: 1.00
Name: B_KR_WK_AF	Len: 106	Check: 2320	Weight: 1.00
Name: B_NL_3202A	Len: 106	Check: 4510	Weight: 1.00
Name: B_TW_TWCYS	Len: 106	Check: 5491	Weight: 1.00
Name: B_US_BC_L0	Len: 106	Check: 3142	Weight: 1.00
Name: B_US_DH123	Len: 106	Check: 4669	Weight: 1.00
Name: B_US_JRCSE	Len: 106	Check: 4070	Weight: 1.00
Name: B_US_MNCG_	Len: 106	Check: 3291	Weight: 1.00
Name: B_US_P896_	Len: 106	Check: 2280	Weight: 1.00
Name: B_US_RF_M1	Len: 106	Check: 3104	Weight: 1.00
Name: B_US_SF2_K	Len: 106	Check: 3857	Weight: 1.00
Name: B_US_WEAU1	Len: 106	Check: 3817	Weight: 1.00
Name: B_US_WR27_	Len: 106	Check: 3329	Weight: 1.00
Name: B_US_YU2_M	Len: 106	Check: 5184	Weight: 1.00
Name: BF1_BR_93B	Len: 106	Check: 3243	Weight: 1.00
Name: C_BR_92BR0	Len: 106	Check: 7645	Weight: 1.00
Name: C_BW_96BW0	Len: 106	Check: 5235	Weight: 1.00
Name: C_BW_96BW1	Len: 106	Check: 6477	Weight: 1.00
Name: C_BW_96BW1	Len: 106	Check: 6400	Weight: 1.00
Name: C_BW_96BW1	Len: 106	Check: 2981	Weight: 1.00
Name: C_ET_ETH22	Len: 106	Check: 8303	Weight: 1.00
Name: C_IN_93IN1	Len: 106	Check: 8376	Weight: 1.00
Name: C_IN_93IN9	Len: 106	Check: 6231	Weight: 1.00
Name: C_IN_93IN9	Len: 106	Check: 7626	Weight: 1.00
Name: C_IN_94IN1	Len: 106	Check: 6889	Weight: 1.00
Name: C_IN_95IN2	Len: 106	Check: 8199	Weight: 1.00
Name: CRF01_AE_C	Len: 106	Check: 4437	Weight: 1.00
Name: CRF01_AE_C	Len: 106	Check: 4082	Weight: 1.00
Name: CRF01_AE_C	Len: 106	Check: 3725	Weight: 1.00
Name: CRF01_AE_T	Len: 106	Check: 3201	Weight: 1.00

Name: CRF01_AE_T	Len: 106	Check: 3137	Weight: 1.00
Name: CRF01_AE_T	Len: 106	Check: 3484	Weight: 1.00
Name: CRF01_AE_T	Len: 106	Check: 3491	Weight: 1.00
Name: CRF01_AE_T	Len: 106	Check: 2300	Weight: 1.00
Name: CRF01_AE_T	Len: 106	Check: 2481	Weight: 1.00
Name: CRF02_AG_F	Len: 106	Check: 2748	Weight: 1.00
Name: CRF02_AG_F	Len: 106	Check: 4618	Weight: 1.00
Name: CRF02_AG_G	Len: 106	Check: 400	Weight: 1.00
Name: CRF02_AG_N	Len: 106	Check: 5979	Weight: 1.00
Name: CRF02_AG_S	Len: 106	Check: 5296	Weight: 1.00
Name: CRF02_AG_S	Len: 106	Check: 4213	Weight: 1.00
Name: CRF03_AB_R	Len: 106	Check: 952	Weight: 1.00
Name: CRF03_AB_R	Len: 106	Check: 431	Weight: 1.00
Name: CRF04_cpx_	Len: 106	Check: 6986	Weight: 1.00
Name: CRF04_cpx_	Len: 106	Check: 8606	Weight: 1.00
Name: CRF04_cpx_	Len: 106	Check: 5826	Weight: 1.00
Name: CRF05_DF_B	Len: 106	Check: 5193	Weight: 1.00
Name: CRF05_DF_B	Len: 106	Check: 5092	Weight: 1.00
Name: CRF06_cpx_	Len: 106	Check: 3214	Weight: 1.00
Name: CRF06_cpx_	Len: 106	Check: 3831	Weight: 1.00
Name: CRF06_cpx_	Len: 106	Check: 4862	Weight: 1.00
Name: CRF06_cpx_	Len: 106	Check: 3114	Weight: 1.00
Name: CRF11_cpx_	Len: 106	Check: 4492	Weight: 1.00
Name: CRF11_cpx_	Len: 106	Check: 9106	Weight: 1.00
Name: D_CD_84ZR0	Len: 106	Check: 5829	Weight: 1.00
Name: D_CD_ELI_K	Len: 106	Check: 2669	Weight: 1.00
Name: D_CD_NDK_M	Len: 106	Check: 4007	Weight: 1.00
Name: D_UG_94UG1	Len: 106	Check: 2098	Weight: 1.00
Name: F1_BE_VI85	Len: 106	Check: 4208	Weight: 1.00
Name: F1_BR_93BR	Len: 106	Check: 4525	Weight: 1.00
Name: F1_FI_FIN9	Len: 106	Check: 5556	Weight: 1.00
Name: F1_FR_MP41	Len: 106	Check: 4332	Weight: 1.00
Name: F2_CM_MP25	Len: 106	Check: 5691	Weight: 1.00
Name: F2KU_BE_VI	Len: 106	Check: 4047	Weight: 1.00
Name: G_BE_DRCBL	Len: 106	Check: 3839	Weight: 1.00
Name: G_NG_92NG0	Len: 106	Check: 825	Weight: 1.00
Name: G_SE_SE616	Len: 106	Check: 4456	Weight: 1.00
Name: H_BE_VI991	Len: 106	Check: 2728	Weight: 1.00
Name: H_BE_VI997	Len: 106	Check: 3468	Weight: 1.00
Name: H_CF_90CF0	Len: 106	Check: 5568	Weight: 1.00
Name: J_SE_SE702	Len: 106	Check: 4413	Weight: 1.00
Name: J_SE_SE788	Len: 106	Check: 3659	Weight: 1.00
Name: K_CD_EQTB1	Len: 106	Check: 4999	Weight: 1.00
Name: K_CM_MP535	Len: 106	Check: 4729	Weight: 1.00
Name: N_CM_YBF30	Len: 106	Check: 8961	Weight: 1.00
Name: O_CM_ANT70	Len: 106	Check: 7210	Weight: 1.00
Name: O_CM_MVP51	Len: 106	Check: 8490	Weight: 1.00
Name: O_SN_99SE_	Len: 106	Check: 726	Weight: 1.00
Name: O_SN_99SE_	Len: 106	Check: 9615	Weight: 1.00
Name: U_CD_83C	Len: 106	Check: 6063	Weight: 1.00

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50

00BW0762_1MI	ELIAAVDYRI	GVA.ALIIAL	IIAIVVWTIA	YIEYRKLKQ
00BW0768_2ML	ELTARVDYRL	GVG.ALIVAI	ILAIVVWIWA	YIEYKELLRQ
00BW0874_2ML	GLSEKAGYAL	GVG.ALIVAL	IIVIVVWTIV	YIEYRKLVRQ
00BW1471_2MI	NLLERVDX..	GVG.ALGIAL	IIVIVVWTIV	YIEYRKLVRQ
00BW1616_2MLDLDYKV	AVG.AFTVAL	ILAIVVWILV	YREYRKLRLQ
00BW1686_8	...MEDVILS	FIA.KIDYRI	GIA.AIIVAL	ILAIIVWTIV	YIEYRKLVRQ
00BW1759_3MID	LSA.RVDYRI	GVA.AFIIAL	IIAIVVWTIV	YIEYRKLRLQ
00BW1773_2	MLKLATIVDY	ILAAKVDYRV	GIG.ALIAAL	IITIVVWIIV	YREYRKLRLQ

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00BW1783_5 ... IVDVIFS LTD.RVDYRI AVA.ALTIAL IIAIVVWTIV YIEYRKLVRQ
00BW1795_6 .....MVD WTKXKVDYRI AVV.AFIVAL IIAIVVWTIV YIEYRKLVRQ
00BW1811_3 .....MLAIDYSL GVG.ALLVAL FIAIID.... ...RKLVRQ
00BW1859_5 .....ML ELTARVDYRL GVG.ALIVAL IIAIVVWTIA SLEYRKLVRQ
00BW1880_2 .....MLS LMT.RVDYRI AVA.AFIVAL ILAIVVWTIA YLEYRKLVRQ
00BW1921_1 .....MLD LAA.IVDYRI TIV.AFAIAL FIAIVVWTIA YLEYRKLVRQ
00BW2036_1 .....ML DLIAKVDYRV GIG.ALIVAL IIAVVVWIIA YIEYRKLVRQ
00BW2063_6 .....MID WTE.QVDYRI AIVXSFIVAL IIAIVVWTIA YIEYRKLVRQ
00BW2087_2 .....ML SLIERIDYRL GVG.ALIVAL IIVVIVWTIV YIEYRKLVRQ
00BW2127_2 .....ML DLAARVDYRL GVG.ALVAL IIAIVVWTIV YIEYRKLVRQ
00BW2276_7 .....M VDLGRVDYRL GVG.ALIVAL IIAIVVWIIV YIEYRKLVRQ
00BW3819_3 .....ML DLLTRVDYRL GVG.ALIVAL IIAIVVWTIA YIEYRKLVRQ
00BW3842_8 .....MF DLLAGVDYRL GVG.ALIAL IIAIVVWVIA YIEYKWLVRQ
00BW3871_3 .....MVD LLE.KVDYRI GIA.AFTVAL LIAIVVWIIA YIEYRKLVRQ
00BW3876_9 .....M LDLTQIGYEL GIG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
00BW3886_8 .....MLAARDYRL GVG.ALTVAL ILVIVVWTIV YIEYRKLVRQ
00BW3891_6 .....ML DLLAGVDYRI GVG.AFLVAL SIAIVVWTIV YIEYRKLVRQ
00BW3970_2 .....MF SLLERIDYRL GVG.ALLVAL IIAIVVWAIV YIEYRKLVRQ
00BW5031_1 .....M FALFEVDYRL TIG.AFIVAL FLAIVVWTIA YIEYRKLVRQ
96BW01B21 .....ML ELIAKIDYRL GGG.ALIVAL SIAIVVWIIA YIEYKLLVRQ
96BW0407 .....ML SLAA.IDYRI GVG.AFVVAL IIAIVVWIIV YIEYRKLVRQ
96BW0502 .....MI NFLAKVDYRL GVG.ALIVAF IIAIVVWIIA YIEYRKLVRQ
96BW06_J4 .....MID LLA.RVDYRI GLA.AFVVAL LIAIVVWTIV YIEYRKLVRQ
96BW11_06 .....MVD LLA.KVDYKI AVA.AFIAL IIAIVVWIIV YVEYRKLVRQ
96BW1210 .....ML YLLEKVDYRL GVG.ALIAL IIAIVVWTIA YIEYRKLVRQ
96BW15B03 .....MVN FLAAKVDYRL GVG.ALIVAL IIAIVVWSIV YIEYKLLVRQ
96BW16_26 .....MF SLLAKVDYRV GVG.ALIVAL IIAIVVWIIV YIEYRKLVRQ
96BW17A09 .....ML NLLAKVDYRL GVG.ALIVAL IIAIVVWIIA YIEYRKLVRQ
96BWMO1_5 .....MID WTA.RVDYRV AVV.AFIVAL ILAIVVWIIA YIEYRKLVRQ
96BWMO3_2 .....ML SLAALVDYRL GVG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
98BWMC12_2 .....MV VLGEKEIYIL GIG.ALIVAL IIAIVVWSIA YIEYRKLVRQ
98BWMC13_4 .....MSN WTA.RVDYRI AIA.AFIVAL IIAIVVWTIV YIEYRKLVRQ
98BWMC14_a .....MLD LTE.GVDYRI GIA.AFAVAL FIAIVVWIIV YIEYRKLVRQ
98BWMO14_1 .....ML ELLEKVDYKI TVA.AFIVAL IIAIVVWTIA YIEYRKLVRQ
98BWMO18_d .....ML DLIARVDYRL GVG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
98BWMO36_a .....ML AFLARVDYRL GVG.AFIAL IIAIVVWTIA YIEYRKLVRQ
98BWMO37_d .....ML NLVARVDYRL GVG.ALIVAL IIAIVVWTLV YIEYRKLVRQ
99BW3932_1 .....MLLENIDYRL GVG.ALIVAL IIVVIVWTIV YIEYRKLVRQ
99BW4642_4 .....MLD LMTARVDYRL GVG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
99BW4745_8 .....MI NLIARVDYRL GVG.ALIAL IIAIVVWTIA YIEYRKLVRQ
99BW4754_7 .....ML.ELDYRI GIA.AFIAL IIAIVVWTIV YIEYRKLVRQ
99BWMC16_8 .....MF NLAARVDYRL GVG.ALVIAG IIAIVVWTIV YIEYRKLVRQ
A2_CD_97CD .....MSPLAILS IVG..LVVAS ILAIVVWTVV FIEYRKLVRQ
A2_CY_94CY .....MLPLVILA IVG..LIVAL ILAIVVWTIV FIEYRKLVRQ
A2D_97KR .....MNSLQILS IVG..LIVAF ILAVVWTVV FIEYRKLVRQ
A2G_CD_97C .....MQALEISA IVG..LIVAF IAATVWTVV YIEYRKLVRQ
A_BY_97BL0 .....MTPLXIYA IVA..LVVVF VIXXVWTVV GIXYXLLKQ
A_KE_Q23_A .....MSPLEISA IVG..LIVAL ILAIVVWTIV GIEYKLLVRQ
A_SE_SE659 .....MQSLVILA IVA..LVVVL IIAIVVWTIV FIEWGRLVRQ
A_SE_SE725 .....MLPLSTIWA IIG..LIVAL ILAIVVWTIV GIEYKLLVRQ
A_SE_SE753 .....MIPLQIWA IAG..LIVAL ILAIAWTIV GIEYKLLVRQ
A_SE_SE853 .....MSA LEISALEIWS IVG..LVVAL ILAIVVWTIV GIECKRLVRQ
A_SE_SE889 .....MTPLEIWA IVG..LVVVS IIAIVVWTIV GIEYKLLVRQ
A_SE_UGSE8 .....MSPLEIWA IVG..LIVAL ILAIVVWTIV GLEYKLLVRQ
A_UG_92UG0 .....MQLLEICA VVG..LVVAL IIAIVVWTIV GIEYKLLVRQ
A_UG_U455 .....MTPLEIWA ITG..LIVAL ILAIVVWTIV GIE.KKLLVRQ
AC_IN_2130 .....MLNLNYEL AVG.ALIVAL IIAIVVWTIV YVEYRKLVRQ
AC_RW_92RW .....MTSLEIYA IVA..LIVAL IIVVIVWTLA GIEYKLLVRQ
AC_SE_SE94 .....ML DLLAEIDYRI GVG.AFIAL IIAVVVWIIA YIEYRKLVRQ
ACD_SE_SE8 .....MQPLEICS IVG..LIVAI ILAIAWTIV GIEYKLLVRQ

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ACG_BE_VI1 .....ML ELLAQVDYRI GVG.ALILAL FIAIVVWIIA YLEYRKLVRQ
AD_SE_SE69 ..... ..MQSLVILS IVA..LVVAL VIAIVVWTIV FIEYRRRLERQ
AD_SE_SE71 ..... ..MLSLHICA IVG..LLVAL IIAIVVWTIV GIEYKRLLRQ
ADHK_NO_97 ..... ..MYILGI GIG.ALIVAF IIVIVVWTIV YLEYRKLVRQ
ADK_CD_MAL ..... ..IQPLVILA IVA..LVVTL IIAIVVWTIV FIEIRKIRRO
AG_BE_VI11 ..... ..MQSLEIAA VVG..LVVAF IAAIIVWTIV FIEYRKIRKQ
AG_NG_92NG ..... ..MQSLEIAA IAG..LVVAA IAAIVVWTI. ....KIKKQ
AGHU_GA_VI ..... ..MYILGI GIG.ALVAF IIAIVVWTIA YIEYRKLRLRQ
AGU_CD_Z32 ..... ..MQFLEIAS IVG..LVVAV LAAIVVW... ..IEYRKIRKE
AJ_BW_BW21 ..... ..MRPLQIAA IVG..VIVAI FLAIVVWTIV YIEYRKLVRQ
B_AU_VH_AF ..... ..MQSLQIVA IVA..LVVVT IIAIVVWTIV FIEYRRILRQ
B_CN_RL42 ..... ..MQALTILA IVA..LVVVA IIAIVVWTIV LLEYRKILRQ
B_DE_D31_U ..... ..MQSLQVAA IVA..LVVVA IIAIVVWTIV FIEYRKILRQ
B_DE_HAN_U ..... ..MLSLQIAA IVA..LVVAA IIVIVVWTIV VIEYRKLRLRQ
B_FR_HXB2 ..... ..TQPIPIVA IVA..LVVAI IIAIVVWSIV IIEYRKILRQ
B_GA_OYI_M ..... ..IYSLQILA IVA..LVVVT IIAIVVWTIV LLEYRKILRQ
B_GB_CAM1 ..... ..MLPLQIA IVA..LVVVA IIAIVVWTIV FIEYRKIRRO
B_GB_GB8_A ..... ..IQILT IVA..LVVAG IVAIVVWIIV FIEYRKILKK
B_GB_MANC ..... ..IVSLQIVA IVA..LVVVT IIAIVVWTIV FIEYRKILRQ
B_KR_WK_AF ..... ..MQLLAILA IVG..LVVAA ILAIVVWFIV FIEYKKILKQ
B_NL_3202A ..... ..MQPLVVAA IVA..LVVVA IIAIVVWSIV FIEYRKILRQ
B_TW_TWCYS ..... ..MQPLHILA IVA..LVVAA IIAIVVWTIV LLEYRKILRQ
B_US_BC_L0 ..... ..MQPIQIAA IVA..LVVVG IIAIVVW... ..KILRQ
B_US_DH123 ..... ..MQPLVILA IVA..LVVAL IIVIVVWSIV LIEYRKILRQ
B_US_JRCSE ..... ..MQPLQILA IVA..LVVAG IIAIVVWSIV LIEYRKILRQ
B_US_MNCG ..... ..MQPLVIAA IVA..LVVAG IIAIVVS..IV FIEYRKIRRO
B_US_P896 ..... ..MLSLQILA IVA..LVVAA IIAIVVWSIV FIEYRKILRQ
B_US_RF_M1 ..... ..MQSLEILA IVA..LVVAA ILAIVVWTIV GIEIRKTLRQ
B_US_SF2_K ..... ..MQSLQILA IVS..LVVVA IIAIVVWTIV LIEYRKILRQ
B_US_WEAU1 ..... ..MQSLQILA IVA..LVVAG IIAIVVWSIV LIEYRKILRQ
B_US_WR27 ..... ..MPLYILA VVA..LVVLA IIAIVVWTIV FIEYRKILRQ
B_US_YU2_M ..... ..LQSLQVLA IVA..LVVAT IIAIVVWTIV FIEYRKILRQ
BF1_BR_93B ..... ..MSYLLV IGLAALIAAL IIAIVVWTIA YIEYRELVRQ
C_BR_92BR0 .....ML ELIGRIDYRL GVG.ALIVAL IIVIVVWTIA YIEYRKLVRQ
C_BW_96BW0 .....MI SLAARVDYRI GVG.AFIVAL IIAIVVWTIV YIEYRKLVRQ
C_BW_96BW1 .....MVD LLA.KVDYKI AVA.AFIIAL IIAIVVWIIV YVEYRKLVRQ
C_BW_96BW1 .....ML YLLEKVDYRL GVG.ALIIAL IIAIVVWTIA YIEYRKLVRQ
C_BW_96BW1 .....MVN FLAAKVDYRL GVG.ALIVAL IIAIVVWSIV YIEYKLLKQ
C_ET_ETH22 .....MV DLLAKVDYRI VIV.AFIVAL IIAIVVWTIA YIEYRKLVRQ
C_IN_93IN1 ..... ..MIDLYRL GVG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
C_IN_93IN9 ..... ..MLDLDYKL AVG.ALIVAL IIAIVVWIIA YIEYRKLVRQ
C_IN_93IN9 ..... ..IIDLDYRL GVG.ALIVAF IIAIVVWTIV YIKYRKLVRQ
C_IN_94IN1 ..... ..MLDLKL AVG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
C_IN_95IN2 ..... ..MVNLDYKL GVG.ALIVAL IIAIVVWTIV YIEYRKLVRQ
CRF01_AE_C ..... ..MSALQIA IVG..LIVAL ILAIVVWTIV FIEYKILRQ
CRF01_AE_C ..... ..RLPLHICA IVG..LIVAL IIAIVVWTIV AIEYKILRQ
CRF01_AE_C ..... ..MLPLQISA IVR..LIVAL ILAIVVWTLV AIEYRILR.Q
CRF01_AE_T ..... ..MSPLEISA IVG..LIVAI ILVIVVWTIV AIEFKILRQ
CRF01_AE_T ..... ..MSPLEISA IVG..LIVAL ILAIVVWTIV AIEFKILRQ
CRF01_AE_T ..... ..MHLWKLA IVG..LLVAL ILAIVVWTIV AIEFKILRQ
CRF01_AE_T ..... ..MTPLEISA VVG..LIVVL ILAIVVWTIV GILKKILR.Q
CRF01_AE_T ..... ..MTPLEISA IVG..LIVAL ILAIVVT..IV AIEVKKILRQ
CRF01_AE_T ..... ..MTPLQISA IVG..LIVAL ILAIVVT..IV IIEYKKILKQ
CRF02_AG_F ..... ..MQSLEITA IVG..LVVAF IAAIVVWAIV FIEYRKIRKQ
CRF02_AG_F ..... ..MKSLEIAA IVG..LVVAI IAGIVVWTIV VIEYRKIRKQ
CRF02_AG_G ..... ..MQSLEIAA IVG..LVVAF IAAIVVWIIV YIEYRKIRKQ
CRF02_AG_N ..... ..MQPLTITA IVG..LVVAF IAAIVVWSIV YIEYRKIRKQ
CRF02_AG_S ..... ..MNSLDIVA IVG..LVVAF IAAIVVWTIV YIEYRKIRKQ
CRF02_AG_S ..... ..MQPLAVAA IVG..LVVAF ILAIVVWTIV FIEYRKIRKQ
CRF03_AB_R ..... ..MQSLAIAA IVA..LVVVG IIAIVVGSIV FIEYRKILRQ

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CRF03_AB_RMQFLVIAA	IVA..LVVGG	IIAIVVWSIV	FIEYRKILRQ
CRF04_cpxMLFWEIWA	IVG..LVVAL	IIVIVVWTLV	FIEYKKLRRQ
CRF04_cpxM	SSLSSLEIWT	IVA..LIVAL	IIAIVVWTIV	YIEYKKLQKQ
CRF04_cpxM	SSMSSLQVWA	ITA..LIVAL	IIAIVVWTIA	LIEYRKLLRQ
CRF05_DF_BMSDLLT	IADVVALIVAL	IIAIVVWIIV	YIEYKKLVRQ
CRF05_DF_BMSDLLA	VAIAAFIVAL	IIAIVVWTIV	YIEYKKLVRQ
CRF06_cpxMQALEIAA	IVG..LVVAF	LAAIVVWTIV	FIQYREIRKQ
CRF06_cpxMQSLEISA	IVG..LVVAF	LAAIVVWTIV	FIQYREIRKQ
CRF06_cpxMQPLEISA	VVG..LIVAF	LAAIVVWTIV	YIYREIRKQ
CRF06_cpxMQPLEISA	IVG..LIVAF	LAAIVVWTIV	FILHRQIKKQ
CRF11_cpxMIPLQIAG	IVA..LIVAA	IIVIVVWTIV	FIEYRKLLKQ
CRF11_cpxMITLRTVK	HSS..ISQHL	LIAIVVWTIA	GIEYRRLLRH
D_CD_84ZROMQSLQILA	IVA..LVVAL	IIAIVVWTIV	FIEYRRIKQ
D_CD_ELI_KMQPLGIIA	IAA..LVVAI	IIAIVVWTIV	FIEYRRIKKQ
D_CD_NDK_MMQPLVIIA	IAA..LVVAI	IIAIVVWTIV	YIEYRRIKQ
D_UG_94UG1MQPLEILA	IVA..LVVAL	IIAIVVWTIV	FIECKKLRRQ
F1_BE_VI85MSYLLA	IGIAALIVAL	IIAIVVWTIV	YIEYKKLVRQ
F1_BR_93BRMSNLLA	IGIAALIVAL	IITIVVWTIA	YIEYKKLVRQ
F1_FI_FIN9MSDLLA	ITIVAFIVAL	IIVIVVWTIV	FIEYKKLVRQ
F1_FR_MP41MSNLYV	LSIVAFIALL	IIAIVVWTIV	FIEYKKLLRQ
F2_CM_MP25MSLSLI	VVIAAYIVVL	IIAIVVWTIV	YIEYKKILRQ
F2KU_BE_VIMNL.LL	VGIGALIVAF	IIAIVVWTIA	YIEYRKVLKQ
G_BE_DRCBLMQPLEISA	IVG..LIVAS	IIAIVVWTIV	FIEYRKIRKQ
G_NG_92NGOMQALEIS.LIVAF	IIAIVVWSIV	FIEYRKIRKQ
G_SE_SE616MQSLVILA	IVG..LIVAF	IIAIVVWTIV	FIEYREIRKQ
H_BE_VI991MNILGI	GIG.ALVVAF	IIAIVVWTIA	YIEYRKLK.Q
H_BE_VI997MYIIGI	GIG.ALIVAF	IIAIVVWTIV	YIEYRKLKQ
H_CF_90CF0MYILGL	GIG.ALVVTI	IIAIVVWTIV	YIEYKKLVRQ
J_SE_SE702MVSLQIVA	IVA..LIVAF	FLAICVWTIV	YIEYKKLLRQ
J_SE_SE788MIPLQIAA	IVA..FIVAI	FLAIGMWTIV	YIEYKKLLRQ
K_CD_EQTB1MVPLT	VGIIALVAAL	IIAIVVWTIA	YIEYRKVVVRQ
K_CM_MP535MVSLA	ISIVALVVAL	IIAIVVWTIV	YIEYRKLVKQ
N_CM_YBF30MLSL	LGFIALLCAAV	SIAVIVWALL	YIEYKKIKLQ
O_CM_ANT70MHHRDLA	III..ISALL	FINVILWGF	LRKYLEQKEQ
O_CM_MVP51MHQENLLA	LIA..LSALC	LINVLIWLFN	LRIYLVQRKQ
O_SN_99SEMHHRDLA	LIT..TSALL	LTNVVLWTFI	LRQYLKQKKQ
O_SN_99SEMHHRDLT	LII..ISALL	LTNVILWAFI	LRQYLKQKKQ
U_CD_83CMSILQIVA	IVA..IIVAL	IIAIVVWTIV	YIEYKRLLRQ

51

100

00BW0762_1	KKIDR....L	IKRIIERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD
00BW0768_2	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGQLRLLD
00BW0874_2	RKID....L	IKRIRERAED	SGNESDGD.T	EEL....STM	VDMGNLRLLD
00BW1471_2	KKIDQ....L	VKRIREREED	SGNESDGD.I	EEL....STM	VDMGHLRLLD
00BW1616_2	KRIDN....L	IKRIRERAED	SGNESDGD.T	EEL....STM	VDMGNLRLLD
00BW1686_8	RKIDR....L	IERIKEREED	SGNESEGD.T	EEL....ATM	VDMGQLRLLD
00BW1759_3	RKINW....L	IERIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLH
00BW1773_2	KKIDR....V	LEKIRERAED	SGNESEGD.L	EEL....STL	VDVEHLRLVD
00BW1783_5	RKIDR....L	IERIRERAED	SGNESDGD.Q	EEL....STM	VDMGHLRLLD
00BW1795_6	RKINW....L	IERIRERAED	SGNESDGD.Q	EEL....ATM	VDMGHLRLLD
00BW1811_3	AKIDK....I	IKRIRERAED	SGNESEGD.I	EEL....STM	VDMGHLRLMD
00BW1859_5	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD
00BW1880_2	KKIDW....L	IERIRERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD
00BW1921_1	RKIDR....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGQLRLLG
00BW2036_1	RKIDW....L	IKRIRERAED	SGNESEGD.I	EEL....ATM	VDMGHLRLLD
00BW2063_6	RKIDW....L	IKRIRERAED	SGNESDGD.H	EEL....ATM	VDLGHLRLLD
00BW2087_2	RKLDW....L	VKRIRERAED	SGNESDGD.V	EEL....STM	VDMGHLRLLD
00BW2127_2	RKIDW....L	IKRIGERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD
00BW2276_7	RKIDW....L	VKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHIRLLD
00BW3819_3	RKIDW....L	IKRIREREED	SGNESEGD.T	EEL....AAM	VDMGHLELLG

00BW3842_8 KKIDW....L IERIRERAED NGNESEGD.T EEL....ATM VDMGHLRLLD
 00BW3871_3 RKIDW....L IKRIRERAED SGNESEGD.T EEL....ATM VDMGQLRLLD
 00BW3876_9 RKIDR....L IKRIRERAED SGNESEGD.I EEL....BAI VDMGHLRLLG
 00BW3886_8 RKIDW....L IKRIRERAED SGNESEGD.I EDL....AMV VDMGQLRLLD
 00BW3891_6 KRIDR....L IERIRERAED SGNESEGD.I EEL....STM VDMGHLRLLD
 00BW3970_2 RRLDW....L VKRIRERAED SGNESEGD.N EEL....STV VDLGHLRLLD
 00BW5031_1 RRIDQ....L VKRIRERAED SGNESDGD.T EEL....STM VDMGHLRLLD
 96BW01B21 RRINW....L IERIRERAED SGNESEGD.T EEL....STM VDMGHLRLLD
 96BW0407 RKIDW....L VKRIRERAED SGNESDGD.T EEL....STM VDMGHLRLLD
 96BW0502 RKIDR....L IRKIRERAED SGNESDGD.I EEL....SAM VDVGHLRLLD
 96BW06_J4 RKIDW....L IKRIRERAED SGNESEGD.T EEL....ATM VDMGQLRLLD
 96BW11_06 RKIDW....L IERIRERAED SGNESDGD.H EEL....STM VDMGHLRLLD
 96BW1210 RRIDR....L VERIREREED SGNESEGD.I EEL....STM VDMGHLRLLD
 96BW15B03 KNIDW....L IKRIRERAED SGNESEGD.T EEL....ATM VDMGHLRLLD
 96BW16_26 KKIDR....L IERIRERAED SGNDSEGD.I EDL....STM VDMGHLRLLD
 96BW17A09 RKLDE....L VKRIRERAED SGNESDGD.I EEL....STM VDMGHLRLLD
 96BWM01_5 RKIDC....L IKRIRERAED SGNESDGD.Q EEL....ATM VDMGRLRLLD
 96BWM03_2 RKINW....L VKRIRERAED SGNESEGD.T EEL....ATM VDLHFGLLD
 98BWM012_2 RRIDQ....L IKRIGERAED SGNESDGD.T EEL....STL VDMGHLRLLD
 98BWM013_4 RKIDR....L IKRIRERAED SGNESDGD.Q DEL....ATM VDMGHLRLLD
 98BWM014_a RKIDW....L IERIRERAED SGNESEGD.T EEL....ATM VDMGQLRLLD
 98BWM014_1 RKIDC....L IKRIRERAED SGNESDGD.T EEL....STM VDMGNLRLLD
 98BWM018_d RKIDW....L IKRIRERVED SGNESDGD.T EEL....STL VDMGNLRLLD
 98BWM036_a KKIDR....L IERIRERAED SGNESEGD.T EEL....STM VDMGHLRLLD
 98BWM037_d RKIDQ....L VKRIRERAED SGNESEGD.I EEL....STM VDMGNLRLLD
 99BW3932_1 RKIDW....L IKRIRERAED SGNESEGD.T EEL....ATM VDMGHLRLLD
 99BW4642_4 RRIDW....L IKRIRERAED SGNESEGD.T EEL....ATM VDMGHLRLLD
 99BW4745_8 KKIDW....L IKRIRERAED SGNESEGD.T EGL....STM VDMGHLRLLD
 99BW4754_7 RKIDR....L IERIRERAED SGNESDGD.Q EEL....SAM VDMGHLRLLD
 99BWM016_8 RKINE....I IKRIRERAED SGNESDGD.M EEL....STM VDLGHLGLLD
 A2_CD_97CD RKIDW....L LERISERAED SGNESDGD.T EEL....SKM VGMGNLGFWD
 A2_CY_94CY RKIDW....L IKRISERAED SGNESDGD.T EEL....SAL VERGHLDLFGD
 A2D_97KR NKIDW....L IKRISERAED SGNESEGD.T EEL....STL MEMGNLDFGD
 A2G_CD_97C KRIER....L LDRIGERAED SGNESEGD.A EEL....AKL VEMGGFDPWV
 A_BY_97BL0 RKIDR....L XERXXXRAED SGNESEGD.A XEL....STL MEVXNYALLD
 A_KE_Q23_A RKIDR....L IERIRERAED SGNESDGD.T EEL....STL IDMGDYDLGD
 A_SE_SE659 R.KDR....L IERIRERAED SGNESDGD.T EEL....SAL IEMGNYNLGF
 A_SE_SE725 RKIDK....L VERIRERAED SGNESDGD.T NEL....AAL IEMGNYNLGD
 A_SE_SE753 KEIDG....L VERIAERAED SGNESDGD.T EEL....STL IEMGNYDLGV
 A_SE_SE853 RKIDR....L IERIRERAED SGNESEGD.T EEL....SAL IEMGNYDLGN
 A_SE_SE889 RKIDR....L IRRISERAED SGNESDGD.T DEL....AKL VEMGNYDLGD
 A_SE_UGSE8 RKIDR....L IERIRERAED SGNESDGD.T EEL....STL IELG DYDLGD
 A_UG_92UG0 RKIDR....L VDRIRERAED SGNESDGD.R EEL....SLL VDMG DYDLGD
 A_UG_U455_ KKIDR....L LNRIRERAED SGNESDGD.T EEL....SLL VEMGNYDLGV
 AC_IN_2130 RKIDR....L IKRIRERAED SGNESEGD.T EEL....STM VDMGQLRLLD
 AC_RW_92RW RKIDR....L IKKIRERAED SGNESDGD.I DEL....SKL VGVGNYDLGD
 AC_SE_SE94 RKIDW....L IKRIRERAED SGNESDGD.T EEL....STM VDMGHLRLLD
 ACD_SE_SE8 KKIDR....L IERIRERAED SGNESDGD.T EEL....AAL VEMGNYDPGD
 ACG_BE_VI1 RKIDW....L VKRIRERAED SGNESEGD.T EEL....STM VDMGELRLMD
 AD_SE_SE69 KRIDW....L IDRIRERAED SGNESEGDRD ELS....EL. VEMGHPAPWD
 AD_SE_SE71 RKIDR....I LDRIRVRAED SGNESDGD.T EEL....SKL IDMGNYDLGD
 ADHK_NO_97 KRIDQ....L IERIRERAED SGNESDGD.T EEL....SEL VEMGRLNLGY
 ADK_CD_MAL RKIDR....L IDRIRERAED SGNESEGDTE ELS....KL. VEMGHDPAPWD
 AG_BE_VI11 KKIEK....L PDRIRERAED SGNESEGD.T DEL....ATL VERGNFDPWV
 AG_NG_92NG EKIDR....L LDRIRERAED SGNESEGD.T EEL....ATL VDMVDFDPWV
 AGHU_GA_VI RKIDW....L IRRISERAED SGNESDGD.T EEL....STL VEMGNHNPY
 AGU_CD_Z32 KKIEY....L IDRIRKRAED SGNESEGD.T EEL....STL MEMGDFHPWV
 AJ_BW_BW21 KKIDR....I IDRIGERAED SGNESDGD.T DEL....HKL VEMGPHDLWN
 B_AU_VH_AF RKIDR....L IDRIAERAED SGNESEGD.Q EEL....AAL VEMGHHPAPWD
 B_CN_RL42_ RKIDR....L IDRIRERAED SGNESDGD.Q EEL....SAF MEMGHHPAPWD

B_DE_D31_U	RKIDR....L	IDRIIERAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_DE_HAN_U	RKINR....L	IDRLTERAED	SGNESEGD.Q	EEL....SAL	VERGHLAPWD
B_FR_HXB2	RKIDR....L	IDRLIERAED	SGNESEGEIS	ALV....EMG	VEMGHHAPWD
B_GA_OYI_M	RKIDR....L	IDRIRERAED	SGNDSEGD.Q	EEL....SAL	VEMGHHAPWD
B_GB_CAM1	KQVDR....L	IDRIIERAED	SGNESEGD.Q	EEL....SAL	MEMGHNAPWD
B_GB_GB8_A	KKIDR....L	IDRIIERAED	SDNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_GB_MANC	RKIDR....L	IDRIRERAED	SGNESEGD.Q	EEL....SEL	VEMGHLVPWD
B_KR_WK_AF	KKIDR....L	IDRIRERAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_NL_3202A	RKIDR....L	IDRIAERAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_TW_TWCYS	RKIDR....L	IDRIRERAED	SGNESEGD.Q	DEL....SAL	VEMGYHAPWD
B_US_BC_L0	RKIDR....L	IKRISKRAED	SGNESEGD.Q	EEL....SAL	VEMGHHALWD
B_US_DH123	KKIDR....L	IDRIRERAED	SGNESDGD.Q	EEL....SAL	VERGHLAPWD
B_US_JRCSF	RKIDR....L	IDKIRERAED	SGNESEGD.Q	EEL....SAL	VERGHLAPWD
B_US_MNCG	RKIDR....L	IDRISERAED	SGNESEGD.Q	EEL....SAL	VGMGHDAPWV
B_US_P896	RKIDR....L	IDRIREREED	SGNESEGD.Q	EEL....AAL	ERG.HLAPWD
B_US_RF_M1	KKIDR....L	IDRIRERAED	SGNESDGD.E	EEL....SAL	VEMGHHAPWD
B_US_SF2_K	R.IDR....L	IDRIREKAED	SGNESEGD.Q	EEL....SAL	VEMGHLAPWD
B_US_WEAU1	RKIDR....L	IDRIRDRAED	SGNESEGD.Q	EEL....SAL	VEMGHHAPWD
B_US_WR27	RKIDR....L	IDRIRERAED	SGNESEGD.Q	EEL....SAL	MEMGHHAPWD
B_US_YU2_M	RKIDR....L	INRITERAED	SGNESDGD.Q	EEL....SAL	VERGHLAPWD
BF1_BR_93B	RKINR....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEMGPFIPGD
C_BR_92BR0	RRIDW....L	VKRIRERAED	SGNESGGD.T	EEL....ETM	VDMGHLRLLD
C_BW_96BW0	RKIDW....L	VKRIRERAED	SGNESDGD.T	EEL....STM	VDMGHLRLLD
C_BW_96BW1	RKIDW....L	IERIRERAED	SGNESDGD.H	EEL....STM	VDMGHLRLLD
C_BW_96BW1	RRIDR....L	VERIREREED	SGNESEGD.I	EEL....STM	VDMGHLRLLD
C_BW_96BW1	KNIDW....L	IKRIRERAED	SGNESEGD.T	EEL....ATM	VDMGHLRLLD
C_ET_ETH22	RRIDR....L	IKRTERAED	SGNESDGD.T	EEL....STM	VDMGNLRLLD
C_IN_93IN1	SKINW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
C_IN_93IN9	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
C_IN_93IN9	RRIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGHLRLLD
C_IN_94IN1	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
C_IN_95IN2	RKIDW....L	IKRIRERAED	SGNESEGD.T	EEL....STM	VDMGRLRLLD
CRF01_AE_C	RKIDR....L	IERIRERAED	SGNGSEGD.T	NEL....ATL	VEVGDFDPWV
CRF01_AE_C	RKIDR....L	VQRISERAED	SGNESEGD.T	EEL....AKL	VEMGDFDPWV
CRF01_AE_C	RKIDR....L	IERIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIREREED	SGNESEGD.T	DKL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AQL	VEMEDFDPWV
CRF01_AE_T	RKIDR....L	VKRIRERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF01_AE_T	RKIDR....L	IKRIGERAED	SGNESEGD.T	DEL....AKL	VEMGDFDPWV
CRF02_AG_F	KKIDK....L	LDRIRERAED	SGNESDGD.A	EEL....STL	MEMGYD.HIL
CRF02_AG_F	KKIDK....L	LDRIRERAED	SGNESDGD.T	EEL....STL	LEMGYD.NIL
CRF02_AG_G	KKIDK....L	LDRIREREED	SGNESEGD.A	EEL....SKL	MEMGHD.FWI
CRF02_AG_N	KKIDR....L	LDRIRERAED	SGNESDGD.T	EEL....STL	MEMGYE.YIL
CRF02_AG_S	KKIDR....L	LDRIRERAED	SGNESDGD.T	EEL....STL	MEMGYD.NIL
CRF02_AG_S	GKIDK....L	LDRIRERAED	SGNESDGD.T	EEL....STL	LEMGYDNAAL
CRF03_AB_R	RKIDR....L	IDRIRERAED	SGNESEGD.Q	E.....AL	MEMGHLVPWD
CRF03_AB_R	RKIDR....L	IDRIRERAED	SGNESEGD.Q	E.....AL	MEMGHLAPWD
CRF04_cpx	RRIDS....L	YNRIRERAED	SGNESDGD.A	EEL....STL	VGMGNFDPWV
CRF04_cpx	RKIDR....L	YKRIRERAED	SGNESDGD.T	EEL....STL	VGMGDFDPWV
CRF04_cpx	RKIDR....L	CKRIIERAED	SGNDSGD.T	EEL....STL	VDMGDFHPLV
CRF05_DF_B	RKINR....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEVGPFIPGD
CRF05_DF_B	RKINR....L	YKRIRERAED	SGNESEGD.A	EEL....AAL	GEMGPFIPGN
CRF06_cpx	KKIEK....L	LDRIRERAED	SGNESEGD.T	DEL....ATL	MEMGDFDPWV
CRF06_cpx	RKIEK....L	LNRIERAED	SGNESEGD.T	EEL....AAF	MEMGNFDPWV
CRF06_cpx	KKIEK....L	LDRIRERAED	SGNESEGD.T	DEL....ATL	MEMGNFDPWV
CRF06_cpx	KKIEK....L	LDRIREREED	SGNDSGD.T	EEL....ATL	MEMGNFDPWV
CRF11_cpx	KKIDR....L	IDRIRERAED	SGNESEGD.T	EEL....ARL	VEMGPHDQWN
CRF11_cpx	R.....K	DRLRIRRAED	SGNESEGD.T	EEL....AQL	VEMGPHDLWN

D_CD_84ZR0	RKIDW....L	IDRIREREED	SGNESEGDKE	ELS....TL	VEMGHHPWD
D_CD_ELI_K	RRIDC....L	LDRITERAED	SGNESEGDRE	KL....KL	VEMGHHPWD
D_CD_NDK_M	RKIDC....L	IDRIRERAED	SGNESEGERE	ELS....KL	VEMGHHPWD
D_UG_94UG1	RKIDW....L	IDRIRERAED	SGNESEGDKE	ELS....AL	VEMGHDPWD
F1_BE_VI85	RKINK....L	YKRIRERAED	SGNESEGD.A	BEL....AAL	GEMGPFIPGD
F1_BR_93BR	RKINR....L	YKRISERAED	SGNESEGD.A	BEL....AAL	GEVGPFIPGD
F1_FI_FIN9	RKINR....L	YIRIRERAED	SGNESEGD.A	BEL....AAL	GKMGPFIIPGD
F1_FR_MP41	RKINR....L	YERIRERAED	SGNESEGD.A	BEL....AAL	GEMGSFISGD
F2_CM_MP25	KRINR....L	YERIIRAED	SGNESEGD.A	BEL....AAL	GEVGPLIPGD
F2KU_BE_VI	BRINQ....L	YNRLIERAED	SGNESEGE.A	BEL....AAL	GEVGHLVLGN
G_BE_DRCBL	KRIEK....L	LDRIRERAED	SGNESEGD.T	BEL....ATL	MELGDFDPWV
G_NG_92NG0	KKIEK....L	LDRIRERAED	SGNESEGD.T	BEL....ATL	MEMGDFDPWV
G_SE_SE616	KRIGK....L	LDRIRERAED	SGNESDGD.T	BEL....VTL	VEMGDFDPWV
H_BE_VI991	RKIDR....L	IERIRERAED	SGNESDGD.T	BEL....SKL	VEMGHLNLGY
H_BE_VI997	KKIDR....L	IQRIEGAED	SGNESD....	EEL....STM	VERGHLTFGY
H_CF_90CF0	KKIDR....L	IERIGERAED	SGNESDGD.T	BEL....SKL	MEMGHLNLGY
J_SE_SE702	RKIDK....L	INRIRERAED	SGNESDGD.T	DEL....AEL	VEMGPHDLWN
J_SE_SE788	RKIDK....L	IDRIRERAED	SGNESDCD.T	BEL....ADL	VERCPHDLWN
K_CD_EQTB1	KRINW....L	FDRIRERAED	SGNESEGD.T	EEL....AAL	GETGHLILGD
K_CM_MP535	KRINW....L	IDRIRERAED	SGNESEGD.A	EEL....ADI	GELGHLILGN
N_CM_YBF30	EKIKH....I	RQRIREREED	SGNESDGD.A	EWLDGDEEWL	VTLLSSSKLD
O_CM_ANT70	DRKEREILER	LRRIREIRDD	SDYESNGE..	EEQ....EV	MDLVLSHGFD
O_CM_MVP51	DRREQEILER	LRRIKEIRDD	SDYESNEE..	EEQ....EV	MELIHSHGFA
O_SN_99SE	DKREREILER	LRRIRQIEDD	SDYESDGT..	EEQ....EV	RDLVHSYGFD
O_SN_99SE	DRREREILER	LRRIRQIEDD	SDYESDGK..	EEQ....EV	RDLVHGYGFD
U_CD___83C	RKIDW....L	IDRIRERAED	SGNESEGD.T	EEL....STL	VEMEPDNFRN

101

00BW0762_1	ANGL..
00BW0768_2	GNDL..
00BW0874_2	VNDL..
00BW1471_2	VNDL..
00BW1616_2	DL....
00BW1686_8	VNVL..
00BW1759_3	DNNL..
00BW1773_2	INH...
00BW1783_5	AHDL..
00BW1795_6	ANNL..
00BW1811_3	IINY..
00BW1859_5	INDL..
00BW1880_2	ANDL..
00BW1921_1	HGL...
00BW2036_1	VHDL..
00BW2063_6	ANDL..
00BW2087_2	VNDL..
00BW2127_2	DL....
00BW2276_7	GNDL..
00BW3819_3	AHDL..
00BW3842_8	L.....
00BW3871_3	VNDI..
00BW3876_9	INN...
00BW3886_8	VNNL..
00BW3891_6	VNDV..
00BW3970_2	VTDL..
00BW5031_1	VNDL..
96BW01B21	DNAL..
96BW0407	DI....
96BW0502	VNN...
96BW06_J4	NL....
96BW11_06	ANDL..

96BW1210	ADGL..
96BW15B03	L.....
96BW16_26	INN...
96BW17A09	VNDL..
96BWM01_5	TNDL..
96BWM03_2	INL...
98BWMC12_2	DNEL..
98BWMC13_4	VNDL..
98BWMC14_a	VM....
98BWM014_1	ANDL..
98BWM018_d	ANDL..
98BWM036_a	AHDL..
98BWM037_d	ANDL..
99BW3932_1
99BW4642_4	VNDL..
99BW4745_8	DL....
99BW4754_7	VNDL..
99BWMC16_8	ANDL..
A2_CD_97CD	DNDV..
A2_CY_94CY	VNNV..
A2D___97KR	AND...
A2G_CD_97C	GDNL..
A_BY_97BL0	DNNV..
A_KE_Q23_A	NNIL..
A_SE_SE659	DNNL..
A_SE_SE725	DNDL..
A_SE_SE753	GNNL..
A_SE_SE853	DNNL..
A_SE_SE889	NNNL..
A_SE_UGSE8	DNNL..
A_UG_92UG0	DNNL..
A_UG_U455_	DNNL..
AC_IN_2130	VNGL..
AC_RW_92RW	VNNL..
AC_SE_SE94	VNNL..
ACD_SE_SE8	DINL..
ACG_BE_VI1	AIDL..
AD_SE_SE69	VDDM..
AD_SE_SE71	DNNL..
ADHK_NO_97	VADL..
ADK_CD_MAL	VDDL..
AG_BE_VI11	GDNL..
AG_NG_92NG	GDNL..
AGHU_GA_VI	VNDL..
AGU_CD_Z32	GDNL..
AJ_BW_BW21	VNDL..
B_AU_VH_AF	VDDL..
B_CN_RL42_	VDDL..
B_DE_D31_U	VDDL..
B_DE_HAN_U	VNDQ..
B_FR_HXB2_	VDDL..
B_GA_OYI_M	VDDM..
B_GB_CAM1_	VNDL..
B_GB_GB8_A	VDDL..
B_GB_MANC_	VDDL..
B_KR_WK_AF	VDDL..
B_NL_3202A	VDDL..
B_TW_TWCYS	VNDQ..
B_US_BC_L0	IDDL..
B_US_DH123	IDDL..

B_US_JRCSF	INDL..
B_US_MNCG	INDL..
B_US_P896	VDDL..
B_US_RF_M1	VDDL..
B_US_SF2_K	VDDL..
B_US_WEAU1	IDDL..
B_US_WR27	VDDL..
B_US_YU2_M	VDDL..
BF1_BR_93B	IDNL..
C_BR_92BR0	GNDL..
C_BW_96BW0	DN....
C_BW_96BW1	ANDL..
C_BW_96BW1	ADGL..
C_BW_96BW1	L.....
C_ET_ETH22	VNDL..
C_IN_93IN1	VNDL..
C_IN_93IN9	VNDL..
C_IN_93IN9	VNDM..
C_IN_94IN1	VNDL..
C_IN_95IN2	VNDL..
CRF01_AE_C	GDNL..
CRF01_AE_C	GDNL..
CRF01_AE_C	GDNV..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNV..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF01_AE_T	GDNL..
CRF02_AG_F	DNDNL.
CRF02_AG_F	DNDNL.
CRF02_AG_G	DNL...
CRF02_AG_N	DNDNL.
CRF02_AG_S	DNDNL.
CRF02_AG_S	DIDNL.
CRF03_AB_R	ADDL..
CRF03_AB_R	ADDL..
CRF04_cpx	GDNL..
CRF04_cpx	GNNV..
CRF04_cpx	GNNL..
CRF05_DF_B	INNLL..
CRF05_DF_B	INNLL..
CRF06_cpx	GDNL..
CRF06_cpx	GDNL..
CRF06_cpx	GDNL..
CRF06_cpx	GDNL..
CRF11_cpx	VNDL..
CRF11_cpx	VNDL..
D_CD_84ZR0	VDDDL.
D_CD_ELI_K	IDDL..
D_CD_NDK_M	VDDL..
D_UG_94UG1	ADDM..
F1_BE_VI85	INNLL..
F1_BR_93BR	INNLL..
F1_FI_FIN9	VNNLL..
F1_FR_MP41	INNLL..
F2_CM_MP25	INNLL..
F2KU_BE_VI	IHNLL..
G_BE_DRCBL	GDNL..
G_NG_92NG0	GNNLL..

50458025 032803

G_SE_SE616	GDNL..
H_BE_VI991	VADL..
H_BE_VI997	VADL..
H_CF_90CF0	VADL..
J_SE_SE702	VNDL..
J_SE_SE788	VNDL..
K_CD_EQTB1	INN..
K_CM_MP535	IDNL..
N_CM_YBF30	QGNWV.
O_CM_ANT70	NPMFEP
O_CM_MVP51	NPMFEL
O_SN_99SE	NPMFEL
O_SN_99SE	NPMFEP
U_CD__83C	DNDM..

Table 20. BLASTP Sequences producing significant alignments with S20757 (HBV Polymerase subtype ayw)

			Score (bits)	E: Value
gi 93080 pir	S20757	DNA-directed DNA polymerase (EC 2.7.7....	1553	0.0
gi 8925755 gb	AAF81607.1	DNA polymerase/reverse transcript...	1489	0.0
gi 1514497 emb	CAA68864.1	P [Hepatitis B virus]	1488	0.0
gi 27466573 gb	AAO12632.1	polymerase [Hepatitis B virus]	1482	0.0
gi 5257489 gb	AAD41360.1	polymerase [Hepatitis B virus]	1482	0.0
gi 118876 sp	P03156 DPOL_HPBVY	P protein [Includes: DNA-dir...	1482	0.0
gi 27466565 gb	AAO12625.1	polymerase [Hepatitis B virus]	1481	0.0
gi 67003 pir	JDVLVB	DNA-directed DNA polymerase (EC 2.7.7....	1480	0.0
gi 59433 emb	CAA46352.1	polymerase ORF [Hepatitis B virus]	1480	0.0
gi 6692498 gb	AAF24666.1	polymerase [Hepatitis B virus]	1479	0.0
gi 6692505 gb	AAF24673.1	polymerase [Hepatitis B virus]	1479	0.0
gi 2117935 pir	S71785	DNA-directed DNA polymerase (EC 2.7....	1477	0.0
gi 28436101 dbj	BAC57445.1	polymerase [Hepatitis B virus]	1476	0.0
gi 631984 pir	S47406	DNA-directed DNA polymerase (EC 2.7.7....	1475	0.0
gi 1359687 emb	CAA66431.1	polymerase [Hepatitis B virus]	1474	0.0
gi 18621117 emb	CAC87021.1	polymerase [Hepatitis B virus]	1474	0.0
gi 28436091 dbj	BAC57437.1	polymerase [Hepatitis B virus]	1473	0.0
gi 6692512 gb	AAF24680.1	polymerase [Hepatitis B virus]	1472	0.0
gi 22135695 gb	AAM09037.1	polymerase [Hepatitis B virus]	1471	0.0
gi 18621125 emb	CAC87015.1	polymerase [Hepatitis B virus]	1471	0.0
gi 1359679 emb	CAA66424.1	polymerase [Hepatitis B virus]	1470	0.0
gi 6692492 gb	AAF24660.1	polymerase [Hepatitis B virus]	1468	0.0
gi 2182121 gb	AAB59972.1	DNA polymerase [Hepatitis B virus]	1467	0.0
gi 4140295 emb	CAA10539.1	polymerase [Hepatitis B virus]	1467	0.0
gi 28436096 dbj	BAC57441.1	polymerase [Hepatitis B virus]	1466	0.0
gi 2829156 gb	AAC40810.1	polymerase [Hepatitis B virus]	1464	0.0
gi 27466519 gb	AAO12604.1	polymerase [Hepatitis B virus] >...	1463	0.0
gi 118869 sp	P24024 DPOL_HPBVA	P protein [Includes: DNA-dir...	1462	0.0
gi 27466525 gb	AAO12672.1	polymerase [Hepatitis B virus]	1461	0.0
gi 762933 emb	CAA59514.1	polymerase [Hepatitis B virus]	1461	0.0
gi 22135690 gb	AAM09033.1	polymerase [Hepatitis B virus]	1459	0.0
gi 6063470 dbj	BAA85377.1	DNA polymerase/reverse transcrip...	1455	0.0
gi 6063465 dbj	BAA85373.1	DNA polymerase/reverse transcrip...	1454	0.0
gi 27466605 gb	AAO12660.1	polymerase [Hepatitis B virus]	1451	0.0
gi 2829149 gb	AAC40804.1	polymerase [Hepatitis B virus]	1451	0.0
gi 475987 gb	AAA18583.1	polymerase [Hepatitis B virus]	1450	0.0
gi 313784 emb	CAA42466.1	polymerase [Hepatitis B virus]	1446	0.0
gi 27466597 gb	AAO12653.1	polymerase [Hepatitis B virus]	1444	0.0
gi 15419833 gb	AAK97182.1	AF297620_3 polymerase [Hepatitis ...	1442	0.0
gi 93082 pir	S20752	DNA-directed DNA polymerase (EC 2.7.7....	1441	0.0
gi 27466613 gb	AAO12667.1	polymerase [Hepatitis B virus]	1435	0.0
gi 27466589 gb	AAO12646.1	polymerase [Hepatitis B virus]	1434	0.0
gi 27466538 gb	AAO12618.1	polymerase [Hepatitis B virus]	1432	0.0
gi 27466581 gb	AAO12639.1	polymerase [Hepatitis B virus]	1431	0.0
gi 15419828 gb	AAK97178.1	AF297619_3 polymerase [Hepatitis ...	1429	0.0
gi 27466544 gb	AAO12681.1	polymerase [Hepatitis B virus]	1427	0.0
gi 27466557 gb	AAO12692.1	polymerase [Hepatitis B virus]	1423	0.0
gi 16751312 gb	AAL25951.1	polymerase protein [Hepatitis B ...	1382	0.0
gi 11935073 gb	AAG41955.1	AF305327_2 polymerase [Hepatitis ...	1379	0.0
gi 13491150 gb	AAK27856.1	AF330110_3 polymerase [Hepatitis ...	1368	0.0
gi 6116700 dbj	BAA32859.2	pol protein [Hepatitis B virus]	1368	0.0
gi 3551332 dbj	BAA32886.1	pol protein [Hepatitis B virus]	1368	0.0
gi 28812222 dbj	BAC65108.1	polymerase protein [Hepatitis B...	1368	0.0
gi 6691505 dbj	BAA89330.1	polymerase protein [Hepatitis B ...	1368	0.0
gi 118872 sp	P12900 DPOL_HPBVL	P protein [Includes: DNA-dir...	1368	0.0

gi 560084 dbj BAA04927.1	DNA polymerase [Hepatitis B virus]	1367	0.0
gi 560089 dbj BAA04931.1	DNA polymerase [Hepatitis B virus]	1367	0.0
gi 6116731 dbj BAA32957.2	pol protein [Hepatitis B virus]	1366	0.0
gi 6691495 dbj BAA89322.1	polymerase protein [Hepatitis B ...]	1365	0.0
gi 7188655 gb AAF37833.1 AF222323_2	polymerase [Hepatitis B...]	1365	0.0
gi 6063460 dbj BAA85369.1	DNA polymerase/reverse transcrip...	1364	0.0
gi 3551347 dbj BAA32898.1	pol protein [Hepatitis B virus]	1364	0.0
gi 6691500 dbj BAA89326.1	polymerase protein [Hepatitis B ...]	1363	0.0
gi 28812217 dbj BAC65104.1	polymerase protein [Hepatitis B...]	1363	0.0
gi 3551342 dbj BAA32894.1	pol protein [Hepatitis B virus]	1363	0.0
gi 628080 pir S43491	DNA-directed DNA polymerase (EC 2.7.7...	1363	0.0
gi 12246972 gb AAG49670.1 AF223956_3	polymerase [Hepatitis ...]	1362	0.0
gi 3551293 dbj BAA32852.1	pol protein [Hepatitis B virus]	1362	0.0
gi 12246964 gb AAG49663.1 AF223955_3	polymerase [Hepatitis ...]	1362	0.0
gi 21624231 dbj BAC01103.1	polymerase protein [Hepatitis B...]	1362	0.0
gi 118874 sp P03157 DPOL_HPBVR	P protein [Includes: DNA-dir...	1361	0.0
gi 6009784 dbj BAA85065.1	polymerase [Hepatitis B virus]	1361	0.0
gi 22651880 gb AAN03491.1 AF286594_3	DNA polymerase [Hepati...	1360	0.0
gi 18252591 gb AAL66348.1 AF461043_2	P protein [Hepatitis B...]	1360	0.0
gi 15778326 gb AAL07381.1 AF411409_4	polymerase [Hepatitis ...]	1360	0.0
gi 3551268 dbj BAA32832.1	pol protein [Hepatitis B virus]	1360	0.0
gi 14290241 gb AAK59316.1 AF384371_2	polymerase [Hepatitis ...]	1358	0.0
gi 6063435 dbj BAA85353.1	DNA polymerase/reverse transcrip...	1358	0.0
gi 6063440 dbj BAA85357.1	DNA polymerase/reverse transcrip...	1358	0.0
gi 3551283 dbj BAA32844.1	pol protein [Hepatitis B virus]	1358	0.0
gi 18252536 gb AAL66307.1 AF458664_3	polymerase [Hepatitis ...]	1358	0.0
gi 6009769 dbj BAA85053.1	polymerase [Hepatitis B virus]	1358	0.0
gi 13991865 gb AAK51533.1 AF363961_2	polymerase [Hepatitis ...]	1357	0.0
gi 6063425 dbj BAA85382.1	DNA polymerase/reverse transcrip...	1357	0.0
gi 2626986 dbj BAA23435.1	DNA polymerase [Hepatitis B viru...]	1357	0.0
gi 4490402 emb CAB38767.1	P protein [Hepatitis B virus]	1357	0.0
gi 22415735 gb AAM95242.1	DNA polymerase/reverse transcrip...	1357	0.0
gi 10934057 dbj BAB16885.1	polymerase [Hepatitis B virus]	1356	0.0
gi 18252556 gb AAL66323.1 AF461359_3	polymerase [Hepatitis ...]	1356	0.0
gi 2627009 dbj BAA23455.1	DNA polymerase [Hepatitis B virus]	1356	0.0
gi 560074 dbj BAA04919.1	DNA polymerase [Hepatitis B virus]	1356	0.0
gi 479847 pir S35527	DNA-directed DNA polymerase (EC 2.7.7...	1356	0.0
gi 18252545 gb AAL66314.1 AF461357_2	polymerase [Hepatitis ...]	1356	0.0
gi 1742906 dbj BAA09083.1	DNA polymerase [Hepatitis B virus]	1355	0.0
gi 6009764 dbj BAA85049.1	polymerase [Hepatitis B virus] >...	1355	0.0
gi 2627002 dbj BAA23449.1	DNA polymerase [Hepatitis B virus]	1355	0.0
gi 6063455 dbj BAA85365.1	DNA polymerase/reverse transcrip...	1355	0.0
gi 10441115 gb AAG16953.1 AF182804_4	polymerase [Hepatitis ...]	1354	0.0
gi 6009774 dbj BAA85057.1	polymerase [Hepatitis B virus]	1353	0.0
gi 4490407 emb CAB38771.1	P protein [Hepatitis B virus]	1353	0.0
gi 3582359 dbj BAA32913.1	pol protein [Hepatitis B virus]	1353	0.0
gi 3582355 dbj BAA32874.1	pol protein [Hepatitis B virus]	1353	0.0
gi 12246980 gb AAG49677.1 AF223957_3	polymerase [Hepatitis ...]	1352	0.0
gi 16751307 gb AAL25947.1	polymerase protein [Hepatitis B ...]	1352	0.0
gi 3582375 dbj BAA32925.1	pol protein [Hepatitis B virus]	1352	0.0
gi 15778340 gb AAL07392.1 AF411412_4	polymerase [Hepatitis ...]	1352	0.0
gi 4206637 gb AAD11755.1	DNA polymerase [Hepatitis B virus]	1352	0.0
gi 15425690 dbj BAB64319.1	polymerase [Hepatitis B virus]	1352	0.0
gi 3551352 dbj BAA32902.1	pol protein [Hepatitis B virus]	1352	0.0
gi 3582395 dbj BAA32963.1	pol protein [Hepatitis B virus]	1352	0.0
gi 5114071 gb AAD40205.1 AF090839_2	polymerase [Hepatitis B...]	1352	0.0
gi 9082085 gb AAF82723.1 AF233236_2	pol [Hepatitis B virus]	1352	0.0
gi 6983935 gb AAF34734.1 AF160501_2	polymerase [Hepatitis B...]	1351	0.0
gi 560094 dbj BAA04935.1	DNA polymerase [Hepatitis B virus]	1351	0.0
gi 18032033 gb AAL49990.1	polymerase [Hepatitis B virus]	1351	0.0

gi 18146671 dbj BAB82392.1	polymerase [Hepatitis B virus]	1351	0.0
gi 6006322 dbj BAA84819.1	polymerase protein [Hepatitis B ...]	1350	0.0
gi 18252551 gb AAL66319.1	AF461358_3 polymerase [Hepatitis ...]	1350	0.0
gi 7188649 gb AAF37828.1	AF222322_2 polymerase [Hepatitis B...]	1350	0.0
gi 12060441 dbj BAB20611.1	DNA polymerase [Hepatitis B virus]	1350	0.0
gi 18845085 gb AAL79545.1	AF473543_4 P protein [Hepatitis B...]	1350	0.0
gi 3551322 dbj BAA32878.1	pol protein [Hepatitis B virus]	1350	0.0
gi 12246956 gb AAG49656.1	AF223954_4 polymerase [Hepatitis ...]	1350	0.0
gi 6063430 dbj BAA85349.1	DNA polymerase/reverse transcrip...	1350	0.0
gi 2288872 dbj BAA21665.1	DNA polymerase [Hepatitis B virus]	1350	0.0
gi 1220111 dbj BAA04072.1	DNA polymerase [Hepatitis B virus]	1349	0.0
gi 9454168 gb AAF87689.1	polymerase protein [Hepatitis B v...]	1349	0.0
gi 18146683 dbj BAB82402.1	polymerase [Hepatitis B virus]	1349	0.0
gi 3551278 dbj BAA32840.1	pol protein [Hepatitis B virus]	1349	0.0
gi 3551372 dbj BAA32939.1	pol protein [Hepatitis B virus]	1349	0.0
gi 19849035 gb AAL99437.1	AF405706_3 polymerase [Hepatitis ...]	1349	0.0
gi 3551357 dbj BAA32906.1	pol protein [Hepatitis B virus]	1349	0.0
gi 15778321 gb AAL07377.1	AF411408_4 polymerase [Hepatitis ...]	1348	0.0
gi 15072542 gb AAK81690.1	polymerase protein [Hepatitis B ...]	1348	0.0
gi 21624238 dbj BAC01109.1	polymerase protein [Hepatitis B...]	1348	0.0
gi 12247012 gb AAG49705.1	AF223961_3 polymerase [Hepatitis ...]	1348	0.0
gi 5114086 gb AAD40217.1	AF090842_2 polymerase [Hepatitis B...]	1348	0.0
gi 3582407 dbj BAA32972.1	pol protein [Hepatitis B virus]	1347	0.0
gi 15425698 dbj BAB64325.1	polymerase [Hepatitis B virus]	1347	0.0
gi 18146665 dbj BAB82387.1	polymerase [Hepatitis B virus]	1347	0.0
gi 23194252 gb AAN15074.1	P protein [Hepatitis B virus]	1347	0.0
gi 560079 dbj BAA04923.1	DNA polymerase [Hepatitis B virus]	1347	0.0
gi 10443833 gb AAG17595.1	AF241410_3 polymerase [Hepatitis ...]	1346	0.0
gi 13991870 gb AAK51537.1	AF363962_2 polymerase [Hepatitis ...]	1346	0.0
gi 4007054 emb CAA10426.1	DNA polymerase [Hepatitis B virus]	1346	0.0
gi 3551362 dbj BAA32910.1	pol protein [Hepatitis B virus]	1346	0.0
gi 18146677 dbj BAB82397.1	polymerase [Hepatitis B virus]	1346	0.0
gi 12246988 gb AAG49684.1	AF223958_3 polymerase [Hepatitis ...]	1346	0.0
gi 15211897 emb CAC51286.1	polymerase [Hepatitis B virus]	1345	0.0
gi 18389989 gb AAL68823.1	polymerase [Hepatitis B virus]	1345	0.0
gi 3582363 dbj BAA32916.1	pol protein [Hepatitis B virus]	1345	0.0
gi 10441110 gb AAG16949.1	AF182803_4 polymerase [Hepatitis ...]	1345	0.0
gi 10443841 gb AAG17602.1	AF241411_3 polymerase [Hepatitis ...]	1345	0.0
gi 3551382 dbj BAA32947.1	pol protein [Hepatitis B virus]	1345	0.0
gi 3582387 dbj BAA32950.1	pol protein [Hepatitis B virus]	1344	0.0
gi 3551317 dbj BAA32871.1	pol protein [Hepatitis B virus]	1344	0.0
gi 10441104 gb AAG16944.1	AF182802_3 polymerase [Hepatitis ...]	1343	0.0
gi 118866 sp P03159 DPOL_HPBV2	P protein [Includes: DNA-dir...]	1343	0.0
gi 15425694 dbj BAB64322.1	polymerase [Hepatitis B virus]	1343	0.0
gi 4007049 emb CAA10422.1	DNA polymerase [Hepatitis B virus]	1343	0.0
gi 29123239 gb AAO62971.1	pol protein [Hepatitis B virus]	1343	0.0
gi 4007064 emb CAA10438.1	DNA polymerase [Hepatitis B virus]	1342	0.0
gi 452623 emb CAA53358.1	polymerase [Hepatitis B virus]	1342	0.0
gi 18252541 gb AAL66311.1	AF458665_3 polymerase [Hepatitis ...]	1342	0.0
gi 527443 emb CAA84791.1	DNA polymerase [Hepatitis B virus]	1342	0.0
gi 15211890 emb CAC51280.1	polymerase [Hepatitis B virus]	1342	0.0
gi 329617 gb AAA62812.1	DNA polymerase	1341	0.0
gi 4007079 emb CAA10454.1	DNA polymerase [Hepatitis B virus]	1341	0.0
gi 9454173 gb AAF87693.1	polymerase protein [Hepatitis B v...]	1341	0.0
gi 452628 emb CAA53354.1	polymerase [Hepatitis B virus]	1341	0.0
gi 3582367 dbj BAA32919.1	pol protein [Hepatitis B virus]	1340	0.0
gi 5114066 gb AAD40201.1	AF090838_2 polymerase [Hepatitis B...]	1340	0.0
gi 15419860 gb AAK97203.1	AF297625_3 polymerase [Hepatitis ...]	1340	0.0
gi 4490412 emb CAB38775.1	P protein [Hepatitis B virus]	1340	0.0
gi 18252566 gb AAL66331.1	AF461361_3 polymerase [Hepatitis ...]	1340	0.0

gi	4007059	emb	CAA10430.1	DNA polymerase [Hepatitis B virus]	1340	0.0
gi	5114081	gb	AAD40213.1	AF090841_2 polymerase [Hepatitis B...	1339	0.0
gi	3582371	dbj	BAA32922.1	pol protein [Hepatitis B virus]	1339	0.0
gi	12247003	gb	AAG49697.1	AF223960_4 polymerase [Hepatitis ...	1339	0.0
gi	4033548	emb	CAA10450.1	DNA polymerase [Hepatitis B virus]	1339	0.0
gi	3892581	emb	CAA09962.1	polymerase [Hepatitis B virus]	1339	0.0
gi	5114076	gb	AAD40209.1	AF090840_2 polymerase [Hepatitis B...	1338	0.0
gi	12060436	dbj	BAB20607.1	DNA polymerase [Hepatitis B virus]	1338	0.0
gi	118868	sp	P17100	DPOL_HPBV9 P protein [Includes: DNA-dir...	1337	0.0
gi	27466434	gb	AAO12555.1	polymerase [Hepatitis B virus]	1337	0.0
gi	3582399	dbj	BAA32966.1	pol protein [Hepatitis B virus]	1337	0.0
gi	3551273	dbj	BAA32836.1	pol protein [Hepatitis B virus]	1337	0.0
gi	14285168	gb	AAK58873.1	polymerase [synthetic construct]...	1337	0.0
gi	3582391	dbj	BAA32953.1	pol protein [Hepatitis B virus]	1337	0.0
gi	15419845	gb	AAK97191.1	AF297622_3 polymerase [Hepatitis ...	1337	0.0
gi	118870	sp	P17393	DPOL_HPBVI P protein [Includes: DNA-dir...	1336	0.0
gi	3551377	dbj	BAA32943.1	pol protein [Hepatitis B virus]	1336	0.0
gi	10443825	gb	AAG17588.1	AF241409_3 polymerase [Hepatitis ...	1336	0.0
gi	10443817	gb	AAG17581.1	AF241408_3 polymerase [Hepatitis ...	1336	0.0
gi	29124889	gb	AAO63519.1	pol protein [Hepatitis B virus]	1335	0.0
gi	399401	sp	P31870	DPOL_HPBVM P protein [Includes: DNA-dir...	1335	0.0
gi	6063445	dbj	BAA85339.1	DNA polymerase/reverse transcrip...	1335	0.0
gi	19568078	gb	AAL89566.1	polymerase [Hepatitis B virus]	1334	0.0
gi	27466426	gb	AAO12548.1	polymerase [Hepatitis B virus]	1334	0.0
gi	22655601	gb	AAN04128.1	polymerase [Hepatitis B virus]	1334	0.0
gi	8161369	gb	AAA69721.2	polymerase [Hepatitis B virus]	1334	0.0
gi	10441120	gb	AAG16957.1	AF182805_4 polymerase [Hepatitis ...	1334	0.0
gi	10443809	gb	AAG17574.1	AF241407_3 polymerase [Hepatitis ...	1333	0.0
gi	18146689	dbj	BAB82407.1	polymerase [Hepatitis B virus]	1333	0.0
gi	4007069	emb	CAA10442.1	DNA polymerase [Hepatitis B virus]	1333	0.0
gi	18031709	gb	AAK57744.1	polymerase [Hepatitis B virus]	1333	0.0
gi	18252561	gb	AAL66327.1	AF461360_3 polymerase [Hepatitis ...	1332	0.0
gi	6959503	gb	AAF33121.1	polymerase protein [orangutan hep...	1332	0.0
gi	26224721	gb	AAN76318.1	polymerase [Hepatitis B virus]	1332	0.0
gi	4007074	emb	CAA10446.1	DNA polymerase [Hepatitis B virus]	1332	0.0
gi	18031714	gb	AAK57745.1	polymerase [Hepatitis B virus]	1332	0.0
gi	7434791	pir	S67505	DNA-directed DNA polymerase (EC 2.7....	1332	0.0
gi	15419855	gb	AAK97199.1	AF297624_3 polymerase [Hepatitis ...	1332	0.0
gi	7434793	pir	T13468	DNA-directed DNA polymerase (EC 2.7....	1331	0.0
gi	4323205	gb	AAD16257.1	polymerase [Hepatitis B virus]	1331	0.0
gi	12060194	dbj	BAB20451.1	DNA polymerase [Hepatitis B virus]	1331	0.0
gi	23194347	gb	AAN15122.1	polymerase [Hepatitis B virus]	1330	0.0
gi	20151228	gb	AAM12945.1	DNA polymerase/reverse transcrip...	1330	0.0
gi	23884547	gb	AAN40009.1	pol protein [Hepatitis B virus]	1330	0.0
gi	21431681	gb	AAM53414.1	U87747_3 DNA polymerase/reverse t...	1330	0.0
gi	3551337	dbj	BAA32890.1	pol protein [Hepatitis B virus]	1329	0.0
gi	5019933	gb	AAD37919.1	P protein [Hepatitis B virus]	1329	0.0
gi	15419840	gb	AAK97187.1	AF297621_3 polymerase [Hepatitis ...	1329	0.0
gi	6006331	dbj	BAA84825.1	polymerase protein [Hepatitis B ...	1329	0.0
gi	19568073	gb	AAL89569.1	polymerase [Hepatitis B virus]	1329	0.0
gi	29124918	gb	AAO63539.1	pol protein [Hepatitis B virus]	1328	0.0
gi	329630	gb	AAA45483.1	P protein [Hepatitis B virus]	1328	0.0
gi	15778331	gb	AAL07385.1	AF411410_4 polymerase [Hepatitis ...	1328	0.0
gi	6566410	dbj	BAA88275.1	P protein [Hepatitis B virus]	1328	0.0
gi	4490397	emb	CAB38763.1	P protein [Hepatitis B virus]	1328	0.0
gi	12060187	dbj	BAB20445.1	DNA polymerase [Hepatitis B virus]	1327	0.0
gi	6063450	dbj	BAA85343.1	DNA polymerase/reverse transcrip...	1327	0.0
gi	118877	sp	P03155	DPOL_HPBVZ P protein [Includes: DNA-dir...	1327	0.0
gi	29124883	gb	AAO63514.1	pol protein [Hepatitis B virus]	1325	0.0
gi	4033543	emb	CAA10434.1	DNA polymerase [Hepatitis B virus]	1325	0.0

gi	6692525	gb	AAF24693.1	polymerase [Hepatitis B virus]	1325	0.0
gi	6692559	gb	AAF24727.1	polymerase [Hepatitis B virus]	1325	0.0
gi	23194340	gb	AAN15116.1	polymerase [Hepatitis B virus]	1325	0.0
gi	560064	dbj	BAA04911.1	DNA polymerase [Hepatitis B virus]	1324	0.0
gi	29124898	gb	AAO63526.1	pol protein [Hepatitis B virus]	1324	0.0
gi	29124927	gb	AAO63545.1	pol protein [Hepatitis B virus]	1323	0.0
gi	6692566	gb	AAF24734.1	polymerase [Hepatitis B virus]	1323	0.0
gi	6692553	gb	AAF24721.1	polymerase [Hepatitis B virus]	1323	0.0
gi	6692518	gb	AAF24686.1	polymerase [Hepatitis B virus] >g...	1323	0.0
gi	1359702	emb	CAA66444.1	polymerase [Hepatitis B virus] >...	1323	0.0
gi	29124867	gb	AAO63501.1	pol protein [Hepatitis B virus]	1323	0.0
gi	29124872	gb	AAO63505.1	pol protein [Hepatitis B virus] ...	1323	0.0
gi	27466479	gb	AAO12576.1	polymerase [Hepatitis B virus]	1322	0.0
gi	6692546	gb	AAF24714.1	polymerase [Hepatitis B virus]	1322	0.0
gi	3551312	dbj	BAA32867.1	pol protein [Hepatitis B virus]	1322	0.0
gi	27466487	gb	AAO12611.1	polymerase [Hepatitis B virus]	1322	0.0
gi	118871	sp	P17394 DPOL_HPBVJ	P protein [Includes: DNA-dir...	1321	0.0
gi	9454473	gb	AAF87833.1 AF282917_3	DNA polymerase [Hepatiti...	1321	0.0
gi	19224214	gb	AAL86445.1 AF479684_3	P gene product [Hepati...	1321	0.0
gi	6692572	gb	AAF24740.1	polymerase [Hepatitis B virus]	1321	0.0
gi	3551297	dbj	BAA32855.1	pol protein [Hepatitis B virus]	1321	0.0
gi	3551327	dbj	BAA32882.1	pol protein [Hepatitis B virus]	1320	0.0
gi	1359695	emb	CAA66434.1	polymerase [Hepatitis B virus]	1320	0.0
gi	3551367	dbj	BAA32932.1	pol protein [Hepatitis B virus]	1320	0.0
gi	118873	sp	P17395 DPOL_HPBVO	P protein [Includes: DNA-dir...	1319	0.0
gi	29124862	gb	AAO63497.1	pol protein [Hepatitis B virus]	1319	0.0
gi	18621110	emb	CAC87028.1	polymerase [Hepatitis B virus]	1319	0.0
gi	3582403	dbj	BAA32969.1	pol protein [Hepatitis B virus]	1318	0.0
gi	27261550	gb	AAN85925.1	DNA polymerase [Hepatitis B viru...	1318	0.0
gi	1914703	emb	CAA66699.1	polymerase [Hepatitis B virus]	1318	0.0
gi	4323200	gb	AAD16253.1	polymerase [Hepatitis B virus]	1318	0.0
gi	6573293	dbj	BAA88291.1	P protein [Hepatitis B virus]	1318	0.0
gi	6006341	dbj	BAA84833.1	polymerase protein [Hepatitis B ...	1316	0.0
gi	6566440	dbj	BAA88286.1	P protein [Hepatitis B virus]	1315	0.0
gi	560059	dbj	BAA04907.1	DNA polymerase [Hepatitis B virus]	1315	0.0
gi	14334410	gb	AAK59391.1	polymerase [Hepatitis B virus]	1315	0.0
gi	5019954	gb	AAD37936.1	P protein [Hepatitis B virus]	1315	0.0
gi	16117323	dbj	BAB69785.1	polymerase [Hepatitis B virus]	1315	0.0
gi	7434792	pir	T13473	DNA-directed DNA polymerase (EC 2.7....	1315	0.0
gi	5019965	gb	AAD37945.1	P protein [Hepatitis B virus]	1314	0.0
gi	29124908	gb	AAO63533.1	pol protein [Hepatitis B virus]	1314	0.0
gi	6566428	dbj	BAA88281.1	P protein [Hepatitis B virus]	1313	0.0
gi	29124894	gb	AAO63523.1	pol protein [Hepatitis B virus]	1311	0.0
gi	22135730	gb	AAM09065.1	polymerase [Hepatitis B virus]	1311	0.0
gi	560069	dbj	BAA04915.1	DNA polymerase [Hepatitis B virus]	1311	0.0
gi	15419850	gb	AAK97195.1 AF297623_3	polymerase [Hepatitis ...	1311	0.0
gi	9634217	ref	NP_037757.1	polymerase protein [orangutan h...	1310	0.0
gi	16117333	dbj	BAB69793.1	polymerase [Hepatitis B virus]	1309	0.0
gi	9971630	dbj	BAB12582.1	polymerase protein [Hepatitis B ...	1308	0.0
gi	27466450	gb	AAO12569.1	polymerase [Hepatitis B virus]	1306	0.0
gi	12247036	gb	AAG49726.1 AF223964_3	polymerase [Hepatitis ...	1306	0.0
gi	12247028	gb	AAG49719.1 AF223963_3	polymerase [Hepatitis ...	1305	0.0
gi	5019945	gb	AAD37929.1	P protein [Hepatitis B virus]	1305	0.0
gi	18146701	dbj	BAB82417.1	polymerase [Hepatitis B virus]	1305	0.0
gi	12247020	gb	AAG49712.1 AF223962_3	polymerase [Hepatitis ...	1304	0.0
gi	5019981	gb	AAD37958.1	P protein [Hepatitis B virus]	1304	0.0
gi	3892582	emb	CAA53343.1	polymerase [Hepatitis B virus]	1304	0.0
gi	27466442	gb	AAO12562.1	polymerase [Hepatitis B virus]	1304	0.0
gi	22135715	gb	AAM09053.1	polymerase [Hepatitis B virus]	1301	0.0
gi	12247044	gb	AAG49733.1 AF223965_3	polymerase [Hepatitis ...	1301	0.0

gi	22135725	gb	AAM09061.1	polymerase [Hepatitis B virus]	1301	0.0
gi	11191880	dbj	BAB17962.1	polymerase [Hepatitis B virus]	1300	0.0
gi	3551392	dbj	BAA32961.1	pol protein [Hepatitis B virus]	1300	0.0
gi	6006336	dbj	BAA84829.1	polymerase protein [Hepatitis B ...]	1299	0.0
gi	2627021	dbj	BAA23467.1	DNA polymerase [Hepatitis B virus]	1298	0.0
gi	2627015	dbj	BAA23461.1	DNA polymerase [Hepatitis B virus]	1297	0.0
gi	16117328	dbj	BAB69789.1	polymerase [Hepatitis B virus]	1297	0.0
gi	22135735	gb	AAM09069.1	polymerase [Hepatitis B virus]	1297	0.0
gi	14485226	gb	AAK62976.1	AF384372_2 polymerase [Hepatitis ...]	1296	0.0
gi	3551288	dbj	BAA32848.1	pol protein [Hepatitis B virus]	1295	0.0
gi	11191960	dbj	BAB18032.1	polymerase [Hepatitis B virus]	1294	0.0
gi	11191888	dbj	BAB17969.1	polymerase [Hepatitis B virus] ...	1293	0.0
gi	11191840	dbj	BAB17927.1	polymerase [Hepatitis B virus] ...	1293	0.0
gi	11191920	dbj	BAB17997.1	polymerase [Hepatitis B virus]	1293	0.0
gi	11191904	dbj	BAB17983.1	polymerase [Hepatitis B virus]	1291	0.0
gi	11191952	dbj	BAB18025.1	polymerase [Hepatitis B virus]	1291	0.0
gi	1169410	sp	Q05486 DPOL_HPBVT	P protein [Includes: DNA-di...	1289	0.0
gi	22135705	gb	AAM09045.1	polymerase [Hepatitis B virus]	1288	0.0
gi	452633	emb	CAA53350.1	polymerase [Hepatitis B virus]	1288	0.0
gi	18146695	dbj	BAB82412.1	polymerase [Hepatitis B virus]	1287	0.0
gi	22135710	gb	AAM09049.1	polymerase [Hepatitis B virus]	1287	0.0
gi	11191864	dbj	BAB17948.1	polymerase [Hepatitis B virus]	1286	0.0
gi	59451	emb	CAA48354.1	HBV polymerase [Hepatitis B virus]	1286	0.0
gi	11191848	dbj	BAB17934.1	polymerase [Hepatitis B virus] ...	1286	0.0
gi	22135700	gb	AAM09041.1	polymerase [Hepatitis B virus]	1285	0.0
gi	5019976	gb	AAD37954.1	P protein [Hepatitis B virus]	1281	0.0
gi	22135720	gb	AAM09057.1	polymerase [Hepatitis B virus]	1279	0.0
gi	5019939	gb	AAD37924.1	P protein [Hepatitis B virus]	1276	0.0
gi	1914697	emb	CAA66674.1	polymerase [Hepatitis B virus]	1273	0.0
gi	1914691	emb	CAA66679.1	polymerase [Hepatitis B virus]	1271	0.0
gi	5019970	gb	AAD37949.1	P protein [Hepatitis B virus]	1263	0.0
gi	15425702	dbj	BAB64328.1	polymerase [Hepatitis B virus]	1258	0.0
gi	29124905	gb	AAO63531.1	pol protein [Hepatitis B virus]	1253	0.0
gi	27466464	gb	AAO12704.1	polymerase [Hepatitis B virus]	1248	0.0
gi	27466471	gb	AAO12710.1	polymerase [Hepatitis B virus]	1244	0.0
gi	18252571	gb	AAL66335.1	AF461362_3 polymerase [Hepatitis ...]	1243	0.0
gi	27466511	gb	AAO12597.1	polymerase [Hepatitis B virus]	1239	0.0
gi	27466457	gb	AAO12698.1	polymerase [Hepatitis B virus]	1238	0.0
gi	15211905	emb	CAC51293.1	polymerase [Hepatitis B virus]	1227	0.0
gi	399402	sp	Q02314 DPOL_HPBVP	P protein [Includes: DNA-dir...	1224	0.0
gi	1914708	emb	CAA66684.1	polymerase [Hepatitis B virus]	1220	0.0
gi	27466503	gb	AAO12583.1	polymerase [Hepatitis B virus]	1184	0.0
gi	118867	sp	P12933 DPOL_HPBV4	P protein [Includes: DNA-dir...	1157	0.0
gi	4468850	emb	CAB38229.1	polymerase [Hepatitis B virus]	1122	0.0
gi	1914719	emb	CAA66694.1	polymerase [Hepatitis B virus]	1101	0.0
gi	9630375	ref	NP_046799.1	polymerase [woolly monkey hepat...	1049	0.0
gi	1185115	emb	CAA51254.1	DNA polymerase [Hepatitis B virus]	922	0.0
gi	20800461	gb	AAM28642.1	U87746_4 DNA polymerase/reverse t...	910	0.0
gi	21326585	ref	NP_647604.1	P gene product (AA 304-843); c...	907	0.0
gi	4377612	emb	CAA53339.1	polymerase [Hepatitis B virus]	904	0.0
gi	4377613	emb	CAA53338.1	polymerase [Hepatitis B virus]	901	0.0
gi	1549226	dbj	BAA04073.1	ORF [Hepatitis B virus]	898	0.0
gi	9454414	gb	AAF87797.1	polymerase [Hepatitis B virus]	895	0.0
gi	1550614	dbj	BAA04075.1	ORF [Hepatitis B virus]	893	0.0
gi	59409	emb	CAA32399.1	DNA polymerase [Hepatitis B virus]	879	0.0
gi	118894	sp	P03160 DPOL_WHV1	P protein [Includes: DNA-dire...	727	0.0
gi	9626716	ref	NP_040994.1	A protein [Ground squirrel hepa...	727	0.0
gi	22256032	ref	NP_671813.1	DNA polymerase [Woodchuck hepa...	725	0.0
gi	15637595	gb	AAL04547.1	AF410859_1 polymerase [Woodchuck ...]	725	0.0
gi	15637587	gb	AAL04543.1	AF410855_1 type II mutant polymer...	725	0.0

gi	118895	sp	P12899	DPOL_WHV59	P protein [Includes: DNA-dir...	724	0.0
gi	15637597	gb	AAL04548.1	AF410860_1	polymerase [Woodchuck ...	724	0.0
gi	15637599	gb	AAL04549.1	AF410861_1	polymerase [Woodchuck ...	722	0.0
gi	15637593	gb	AAL04546.1	AF410858_1	defective polymerase [...	721	0.0
gi	118898	sp	P17396	DPOL_WHV8I	P protein [Includes: DNA-dir...	721	0.0
gi	15637591	gb	AAL04545.1	AF410857_1	type I mutant polymera...	721	0.0
gi	15637589	gb	AAL04544.1	AF410856_1	type IV mutant polymer...	717	0.0
gi	118897	sp	P06275	DPOL_WHV8	P protein [Includes: DNA-dire...	706	0.0
gi	3582379	dbj	BAA32928.1		pol protein [Hepatitis B virus]	692	0.0
gi	9885813	gb	AAG01539.1	AF291830_2	polymerase [Hepatitis B...	692	0.0
gi	118875	sp	P03158	DPOL_HPBVW	DNA polymerase	680	0.0
gi	9628830	ref	NP_043864.1		polymerase [Arctic ground squir...	669	0.0
gi	8926931	dbj	BAA98025.1		pol protein [Hepatitis B virus]	669	0.0
gi	8926928	dbj	BAA98023.1		pol protein [Hepatitis B virus]	667	0.0
gi	8926925	dbj	BAA98021.1		pol protein [Hepatitis B virus]	667	0.0
gi	8926934	dbj	BAA98027.1		pol protein [Hepatitis B virus]	655	0.0
gi	13345982	gb	AAK19538.1	AF335734_2	polymerase [Hepatitis ...	583	e-166
gi	12083172	gb	AAG48743.1	AF329861_2	polymerase [Hepatitis ...	583	e-166
gi	13345979	gb	AAK19536.1	AF335733_2	polymerase [Hepatitis ...	583	e-166
gi	12083181	gb	AAG48749.1	AF329864_2	polymerase [Hepatitis ...	582	e-166
gi	12083178	gb	AAG48747.1	AF329863_2	polymerase [Hepatitis ...	582	e-165
gi	12083163	gb	AAG48737.1	AF329858_1	polymerase [Hepatitis ...	581	e-165
gi	12083167	gb	AAG48740.1	AF329859_2	polymerase [Hepatitis ...	581	e-165
gi	13345988	gb	AAK19542.1	AF335736_2	polymerase [Hepatitis ...	580	e-165
gi	13345985	gb	AAK19540.1	AF335735_2	polymerase [Hepatitis ...	578	e-164
gi	2982339	gb	AAC06361.1		DNA polymerase [Hepatitis B virus]	568	e-161
gi	336159	gb	AAA46774.1		polymerase protein	566	e-161
gi	118899	sp	P11292	DPOL_WHVW6	P protein [Includes: DNA-dir...	560	e-159
gi	225532	prf		1305266C	gene P	555	e-157
gi	1107586	emb	CAA56892.1		polymerase [Hepatitis B virus]	540	e-153
gi	1107579	emb	CAA56878.1		polymerase [Hepatitis B virus]	538	e-152
gi	1185116	emb	CAA51255.1		HBsAg [Hepatitis B virus]	465	e-130
gi	59414	emb	CAA32405.1		DNA polymerase [Hepatitis B virus]	459	e-129
gi	21326589	ref	NP_647608.1		P gene product, put.DNA polyme...	458	e-128
gi	1321828	emb	CAA96556.1		polymerase [Hepatitis B virus]	441	e-123
gi	5019960	gb	AAD37941.1		P protein [Hepatitis B virus]	440	e-123
gi	329652	gb	AAA69719.1		coat protein [Hepatitis B virus]	433	e-121
gi	329651	gb	AAA69720.1		coat protein [Hepatitis B virus]	429	e-120
gi	27466495	gb	AAO12590.1		polymerase [Hepatitis B virus]	429	e-120
gi	21218028	dbj	BAB96528.1		large S protein [Hepatitis B vi...	413	e-115
gi	1321832	emb	CAA96561.1		polymerase [Hepatitis B virus]	410	e-114
gi	27450190	gb	AAO14552.1	AF460225_1	polymerase [Hepatitis ...	385	e-106
gi	27450188	gb	AAO14551.1	AF460224_1	polymerase [Hepatitis ...	384	e-106
gi	27450192	gb	AAO14553.1	AF460226_1	polymerase [Hepatitis ...	383	e-106
gi	27450198	gb	AAO14556.1	AF460229_1	polymerase [Hepatitis ...	382	e-105
gi	27450196	gb	AAO14555.1	AF460228_1	polymerase [Hepatitis ...	382	e-105
gi	27450194	gb	AAO14554.1	AF460227_1	polymerase [Hepatitis ...	382	e-105
gi	27450200	gb	AAO14557.1	AF460230_1	polymerase [Hepatitis ...	375	e-103
gi	27450202	gb	AAO14558.1	AF460231_1	polymerase [Hepatitis ...	375	e-103
gi	3328370	gb	AAC26832.1		DNA polymerase [Hepatitis B virus]	374	e-103
gi	23380174	gb	AAM83022.1		polymerase [Hepatitis B virus]	373	e-103
gi	23380081	gb	AAM82960.1		polymerase [Hepatitis B virus]	373	e-103
gi	23380171	gb	AAM83020.1		polymerase [Hepatitis B virus]	372	e-102
gi	23380180	gb	AAM83026.1		polymerase [Hepatitis B virus]	370	e-102
gi	23380177	gb	AAM83024.1		polymerase [Hepatitis B virus]	369	e-102
gi	23380072	gb	AAM82954.1		polymerase [Hepatitis B virus]	369	e-101
gi	23380084	gb	AAM82962.1		polymerase [Hepatitis B virus]	368	e-101
gi	23380078	gb	AAM82958.1		polymerase [Hepatitis B virus]	368	e-101
gi	23380066	gb	AAM82950.1		polymerase [Hepatitis B virus]	368	e-101
gi	23380111	gb	AAM82980.1		polymerase [Hepatitis B virus]	368	e-101

gi	23380063	gb	AAM82948.1	polymerase [Hepatitis B virus]	367	e-101
gi	23380087	gb	AAM82964.1	polymerase [Hepatitis B virus]	367	e-101
gi	3335627	gb	AAD13662.1	DNA polymerase [Hepatitis B virus]	366	e-101
gi	23380069	gb	AAM82952.1	polymerase [Hepatitis B virus]	366	e-101
gi	23380090	gb	AAM82966.1	polymerase [Hepatitis B virus]	366	e-101
gi	23380060	gb	AAM82946.1	polymerase [Hepatitis B virus]	366	e-101
gi	23380105	gb	AAM82976.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380132	gb	AAM82994.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380093	gb	AAM82968.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380183	gb	AAM83028.1	polymerase [Hepatitis B virus]	365	e-100
gi	23380120	gb	AAM82986.1	polymerase [Hepatitis B virus]	365	e-100
gi	13991875	gb	AAK51541.1	AF363963_2 truncated polymerase [...	365	e-100
gi	23380129	gb	AAM82992.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380186	gb	AAM83030.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380168	gb	AAM83018.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380075	gb	AAM82956.1	polymerase [Hepatitis B virus]	363	e-100
gi	23380123	gb	AAM82988.1	polymerase [Hepatitis B virus]	361	3e-99
gi	23380135	gb	AAM82996.1	polymerase [Hepatitis B virus]	357	4e-98
gi	23380030	gb	AAM82926.1	polymerase [Hepatitis B virus]	351	3e-96
gi	23380021	gb	AAM82920.1	polymerase [Hepatitis B virus]	351	3e-96
gi	23379934	gb	AAM82862.1	polymerase [Hepatitis B virus]	350	8e-96
gi	23380036	gb	AAM82930.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23380156	gb	AAM83010.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379922	gb	AAM82854.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379943	gb	AAM82868.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379967	gb	AAM82884.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23379928	gb	AAM82858.1	polymerase [Hepatitis B virus]	349	1e-95
gi	23380057	gb	AAM82944.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23379925	gb	AAM82856.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23380141	gb	AAM83000.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23380165	gb	AAM83016.1	polymerase [Hepatitis B virus]	348	2e-95
gi	23379997	gb	AAM82904.1	polymerase [Hepatitis B virus]	348	3e-95
gi	23380147	gb	AAM83004.1	polymerase [Hepatitis B virus]	348	3e-95
gi	23379868	gb	AAM82818.1	polymerase [Hepatitis B virus]	348	3e-95
gi	23379958	gb	AAM82878.1	polymerase [Hepatitis B virus]	348	3e-95
gi	23379904	gb	AAM82842.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23379931	gb	AAM82860.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23380159	gb	AAM83012.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23380144	gb	AAM83002.1	polymerase [Hepatitis B virus]	347	3e-95
gi	23379892	gb	AAM82834.1	polymerase [Hepatitis B virus]	347	4e-95
gi	23380000	gb	AAM82906.1	polymerase [Hepatitis B virus]	347	4e-95
gi	23380042	gb	AAM82934.1	polymerase [Hepatitis B virus]	347	4e-95
gi	23380003	gb	AAM82908.1	polymerase [Hepatitis B virus]	347	5e-95
gi	23379886	gb	AAM82830.1	polymerase [Hepatitis B virus]	347	5e-95
gi	23380009	gb	AAM82912.1	polymerase [Hepatitis B virus]	347	6e-95
gi	23380153	gb	AAM83008.1	polymerase [Hepatitis B virus]	347	6e-95
gi	23379973	gb	AAM82888.1	polymerase [Hepatitis B virus]	347	6e-95
gi	23380045	gb	AAM82936.1	polymerase [Hepatitis B virus]	346	7e-95
gi	23379877	gb	AAM82824.1	polymerase [Hepatitis B virus]	346	8e-95
gi	23380138	gb	AAM82998.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23379871	gb	AAM82820.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23380162	gb	AAM83014.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23379946	gb	AAM82870.1	polymerase [Hepatitis B virus]	346	9e-95
gi	23379895	gb	AAM82836.1	polymerase [Hepatitis B virus]	346	1e-94
gi	23379913	gb	AAM82848.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379916	gb	AAM82850.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379991	gb	AAM82900.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23380012	gb	AAM82914.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379889	gb	AAM82832.1	polymerase [Hepatitis B virus]	345	1e-94
gi	23379949	gb	AAM82872.1	polymerase [Hepatitis B virus]	345	1e-94

gi 23380039	gb	AAM82932.1	polymerase [Hepatitis B virus]	345	1e-94
gi 23379898	gb	AAM82838.1	polymerase [Hepatitis B virus]	345	2e-94
gi 23379880	gb	AAM82826.1	polymerase [Hepatitis B virus]	345	2e-94
gi 23380033	gb	AAM82928.1	polymerase [Hepatitis B virus]	345	2e-94
gi 23379874	gb	AAM82822.1	polymerase [Hepatitis B virus]	344	3e-94
gi 23379979	gb	AAM82892.1	polymerase [Hepatitis B virus]	344	3e-94
gi 23380015	gb	AAM82916.1	polymerase [Hepatitis B virus]	344	4e-94
gi 23379937	gb	AAM82864.1	polymerase [Hepatitis B virus]	344	4e-94
gi 23379940	gb	AAM82866.1	polymerase [Hepatitis B virus] >...	343	5e-94
gi 23380054	gb	AAM82942.1	polymerase [Hepatitis B virus]	343	7e-94
gi 23379910	gb	AAM82846.1	polymerase [Hepatitis B virus]	343	7e-94
gi 23379901	gb	AAM82840.1	polymerase [Hepatitis B virus]	343	8e-94
gi 23380018	gb	AAM82918.1	polymerase [Hepatitis B virus]	343	9e-94
gi 23380027	gb	AAM82924.1	polymerase [Hepatitis B virus]	342	1e-93
gi 1914714	emb	CAA66689.1	polymerase [Hepatitis B virus]	342	1e-93
gi 23379982	gb	AAM82894.1	polymerase [Hepatitis B virus]	342	2e-93
gi 5019986	gb	AAD37962.1	P protein [Hepatitis B virus]	341	2e-93
gi 23380051	gb	AAM82940.1	polymerase [Hepatitis B virus]	341	2e-93
gi 27450186	gb	AAO14550.1	AF460223_1 polymerase [Hepatitis ...	341	3e-93
gi 5019949	gb	AAD37932.1	P protein [Hepatitis B virus]	341	4e-93
gi 27450210	gb	AAO14562.1	AF460235_1 polymerase [Hepatitis ...	338	2e-92
gi 27450206	gb	AAO14560.1	AF460233_1 polymerase [Hepatitis ...	337	4e-92
gi 1107593	emb	CAA56885.1	polymerase [Hepatitis B virus]	336	7e-92
gi 27450208	gb	AAO14561.1	AF460234_1 polymerase [Hepatitis ...	336	8e-92
gi 27450182	gb	AAO14548.1	AF460221_1 polymerase [Hepatitis ...	336	8e-92
gi 27450184	gb	AAO14549.1	AF460222_1 polymerase [Hepatitis ...	335	2e-91
gi 3820918	emb	CAA08937.1	polymerase [Hepatitis B virus] >...	332	2e-90
gi 3820942	emb	CAA08951.1	polymerase [Hepatitis B virus]	330	5e-90
gi 3820933	emb	CAA08947.1	polymerase [Hepatitis B virus]	326	8e-89
gi 3820945	emb	CAA08953.1	polymerase [Hepatitis B virus]	326	9e-89
gi 3820930	emb	CAA08945.1	polymerase [Hepatitis B virus]	325	3e-88

Query= gi|93080|pir||S20757 DNA-directed DNA polymerase (EC
2.7.7.7) - hepatitis B virus (subtype ayw, patient E)
(832 letters)

cutoff = 3e-88

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,376,942 sequences; 442,405,847 total letters

BLASTP 2.2.5 (Nov-16-2002) (Altschul, S.F., et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402 (1997))
against HBV subtype sequence S20757, cutoff = 3e-88 (to select human sequences).

Table 21: CLUSTALW alignment of 19 HBV polymerase sequences

	10	20	30	40	50	60
JDLVLS	MPLSYQHFRKLLLLDDGTEAGPLEEEELPRLADADLNRRVAEDNLGNLNVSI	PWTHKVG				
JDLVLD	MPLSYQHFRKLLLLDDGTEAGPLEEEELPRLADADLNRRVAEDNLGNLNVSI	PWTHKVG				
JDLVJ3	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
S71785	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
S47406	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
JDLVA1	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
S20752	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
S67505	MPLSCPHFRKLLLLDE--EAGPLEEEELPRLADEGLNRRVAEDNLQLPNVS	PWTHKVG				
JQ2229	MPLSYPHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLQLPNVS	PWTHKVG				
UNK_494016	-----					
UNK_494017	-----					
UNK_494015	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
UNK_494018	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
JDLVLS	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
JDLVLR	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
T13468	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
T13473	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
S43491	MPLSYQHFRKLLLLDN--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
S35527	MPLSYQHFRKLLLLDD--EAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
Prim. cons.	MPLSYQHFRKLLLLDDGTEAGPLEEEELPRLADEGLNRRVAEDNLGNLNVSI	PWTHKVG				
	70	80	90	100	110	120
JDLVLS	FTGLYSSTAPIFNPEWQTPSF	PKIHLQEDI	INRCQQFVG	PLTVNEKRRLK	LIMPARFYPT	
JDLVLD	FTGLYSSTVPIFNPEWQTPSF	PKIHLQEDI	INRCQQFVG	PLTVNEKRRLK	LIMPARFYPT	
JDLVJ3	FTGLYSSTVPSFNPQWQTPSF	PD IHLQEDI	INCKQFVG	PLTVNEKRRLK	LIMPARFYPN	
S71785	FTGLYSSTVPVFNPHWKTPSF	PN IHLQDI	IKKCEQFVG	PLTVNEKRRLQ	LIMPARFYPN	
S47406	FTGLYSSTVPVFNPHWKTPSF	PN IHLQDI	IKKCEQFVG	PLTVNEKRRLQ	LIMPARFYPK	
JDLVA1	FTGLYSSTVPVFNPHWKTPSF	PN IHLQDI	IKKCEQFVG	PLTVNEKRRLQ	LIMPARFYPK	
S20752	FTGFYSSTVPVFNPHWETPSF	PN IHLQDI	IKKCEQFVG	PLTVNEKRRLQ	LIMPARFYPK	
S67505	FTGLYSSTVPVFNPKWQTPSF	PD IHLQDI	INCKEQFVG	PLTVNEKRRLK	LIIAARFYPN	
JQ2229	FTGLYSSTVPAFNPWNSTPSF	PD IHLQDI	ISKCEQFVG	PLTKNELRRLK	LVMARFYPK	
UNK_494016	-----					
UNK_494017	-----					
UNK_494015	FTGLYSSTVPVFNPDWKTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
UNK_494018	FTGLYSSTVPVFNPDWKTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
JDLVLS	FTGLYSSTVPVFNPEWQTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPK	
JDLVLR	FTGLYSSTVPVFNPEWQTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
T13468	FTGLYSSTVPVFNPEWQTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
T13473	FTGLYSSTVPVFNPEWQTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
S43491	FTGLYSSTVPVFNPEWQTPSF	PHIHLQEDI	IDRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
S35527	FTGLYSSTVPVFNPECQTPSF	PHIHLQEDI	INRCQQYVG	PLTVNEKRRLK	LIMPARFYPN	
Prim. cons.	FTGLYSSTVPVFNPEWQTPSF	PHIHLQEDI	INRCQQFVG	PLTVNEKRRLK	LIMPARFYPN	
	130	140	150	160	170	180
JDLVLS	HTKYLPLDKGIKPYYPDQV	VNHYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
JDLVLD	HTKYLPLDKGIKPYYPDQV	VNHYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
JDLVJ3	VTKYLPDKGIKPYYPEHVN	HYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
S71785	VTKYLPDKGIKPYYPEHVN	HYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
S47406	VTKYLPDKGIKPYYPEHVN	HYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
JDLVA1	VTKYLPDKGIKPYYPEHVN	HYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
S20752	VTKYLPDKGIKPYYPEHVN	HYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		
S67505	APKYLPLDKGIKPYYPEHVN	HYFQTRHYLHTLWK	GILYKRETT	SASFCGSPYSWEQE		

JQ2229 VTKYFPMDDKGIKPYYPBHAVNHYFKTRHYLHTLWKAGILYKRESTRSASFCSGSPYSWEQE
 UNK_494016 -----
 UNK_494017 -----
 UNK_494015 LTKYLPLDKGIKPYYPBYAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 UNK_494018 LTKYLPLDKGIKPYYPBYAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 JDVLVS LTKYLPLDKGIKPYYPBHAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 JDVLVR LTKYLPLDKGIKPYYPBHAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 T13468 LTKYLPLDKGIKPYYPBHAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 T13473 LTKYLPLDKGIKPYYPBHAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 S43491 LTKYLPLDKGIKPYYPBHAVNHYFQTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE
 S35527 LTKYLPLDKGIKPYYPBHAVNHYFKTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE

Prim. cons. LTKYLPLDKGIKPYYPBHAVNHYFQTRHYLHTLWKAGILYKRETRRSASFCSGSPYSWEQE

	190	200	210	220	230	240
JDVLKS	LQHGRLVIKTSQRHGDES	FCSQPSGILSRSSV	GPCIRSQLKQSR	LGLQPHQG	PLASSQPG	
JDVLVD	LQHGRLVIKTSQRHGDES	FCSQSSGILSRSSV	GPCIRSQLKQSR	LGLQPRQGR	LASSQPS	
JDVLJ3	LQHGRLVLQTSR	HGDKSFRPQSSGILSR	SPVGP	CIQSQLRQSR	LGPQPTQ	QGLAQ
S71785	LQHG-----	AESFHQSSGILSRPPV	GSSLSQSKHRKS	SRLGLQSQQGH	LARRQQG	
S47406	LQHG-----	AESFHQSSGILSRPPV	GSSLSQSKHKS	SRLGLQSQQGH	LARRQQG	
JDVLA1	LQHG-----	AESFHQSSGILSRPPV	GSSLSQSKHCKS	SRLGLQSQQGH	LARRQQG	
S20752	LQHG-----	AESIHQSSGILSRPPV	GSSLSQSKHRKS	SRLGLQSQQGH	LARRQQG	
S67505	LQHG-----	AEPVCQQSLGILPRAS	VGSPVQSQLKQSR	LGLQSQQR	QLARSHQG	
JQ2229	LQHGSTSLNDTKRHG	TESLCAQSSGILSRPS	SAGSAIQSKFQ	QSRGLQHKQ	QQLANGKQ	
UNK_494016	-----	-----	-----	-----	-----	
UNK_494017	-----	-----	-----	-----	-----	
UNK_494015	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARGKSG	
UNK_494018	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARGKSG	
JDVLVS	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARGKSG	
JDVLVR	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LMARGKSG	
T13468	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARGKSG	
T13473	LQHGRLVFQTSR	HGDKSFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARGQSG	
S43491	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARGKAG	
S35527	LQHGRLVFQTSR	HGDESFCSSGILSRSPV	GPCVRSQKQSR	LGLQPQQGS	LARRNQG	

Prim. cons. LQHGRLVFQTSRHGDESFCSSGILSRSPVGPCVRSQKQSRGLQPQQGS LARGQQG

	250	260	270	280	290	300
JDVLKS	RSGSIRARVHPSTR	RCFVPEPSGSGH	VDPSVMNSSSCL	RQSAVRKAAYSH	LSTSKRQSSS	
JDVLVD	RSGSIRAKAHPSTR	RYFVPEPSGSGH	IDHVMNSSSCL	HQSAVRKAAYSH	LSTSKRQSSS	
JDVLJ3	SGSIRAGIHSTP	WGTVGVEPSSG	HTNHCANSSSCL	HQSAVRKEAYSP	VSTSKRHSSS	
S71785	RSWSIRAGIHPTA	RRPFGVEPSGSGH	TNLASKSASCIY	QSPVRKAAYPA	VSTFEKHSSS	
S47406	RSWSIRAGIHPTA	RRPFGVEPSGSGH	TNLASKSASCLY	QSPVRKAAYPA	VSTFEKHSSS	
JDVLA1	RSWSIRAGIHPTA	RRPFGVEPSGSGH	TNLASKSASCLH	QSPVRKATYPS	VSTFEKHSSS	
S20752	WSWSIRAGTHPTA	RRPFGVEPSGSGH	TNRASKSASCLY	QSPDRKATYPS	VSTFERHSSS	
S67505	RSGSIRARVHST	TRRSFRVELSGSG	SNHNIASTSSS	CRHQSAVRETAY	SHLSTVERHSSS	
JQ2229	RSGRLRSRVHTP	TRWPAGVEPSS	TRCVNNLASRS	ASCFHQSAVREK	ANPSLSTSKRHT	ST
UNK_494016	-----	-----	-----	-----	-----	
UNK_494017	-----	-----	-----	-----	-----	
UNK_494015	RSGSIWSRVHPT	TRRPFGVEPSGSGH	IDNTASSTSSCL	HQSAVRKTAYSH	LSTSKRQSSS	
UNK_494018	RSGSIWSRVHPT	TRRPFGVEPSGSGH	IDNTASSTSSCL	HQSAVRKTAYSH	LSTSKRQSSS	
JDVLVS	RSGSIRARVPPT	TRRSFGVEPSGSGH	IDNRASSTSSCL	HQSAVRKTAYSH	LSTSKRQSSS	
JDVLVR	RSGSIRARVHPT	TRRSFGVEPSGSGH	IDNSASSTSSCL	HQSAVRKTAYSH	LSTSKRQSSS	
T13468	RSGSIRARVHPT	TRRSFGVEPSGSGH	IDNSARSASSCL	HQSAVRKTAYSH	LSTSKRQSSS	
T13473	RIGSIRARVHPT	TRRSFGVEPSGSGH	IDNSASSPSSCL	HQSAVRKTAYCH	LSTTKRQSSS	
S43491	RSGSIRARVHPT	TRRPFGVEPSGSGH	IDNSASSASSCF	HQSAVRKTAYSH	LSTSKRQSSS	
S35527	RSGRLRARVHPT	TRRSFGVEPSGSGH	IDNSASSSSSCL	HQSAVRKTAYSH	LSTSKRQSSS	

Prim.cons. RSGSIRARVHPTTRRPFVPSGSGHIDNSASSSSSCLHQSAVRKTAYSHLSTSKRQSSS

	310	320	330	340	350	360
JDVLKS	GHAVEFHCLPPSSAR	PQSQGSV	FSCWWLQFRNSKPCSEYCLSHLVNLR	REDRGPCDEHGEH		
JDVLVD	GHAVEFHCLPPNSAGS	QSQSVSSCWWLQFRNSKPCSEYCLSHLVNLR	REDWGPCDEHGEH			
JDVLJ3	GNAVELHHVPPNSRSQ	SQSVLSCWWLQFRNSKPCSEHCLFHIVNLI	DDWGPCAEHGEH			
S71785	GHAVELHNFPPNSARSQ	GERPVFPCWWLQFRNSKPCSDYCLSHIVNLL	EDWGPCTEHGEH			
S47406	GHAVELHNLPPNSRSQ	GERPVFPCWWLQFRNSKPCSDYCLSHIVNLL	EDWGPCAEHGEH			
JDVLA1	GHAVELHNLPPNSARSQ	SERPVSPCWWLQFRNSKPCSDYCLSHIVNLL	EDWGPCAEHGEH			
S20752	GRAVELHNFPPNSARSQ	SERPIFPCWWLQFRNSKPCSDYCLSLIVNLL	EDWGPCAEHGEH			
S67505	GHEVELYSIPPNSARSQ	STGPILSCWWLQFRNSEPCSDYCLSHLVNLL	EDWGPCTEHGEH			
JQ2229	GNAVELNPVPPSSVGSQ	GKGSVLPWWLQFRDTEPCSDYCLSHIINLL	EDWGPCYEHGQH			
UNK_494016	-----LHNIPPSSARSQ	SEGP2FSCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEH			
UNK_494017	-----LHNIPPSSARSQ	SEGP2FSCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEH			
UNK_494015	GHAVE-----					
UNK_494018	GHAVE-----					
JDVLVS	GHAVELHHISPPARSQ	SEGP2FSSWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEH			
JDVLVR	GHAVEFHNIIPPSSARSQ	SEGP2FSCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEH			
T13468	GHAVELHPCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEHNIRIPRTPARVTGGV				
T13473	GHAVETCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEHNIRIPRTPARVTGGV				
S43491	GHAVELHNIIPPSSARSK	SEGPLFPCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEH			
S35527	GHAVELHNIIPPSSARSQ	SEGP2FSCWWLQFRNSKPCSDYCLTHIVNLL	EDWGPCTEHGEH			

Prim.cons. GHAVELHNIIPPSSARSQSEGP2FSCWWLQFRNSKPCSDYCLSHIVNLL

	370	380	390	400	410	420
JDVLKS	HIRIPRTPARVTCCVFLVDKNPHNTAESRLVVD	FSQFSRGITRVSWPKFAIPNLQSLTNL				
JDVLVD	HIRIPRTPARVTGGVFLVDKNPHNTAESRLVVD	FSQFSRGISRVSWPKFAVPNLQSLTNL				
JDVLJ3	RIRTPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGNTRVSWPKFAVPNLQSLTNL				
S71785	HIRIPRTPARVTGGVFLVDKNPHNTAESRLVVD	FSQFSRGNHRVSWPKFAVPNLQSLTNL				
S47406	HIRIPRTPARVTGGVFLVDKNPHNTAESRLVVD	FSQFSRGNYRVSWPKFAVPNLQSLTNL				
JDVLA1	HIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGNHRVSWPKFAVPNLQSLTNL				
S20752	HIRIPRTPARVTGGVFLVDKNPHNTAESRLVVD	FSQFSRGNYRVSWPKFAVPNLQSLTNL				
S67505	HIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGSTRVSWPKFAVPNLQSLTNL				
JQ2229	YIRTPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGTTVSWPKFAVPNLQSLTNL				
UNK_494016	NIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGSTHVS	SWPKFAVPNLQSLTNL			
UNK_494017	NIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGSTHVS	SWPKFAVPNLQSLTNL			
UNK_494015	-----					
UNK_494018	-----					
JDVLVS	NIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGSTHVS	SWPKFAVPNLQSLTNL			
JDVLVR	NIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGSTHVS	SWPKFAVPNLQSLTNL			
T13468	LVDKNPHNTESRLVVD	FSQFSRGSTX-----	VS	SWPKFAVPNLQSLTNL		
T13473	DKNPHNTESX-----	LVVD	FSQFSRGSTQV	SWPKFAVPNLQSLTNL		
S43491	NIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGNTQV	SWPKFAVPNLQSLTNL			
S35527	NIRIPRTPARVTGGVFLVDKNPHNTESRLVVD	FSQFSRGSTHVS	SWPKFAVPNLQSLTNL			

Prim.cons. HIRIPRTPARVTGGVFLVDKNPHNTESRLVVD

	430	440	450	460	470	480
JDVLKS	LSSNLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARLSSNSRINN	QYGT			
JDVLVD	LSSNLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARLSSNSRINN	QYGT			
JDVLJ3	LSSDLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARLSSNSRI	INHQR			
S71785	LSSNLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARVSSNSRI	FNHQR			
S47406	LSSNLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARLSSNSRI	FNHQR			
JDVLA1	LSSNLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARLSSD	SRI			
S20752	LSSNLSWLSLDVSAAGFYHILPLHPAAMP	HLIGSSGV	SRYVARLSSNSRNMNN	QYGT		
S67505	LSSNLSWLSLDVSAAFYHILPLHPAAMP	HLIGSSGLSRYVARLSST	SRI			

JQ2229 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLSRYVARLSSTSRINHGHQHTLQNL
 UNK_494016 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINYQHGTMQNL
 UNK_494017 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINYQHGTMQNL
 UNK_494015 -----
 UNK_494018 -----
 JDVLVS LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINHGHGTMQDL
 JDVLVR LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINHGHGTMQDL
 T13468 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINXQHGTMQDL
 T13473 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINXQHGTMQDL
 S43491 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLQRYVARLSSTSRNINYQHGTMQDL
 S35527 LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLPRYVARLSSTSRNINYQHGTMQDL

Prim. cons. LSSNLSWLSLDVSAAFYHPLHPAAMPHELLVGSSGLSRYVARLSSTSRNINHGHGTMQNL

	490	500	510	520	530	540
JDVLKS	HDSCSRQLYVSLM	LLYKTYGWLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
JDVLVD	HDSCSRQLYVSLM	LLYKTYGWLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
JDVLJ3	HDSCSRNLYVSLM	LLYKTYGWLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
S71785	HDYCSRNLYVSL	LLLYQTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
S47406	HDYCSRNLYVSL	LLLYQTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
JDVLA1	HDSCSRNLYVSL	LLLYQTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
S20752	HDSCSRQLYVSL	MLLYQNFQWLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
S67505	HDHCSRNLFVSL	MLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSSICS	VVR
JQ2229	HNSCTRNLYVSL	LLLFQTLGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
UNK_494016	HDSCSRNLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
UNK_494017	HDSCSRNLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDVLVS	HDSCSRNLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
JDVLVR	HDSCSRNLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
T13468	HESCSRNLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
T13473	HDSCSKHLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
S43491	HDSCSKHLYVSL	LLLYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR
S35527	HDSCSRNLYVSL	LLLVYKTFGRKLHLY	SHPIVLGFRKIP	MGVGLSPFLLA	QFTSAICS	VVR

Prim. cons. HDSCSRNLYVSLLLLYKTFGRKLHLYSHPIVLGFRKIPMGVGLSPFLLAQFTSAICS

	550	560	570	580	590	600
JDVLKS	RAFPHCLAFSYM	DDVVLGAKSVQH	REFLYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
JDVLVD	RAFPHCLAFSYM	DDVVLGAKSVQH	RESLYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
JDVLJ3	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYAAVTNF	LFLSLGIHLN	PQTKRWGYS	LNFMGY
S71785	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
S47406	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
JDVLA1	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
S20752	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
S67505	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
JQ2229	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
UNK_494016	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
UNK_494017	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDVLVS	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
JDVLVR	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
T13468	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
T13473	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
S43491	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY
S35527	RAFPHCLAFSYM	DDVVLGAKSVQH	LESFYTAVTNF	LFLSLGIHLN	PNKTKRWGYS	LNFMGY

Prim.cons. RAFFPHCLAFSYMDDVVLGAKSVQHLESFTAVTNFLLSLGIHLNPNKTKRWGYSLNFMGY

	610	620	630	640	650	660
JDLVLS	VIGSWGTL	PQDHIVQKIKHC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
JDLVLD	IIGSWGTL	PQDHIVQKIKHC	FRKLPVNR	PIDWKVCQ	RIVGLLGFA	APFTQCGYPALMPLY
JDLVJ3	VIGSWGTL	PQEHIVLKI	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
S71785	VIGSYGSL	PQDHIIQKIK	CEFRKL	PINR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
S47406	VIGCYGSL	PQDHIIQKIK	CEFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
JDLVA1	VIGCYGSL	PQDHIIQKIK	CEFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
S20752	VIGCYGSL	PQEHIIQKIK	CEFRKVP	VNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
S67505	IIGSWGSL	PQDHIVQKIK	QCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
JQ2229	VIGSWGSL	PQDHIVHKIK	CEFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
UNK_494016	VIGSWGTL	PQEHIVQKL	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
UNK_494017	VIGSWGTL	PQEHIVQKL	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDLVLS	VIGSWGTL	PQEHIVLKI	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
JDLVLR	VIGSWGTL	PQEHIVLKL	KQCFRKL	PVNS	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
T13468	VIGSWGTL	PQEHIVQKI	KQCFRKL	PVNR	PIDWKVCQ	XIVGLLGFAAPFTQCGYPALMPLY
T13473	VIGSWGTL	PQDHIVQKL	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
S43491	VIGSWGTL	PQEHIVQKL	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY
S35527	VIGSWGTL	PQEHIVLKL	KQCFRKL	PVNR	PIDWKVCQ	RIVGLLGFAAPFTQCGYPALMPLY

Prim.cons. VIGSWGTLPOEHIVQKIKQCFRKL PVNRPIDWKVCQ RIVGLLGFAAPFTQCGYPALMPLY

	670	680	690	700	710	720
JDLVLS	ACIQAKQA	FTFSPTYKA	FLSKQYMN	LYPVARQR	PGLCQVF	FADATPTGWGLAIGHQRM
JDLVLD	ACIQAKQA	FTFSPTYKA	FLSKQYMN	LYPVARQR	PGLCQVF	FADATPTGWGLAIGHQRM
JDLVJ3	ACIQAKQA	FTFSPTYKA	FLNKKQYL	NLYPVARQR	PGLCQVF	FADATPTGWGLAIGHQRM
S71785	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVF	FADATPTGWGLVMGHQRM
S47406	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVF	FADATPTGWGLVMGHQRM
JDLVA1	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVF	FADATPTGWGLVMGHQRM
S20752	ACIQFKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	PGLCQVF	FADATPTGWGLVMGHQRM
S67505	ACIQAKQA	FTFSPTYKA	FLRTQYLT	LYPVARQR	PGLCQVF	FADATPTGWGLAIGHQRM
JQ2229	ACITAKQA	FTFSPTYKA	FLCKQYMN	LYPVARQR	PGLCQVF	FADATPTGWGLAIGHQRM
UNK_494016	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVF	FADATPTGWGLAIGHRRMR
UNK_494017	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVF	FADATPTGWGLAIGHRRMR
UNK_494015	-----	-----	-----	-----	-----	-----
UNK_494018	-----	-----	-----	-----	-----	-----
JDLVLS	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARRT	ALCQVF	FADATPTGWGLAIGHRRMR
JDLVLR	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVF	FADATPTGWGLAIGHRRMR
T13468	ACIQAKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVF	FADATPTGWGLAIGHRRMR
T13473	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVF	FADATPTGWGLAIGHRRMR
S43491	ACIQSKQA	FTFSPTYKA	FLCKQYLN	LYPVARQR	SGLCQVF	FADATPTGWGLAIGHQRM
S35527	ACIQSKQA	FTFSPTYKA	FLCQYLN	LYPVARQR	SGLCQVF	GDATPTGWGLAIGHRRMR

Prim.cons. ACIQSKQAFTFSPTYKAFLCKQYLNLYPVARQR PGLCQVFADATPTGWGLAIGHQRM

	730	740	750	760	770	780
JDLVLS	FVAPLP	PIHTAELLA	ACFARS	SRGAKL	IGTDNS	VVLSRKYTSFPWLLGCAANWILRGTSFV
JDLVLD	FVAPLP	PIHTAELLA	ACFARS	SRGAKL	IGTDNS	VVLSRKYTSFPWLLGCTANWILRGTSFV
JDLVJ3	FVSPLP	PIHTVELLA	ACFARS	SRGAKL	IGTDNS	VVLSRKYTSFPWLLGCAANWILRGTSFV
S71785	FLAPLP	PIHTAELLA	ACFARS	SRGANI	IGTDNS	VVLSRKYTSFPWLLGCAANWILRGTSFV
S47406	FLAPLP	PIHTAELLA	ACFARS	SRGANI	IGTDNS	VVLSRKYTSFPWLLGCAANWILRGTSFV
JDLVA1	FQAPLP	PIHTAELLA	ACFARS	SRGANI	IGTDNS	VVLSRKYTSFPWLLGCAANWILRGTSFV
S20752	FSAPLP	PIHTAELLA	ACFARS	SRGANI	IGTDNS	VVLSRKYTSFPWLLGCAANWILRGTSFV
S67505	FVAPLP	PIHTAELLA	ACFARS	SRGANI	IGTDNS	VVLSPKYTSFPWLLGCAANWILRRTSFV

JQ2229 FVAPLPIHTAELLAACFARSRSRGATLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 UNK_494016 FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 UNK_494017 FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 UNK_494015 -----
 UNK_494018 -----
 JDVLVS VAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTYFVY
 JDVLVR FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 T13468 FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 T13473 FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 S43491 FVAPLPIHTAELLAACFARSRSRGATLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV
 S35527 FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV

Prim.cons. FVAPLPIHTAELLAACFARSRSRGAKLIGTDNSVVLRSKYTSFPWLLGCAANWILRGTSFV

	790	800	810	820	830	840
JDVLKS	YVPSALNPADDPSRGRLGLSRPLLRLPFQPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					
JDVLVD	YVPSALNPADDPSRGRLGLSRPLLRLPFQPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					
JDVLJ3	YVPSALNPADDPSRGRLGLYRPLLRLPYRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
S71785	YVPSALNPADDPSRGRLGIFRPLLRLPFRPTTGRTSLYADSPSVPSHLPVRVHFASPLHV					
S47406	YVPSALNPADDPSRGRLGLSRPLLRLPFRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
JDVLA1	YVPSALNPADDPSRGRLGLSRPLLRLPFRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
S20752	YVPSALNPADDPSRGRLGLSRPLLCLPFRPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
S67505	YVPSALNPADDPSRGRLGLYRPLLRLPFRPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					
JQ2229	YVPSALNPADDPSRGRLGLYRPLLRLPFQPTTGRTSLYADSPSVPSHLPDRVHFASPLHV					
UNK_494016	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
UNK_494017	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
UNK_494015	-----					
UNK_494018	-----					
JDVLVS	VPSALNPADDPSRGRLGLIRPLLHLRFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHVA					
JDVLVR	YVPSALNPADDPSRGRLGLYRPLLRLPFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
T13468	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
T13473	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
S43491	YVPSALNPADDPSRGRLGLYRPLLHLRPFRTTGRTSLYAVSPSVPSHLPDRVHFASPLHV					
S35527	YVPSALNPADDPSRGRLGLYRPLLHLRPFQPTTGRTSLYAVSPSVPSHLPVRVHFASPLHV					

Prim.cons. YVPSALNPADDPSRGRLGLYRPLLRLPFRPTTGRTSLYAVSPSVPSHLPDRVHFASPLHV

JDVLKS AWRPP
 JDVLVD AWRPP
 JDVLJ3 AWRPP
 S71785 AWRPP
 S47406 AWRPP
 JDVLA1 AWRPP
 S20752 AWRPP
 S67505 AWRPP
 JQ2229 AWRPP
 UNK_494016 AWRPP
 UNK_494017 AWRPP
 UNK_494015 -----
 UNK_494018 -----
 JDVLVS WRPP-
 JDVLVR AWRPP
 T13468 AWRPP
 T13473 AWRPP
 S43491 AWRPP
 S35527 AWRPP

Prim.cons. AWRPP

CLUSTALW alignment of 19 HBV polymerase sequences representing the sybtypes adw (4), ayw (5), ayr (4) and adr (6) (NPS@: Network Protein Sequence Analysis, TIBS Vol. 25, No 3 (291):147-150, Combet C., Blanchet C., Geourjon C. and Deléage G. (March 2000))

CLUSTALW options used :

endgaps=1
gapdist=8
gapext=0.2
gapopen=10.0
hgapresidues=GPSNDQERK
ktuple=1
matrix=gonnet
maxdiv=30
outorder=aligned
pairgap=3
score=percent
topdiags=5
type=PROTEIN
window=5

Table 22. HCV Multiple Sequence Alignment

GCG Multiple Sequence File.

Written by Omega 1.1

Name: BEBE1	Len: 3052	Check: 2605	Weight: 1.00
Name: D89815	Len: 3052	Check: 9655	Weight: 1.00
Name: ED43type_4	Len: 3052	Check: 4987	Weight: 1.00
Name: HC_C2	Len: 3052	Check: 6273	Weight: 1.00
Name: HC_G9	Len: 3052	Check: 217	Weight: 1.00
Name: HCU16326	Len: 3052	Check: 5854	Weight: 1.00
Name: HCV_H_CMR	Len: 3052	Check: 4932	Weight: 1.00
Name: HCV_J1	Len: 3052	Check: 4947	Weight: 1.00
Name: HCV_J483	Len: 3052	Check: 2553	Weight: 1.00
Name: HCV_J8	Len: 3052	Check: 9778	Weight: 1.00
Name: HCV_JK1	Len: 3052	Check: 4917	Weight: 1.00
Name: HCV_JS	Len: 3052	Check: 3982	Weight: 1.00
Name: HCV_K1_R1	Len: 3052	Check: 9084	Weight: 1.00
Name: HCV_K1_R2	Len: 3052	Check: 47	Weight: 1.00
Name: HCV_K1_R3	Len: 3052	Check: 1630	Weight: 1.00
Name: HCV_K1_S1	Len: 3052	Check: 3578	Weight: 1.00
Name: HCV_K1_S2	Len: 3052	Check: 9909	Weight: 1.00
Name: HCV_K1_S3	Len: 3052	Check: 9508	Weight: 1.00
Name: HCV_L2	Len: 3052	Check: 4175	Weight: 1.00
Name: HCV_N	Len: 3052	Check: 1702	Weight: 1.00
Name: HCV12083	Len: 3052	Check: 7564	Weight: 1.00
Name: HCV1480	Len: 3052	Check: 5620	Weight: 1.00
Name: HCVPOLYP	Len: 3052	Check: 2663	Weight: 1.00
Name: HD_1	Len: 3052	Check: 4040	Weight: 1.00
Name: HPCCGAA	Len: 3052	Check: 5414	Weight: 1.00
Name: HPCFG	Len: 3052	Check: 7119	Weight: 1.00
Name: HPCGENANTI	Len: 3052	Check: 9591	Weight: 1.00
Name: HPCGENOM	Len: 3052	Check: 2009	Weight: 1.00
Name: HPCHUMR	Len: 3052	Check: 4863	Weight: 1.00
Name: HPCJ	Len: 3052	Check: 3553	Weight: 1.00
Name: HPCJCG	Len: 3052	Check: 6658	Weight: 1.00
Name: HPCJK046	Len: 3052	Check: 436	Weight: 1.00
Name: HPCJK049	Len: 3052	Check: 9796	Weight: 1.00
Name: HPCJTA	Len: 3052	Check: 2902	Weight: 1.00
Name: HPCJTB	Len: 3052	Check: 4237	Weight: 1.00
Name: HPCK3A	Len: 3052	Check: 2180	Weight: 1.00
Name: HPCPLYPRE	Len: 3052	Check: 6557	Weight: 1.00
Name: HPCPOLP	Len: 3052	Check: 1218	Weight: 1.00
Name: HPCPP	Len: 3052	Check: 3845	Weight: 1.00
Name: HPCUNKCD	Len: 3052	Check: 6214	Weight: 1.00
Name: MKC1A	Len: 3052	Check: 1615	Weight: 1.00
Name: NDM59	Len: 3052	Check: 9717	Weight: 1.00
Name: NZLI	Len: 3052	Check: 2255	Weight: 1.00
Name: SA13	Len: 3052	Check: 9158	Weight: 1.00
Name: Th580	Len: 3052	Check: 37	Weight: 1.00
Name: Type_3a_CB	Len: 3052	Check: 7958	Weight: 1.00
Name: TypeV_D	Len: 3052	Check: 303	Weight: 1.00
Name: VN004	Len: 3052	Check: 3873	Weight: 1.00
Name: VN235	Len: 3052	Check: 7756	Weight: 1.00
Name: VN405	Len: 3052	Check: 7249	Weight: 1.00

1	50
BEBE1	MSTNPKPQRK TKRNTNRRPQ DVKFPGGGQI VGGVYLLPRR GPRLGVRATR
D89815	MSTNPKPQRK TKRNTNRRPQ DVKFPGGGQI VGGVYLLPRR GPRLGVRATR
ED43type_4	MSTNPKPQRK TKRNTNRRPM DVKFPGGGQI VGGVYLLPRR GPRLGVRATR
HC_C2	MSTNPKPQRK TKRNTNRRPQ DVKFPGGGQI VGGVYLLPRR GPRLGVRATR

HC_G9	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRVGVRA
HCU16326	MSTNPKPQRK	TKRNTNRRPQ	DIKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_H_CMR	MSTNPKPQRK	TKRNTNRRPQ	DVEFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_J1	MSTIPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_J483	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_J8	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_JK1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_JS	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_K1_R1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_K1_R2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_K1_R3	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_K1_S1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_K1_S2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_K1_S3	MSTNPKPQRQ	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_L2	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV_N	MSTNPKPQRK	TKRNTNRRPQ	EVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCV12083	MSTLPPKQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRK	GPRLGVRATR
HCV1480	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HCVPOLYP	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HD_1	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCCGAA	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCFG	MSTLPPKQRQ	TKRNTLRRPK	NVKFPAGGQI	VGEVYVLP	GPQLGVREVR
HPCGENANTI	MSTNGKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCGENOM	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCHUMR	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCJ	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCJCG	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCJK046	MSTNPKPQRQ	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCJK049	MSTLPPKQRI	TKRNTNRRPQ	DVKFPGGGQI	VGGVYVLP	GPRLGVRATR
HPCJTA	MSTNPKPQRK	TKRNTYRRPQ	DVKFPGGGQI	VGGVYVLP	GPTLGVRATR
HPCJTB	MSTNPKPQRK	TKRNTYRRPQ	DVKFPGGGQI	VGGVYVLP	GPTLGVRATR
HPCK3A	MSTLPPKQRK	TKRNTIRRPQ	DVKFPGGGQI	VGGVYVLP	GPRLGVRATR
HPCPLYPRE	MSTNPKPQKK	NKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCPOLP	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCPP	MSTNPKPQRK	IKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
HPCUNKCD	MSTNPKPQRK	TKRNTNRRPQ	DIKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
MKC1A	MSTNPKPQRK	IKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
NDM59	MSTNPKPQRK	TKRNTSRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
NZLI	MSTLPPKQRK	TKRNTIRRPQ	DVKFPGGGQI	VGGVYVLP	GPRLGVRATR
SA13	MSTNPKPQRK	TKRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
Th580	MSTLPPKQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
Type_3a_CB	MSTLPPKQRK	TKRNTIRRPQ	DVKFPGGGQI	VGGVYVLP	GPRLGVCATR
TypeV_D	MSTLPPKQRK	TKRNTIRRPQ	DVKFPGGGQI	VGGVYVLP	GPRLGVRATR
VN004	MSTLPPKQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
VN235	MSTLPPKQKR	NQRNTNRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR
VN405	MSTLPPKQRK	TKRNTNRRPM	DVKFPGGGQI	VGGVYLLPRR	GPRLGVRATR

51

100

BEBE1	KTSESRQPRG	RRQPIPKDRR	STGKSWGRPG	YPWPLYRNEG	LGWAGWLLSP
D89815	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
ED43type_4	KTSESRQPRG	RRQPIPKARR	PEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HC_C2	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HC_G9	KTSESRQPRG	RRQPIPKARR	PEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HCU16326	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_H_CMR	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HCV_J1	KTSESRQPRG	RRQPIPKVRR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HCV_J483	KTSESRQPRG	WRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_J8	KTSESRQPRG	RRQPIPKDRR	STGKSWGKPG	YPWPLYGNEG	CGWAGWLLSP
HCV_JK1	KTSESRQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_JS	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	MGWAGWLLSP

HCV_K1_R1	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWACWLLSP
HCV_K1_R2	KTSESRQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV_K1_R3	KTSESRQPRG	RRQPIPKVRR	SEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_K1_S1	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_K1_S2	KTSESRQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV_K1_S3	KTSESRQPRG	RRQPIPKVRR	SEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
HCV_L2	KTSESRQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYANEG	LGWAGWLLSP
HCV_N	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HCV12083	KTSESRQPRG	RRQPIPKARQ	PQGRHWAQPG	YPWPLYGSEG	CGWAGWLLSP
HCV1480	KNSERSQPRG	RRQPIPKARR	PTGRSWGQPG	YPWPLYANEG	LGWAGWLLSP
HCVPOLYP	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	MGWAGWLLSP
HD_1	KTSESRQPRG	RRQLIPKARQ	PEGRSWAQPG	YPWPLYGNEG	MGWAGWLLSP
HPCCGAA	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCFG	KTSESRQPRG	RRQPTPKARP	REGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCGENANTI	KTSESRQPRG	RRQPIPKARQ	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCGENOM	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	FGWAGWLLSP
HPCCHUMR	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCJ	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	MGWAGWLLSP
HPCJCG	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	MGWAGWLLSP
HPCJK046	KTSESRQPRG	RRQPIPKARR	QTGRAWGQPG	YAWPLYGNEG	CGWAGWLLSP
HPCJK049	KTSESRQPRG	RRQPIPKARR	TEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCJTA	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCJTB	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCK3A	KTSESRQPRG	RRKPIPKARR	SEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCPLYPRE	KTSESRQPRG	RRQPIPKARR	PEGRTWAQPG	YPWPLYGNEG	CGWAGWLLSP
HPCPOLP	KTSESRQPRG	RRQPIPKARR	STGKSWGKPG	YPWPLYGNEG	LGWAGWLLSP
HPCPP	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
HPCUNKCD	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
MKC1A	KTSESRQPRG	RRQPIPKARR	PEGRAWAQPG	YPWPLYGNEG	LGWAGWLLSP
NDM59	KTSESRQPRG	RRQPIPKARR	STGKSWGKPG	YPWPLYGNEG	LGWAGWLLSP
NZLI	KTSESRQPRG	RRQPIPKARR	SEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
SA13	KTSESRQPRG	RRQPIPKARR	PTGRSWGQPG	YPWPLYANEG	LGWAGWLLSP
Th580	KTSESRQPRG	RRQPIPKARR	SQGRTWGQPG	YPWPLYGNEG	CGWAGWLLSP
Type_3a_CB	KTSESRQPRG	RRQPIPKARR	SGGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
TypeV_D	KTSESRQPRG	RRQPIPKARR	SEGRSWAQPG	YPWPLYGNEG	CGWAGWLLSP
VN004	KTSESRQPRG	RRQPIPKARR	PGRSWGQPG	YPWPLYGNEG	CGWAGWLLSP
VN235	KTSESRQPRG	RRQPIPKARR	QTGRTWGQPG	YPWPLYGNEG	CGWAGWLLSP
VN405	KTSESRQPRG	RRQPIPKARR	SQGRHWAQPG	YPWPLYGNEG	CGWAGWLLSP

101

150

BEBE1	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPVV	GAPVGGVARA
D89815	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
ED43type_4	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPVGSVARA
HC_C2	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HC_G9	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCU16326	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_H_CMR	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_J1	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_J483	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_J8	RGSRPTWGPT	DPRHRSRNLG	RVIDTITCGF	ADLMGYIPVV	GAPVGGVARA
HCV_JK1	YGSRPRWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_JS	RGSRPNWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_K1_R1	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_K1_R2	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_K1_R3	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_K1_S1	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_K1_S2	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_K1_S3	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_L2	RGSRPSWGPT	DPRHRSRNLG	KVIDTPTCGF	ADLMGYIPLV	GAPLGGGAARA
HCV_N	RGSRPSWGPT	DPRHRSRNLG	KVIDTLTCGL	ADLMGYIPLV	GAPLGGGAARA

HCV12083	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMWYIPV	GAPLGGVAAA
HCV1480	RSSRPNWGP	DPRRKSPNLG	RVIHTLTCGF	PHLMGYIPLV	GGPVGGVSRA
HCVPOLYP	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HD_1	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCCGAA	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCFG	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCGENANTI	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCGENOM	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCCHUMR	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJ	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJCG	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJK046	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJK049	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJTA	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJTB	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCJ3A	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCPLYPRE	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCPOLP	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCPP	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
HPCUNKCD	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
MKC1A	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
NDM59	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
NZLI	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
SA13	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
Th580	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
Type_3a_CB	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
TypeV_D	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
VN004	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
VN235	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA
VN405	RGSRPWGP	DPRRRSRNLG	KVIDTLTCGF	ADLMGYIPLV	GAPLGGGAARA

151

200

BEBE1	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCISVPVS	AVEVRNTSSS
D89815	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
ED43type_4	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AVNYRNVSGI
HC_C2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNASGV
HC_G9	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AVGVRNSSGV
HCU16326	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNASGM
HCV_H_CMR	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNSSL
HCV_J1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNSTGL
HCV_J483	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_J8	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_JK1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_JS	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_K1_R1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_K1_R2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_K1_R3	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_K1_S1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_K1_S2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_K1_S3	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_L2	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV_N	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV12083	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCV1480	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HCVPOLYP	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HD_1	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HPCCGAA	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HPCFG	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HPCGENANTI	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HPCGENOM	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI

HPCUMR	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AYEVHNVSGI
HPCJ	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPVS	AYEVRNVSGG
HPCJCG	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYEVRNVSGI
HPCJK046	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AVNYANKSGI
HPCJK049	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLLTPTA	GLEVRNASGL
HPCJTA	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNASGL
HPCJTB	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNRSGL
HPCK3A	LAHGVRVLED	GINFATGNLP	GCSFSIFLLA	LFSLIHPAA	SLEWRNTSGL
HPCPLYPRE	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPAS	AYQVRNSTGL
HPCPOLP	LAHGVRVLED	GVNFATGNLP	GCSFSIFLLA	LLSCITTPVS	AAEVKNISTG
HPCPP	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNASGV
HPCUNKCD	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPVS	AYEVRNASGM
MKC1A	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTIPAS	AYQVRNASGV
NDM59	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCITVPVS	AVQVKNISDS
NZLI	LAHGVRVLED	GINFATGNLP	GCSFSIFLLA	LFSLIHPAA	SLEWRNTSGL
SA13	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTVPTS	AVPYRNASGV
Th580	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCLTTPAS	ALTYGNSSGL
Type_3a_CB	LAHGVRVLED	GINFATGNLP	GCSFSIFLLA	LFSLIHPAA	SLEWRNTSGL
TypeV_D	LAHGVRVLED	GINFATGNLP	GCSFSIFLLA	LFSLIHPAA	SLEWRNTSGL
VN004	LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AIQVRNASGI
VN235	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AVHYANKSGI
VN405	LAHGVRVLED	GINYATGNLP	GCSFSIFLLA	LLSCLTTPAS	AVHYRNISGI

201

250

BBEB1	YMATNDCSNS	SIVWOLEGAV	LHTPGCVPCV	KTGN.KSRCW	VPVTPNIAIN
D89815	YHVTNDCSNS	SIVYEAADVI	MHAPGCVPCV	RENN.SSRCW	VALTPTLAAR
ED43type_4	YHVTNDCPNS	SIVYEAADHI	MHLPGCVPCV	REGN.QSRCW	VALTPTVAAP
HC_C2	YHVTNDCSNS	SIVYEAADMI	MHNPGCVPCV	RENN.SSRCW	VALTPTLAAR
HC_G9	YHVTNDCPNA	SVVYETENLI	MHLPGCVPYV	REGN.ASRCW	VSLSPTVAAR
HCU16326	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
HCV_H_CMR	YHVTNDCPNS	SIVYEAADAI	LHTPGCVPCV	REGN.ASRCW	VAVTPTVATR
HCV_J1	YHVTNDCPNS	SIVYEAADAI	LHTPGCVPCV	REGN.VSRCW	VAMTPTVATR
HCV_J483	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
HCV_J8	YYATNDCSNS	SITWQLTDAV	LHLPGCVPCV	NDNG.TLHCW	IQVTPNVAVK
HCV_JK1	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HCV_JS	YHVTNDCSNS	SIVYEAADII	MHTPGCVPCV	REKN.ISRCW	VALTPTLAAR
HCV_K1_R1	YHVTNDCSNS	SIVYEAQDMI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HCV_K1_R2	YHVTNDCSNA	SIVYEAADMI	MHTPGCVPCV	REAN.SSRCW	VALTPTLAAR
HCV_K1_R3	YHVTNDCSNS	SIVYEAEDVI	MHTPGCLPCV	RENN.SSRCW	VALTPTLAGR
HCV_K1_S1	YHVTNDCSNS	SIVYEAEDMI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HCV_K1_S2	YHVTNDCSNA	SIVYEAADMI	MHTPGCVPCV	REAN.SSRCW	VALTPTLAAR
HCV_K1_S3	YHVTNDCSNS	SIVYEAEDVI	MHTPGCLPCV	RENN.SSRCW	VALTPTLAGR
HCV_L2	YHVTNDCSNS	SIVYEAADLI	MHTPGCVPCV	REAN.SSRCW	VALTPTLAAR
HCV_N	YHVTNDCSNS	SIVFEAADLI	MRTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HCV12083	YHVTNDCSNS	SIVLEADAMI	LHLPGCLPCV	RVGN.QSTCW	HAVSPTLATP
HCV1480	YHVTNDCPNS	SIVYEAADLI	MHTPGCVPCV	LEDN.VSRCW	VQITPTLSAP
HCVPOLYP	YHVTNDCSNA	SIVYEAADMI	MHTPGCVPCV	RVDN.SSRCW	VALTPTLAAR
HD_1	YHVTNDCSNS	SIVYETADMI	MHTPGCVPCV	REDN.SSRCW	VALTPTLAAR
HPCCGAA	YHVTNDCPNS	SVVYEAADAI	LHTPGCVPCV	REGN.ASRCW	VAVTPTVATR
HPCFG	YLLTNDCSNR	SIVYEAADVI	LHLPGCVPCV	STDNMNTSCW	TPISPTVAVK
HPCGENANTI	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HPCGENOM	YHVTNDCSNS	SIVYEAADLI	MHTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HPCHUMR	YHVTNDCSNA	SIVYEAADLI	MHTPGCVPCV	REGN.SSRCW	VALTPTLAAR
HPCJ	YHVTNDCSNS	SIVYEAADVI	MHTPGCVPCV	RENN.SSRCW	VALTPTLAAR
HPCJCG	YHVTNDCSNS	SIVYEAADMI	MHTPGCVPCV	RESN.FSRCW	VALTPTLAAR
HPCJK046	YHVTNDCPNS	SMVYEAADII	LHLPGCVPCV	RTGN.QSRCW	TPATPTLAIP
HPCJK049	YHVTNDCSNG	SIVYEAADVI	LHLPGCIPCV	RLNN.ASKCW	TPVSPTVAVS
HPCJTA	YHVTNDCSNS	SIVYEAAGMI	MHTPGCVPCV	RENN.ASRCW	VALTPTLAAR
HPCJTB	YHVTNDCSNS	SIVYEAAGMI	MHTPGCVPCV	RENN.VSRCW	VALTPTLAAR
HPCK3A	YHVTNDCSNS	SIVYEAADVI	LHTPGCIPCV	QDGN.TSTCW	TPVTPTVAVR

HPCPLYPRE	YHVTND CPNS	SIVYEADAI	LHTPGCVPCV	REGN. ASRCW	VAMTPTVATR
HPCPOLP	YMTNDCTND	SITWQLQAAV	LHVP GCVPCE	KVGN. TSRCW	IPVSPNVAVQ
HPCPP	YHVTND CSNS	SIVYEADVI	MHTPGCVPCV	RENN. SSRCW	VALTPTLAAR
HPCUNKCD	YHVTND CSNS	SIVYEADMI	MHTPGCVPCV	RENN. SSRCW	VALTPTLAAR
MKC1A	YHVTND CSNS	SIVYEADVI	MHTPGCVPCV	RENN. SSRCW	VALTPTLAAR
NDM59	YMTND CSND	SITWQLQAAV	LHVP GCVPCE	KMGN. ISRCW	IPVSPNVAVQ
NZLI	YVLTND CSNS	SIVYEADVI	LHTPGCVPCV	QDGN. TSTCW	TPVTPTVAVR
SA13	YHVTND CPNS	SIVYEADLI	LHAPGCVP CV	RQGN. VSRCW	VOITPTLSAP
Th580	YHLTND CPRS	SIVLEAEAMI	LHLAGCVPCV	RAGN. ISRCW	HPVSPTLAVP
Type_3a_CB	YVLTND CSNS	SIVYEADVI	LHTPGCVPCV	QNDN. ISTCW	TPVTPTVAVR
TypeV_D	YVLTND CSNS	SIVYEADVI	LHTPGCVPCV	QDGN. TSTCW	TPVTPTVAVR
VN004	YHLTND CSNN	SIVFEAETII	LHLP GCVPCI	KVGN. GSRCW	LSVSPTLAVP
VN235	YHLTND CPNS	SIVYEADFI	MHLP GCVPCI	KSGN. GSSCW	LPATLTIAVP
VN405	YHLTND CPNS	SIIYEADNII	MHTPGCVPCV	KTGN. KSQCW	VPVAPTlava

	251			300	
BEBE1	QPGALTKGLR	AHIDVIVMSA	TLCSALYVGD	VCGALMIAAQ	VVVVSPQH HH
D89815	NASVPTTTTLR	RHVDLLVGTA	AFCSAMYVGD	LCGSVFLISQ	LFTFSPPRHE
ED43type_4	YIGAPLESRL	SHVDLMVGAA	TVCSGLYIGD	LCGGLFLVGQ	MFSFRPRRH W
HC_C2	NASVPTTTTIR	RHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHE
HC_G9	DSRVPVSEVR	RRVDSIVGAA	AFCSAMYVGD	LCGSIFLVGQ	IFTFSPPRHH W
HCU16326	NASVPTTTTLR	RHVDLLVGVA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHE
HCV_H_CMR	DGKLPTTQLR	RHIDLLVGSA	TLCSALYVGD	LCGSVFLVGQ	LFTFSPPRHH W
HCV_J1	DGKLPTATQLR	RHIDLLVGSA	TLCSALYVGD	LCGSVFLIGQ	LFTFSPPRHH W
HCV_J483	NASVPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHE
HCV_J8	HRGALTRSLR	THVDMIVMAA	TACSALYVGD	VCGAVMILSQ	AFMVSPQRHN
HCV_JK1	NSSIPTTTTIR	RHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_JS	NISVPTATIR	RHVDLLVGTA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_K1_R1	NASIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_K1_R2	NSSVPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_K1_R3	NSSIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_K1_S1	NASIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_K1_S2	NSSVPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_K1_S3	NSSIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HCV_L2	DSSIPTATIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFAFSPRRE
HCV_N	NATIHTTTTIR	HHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPLRHQ
HCV12083	NASTPATGFR	RHVDLLAGAA	VVCSSLYIGD	LCGSLFLAGQ	LFAFQPRRH W
HCV1480	SFGAVTALLR	RAVDYLAGGA	AFCSALYVGD	ACGALSLVGQ	MFTYKPRQHT
HCVPOLYP	NASVPTTAIR	RHVDLLVGAA	TFCSAMYVGD	LCGSVFLVAQ	LFTFSPPRHE
HD_1	NASIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHA
HPCCGAA	DGKLPTTQLR	RHIDLLVGSA	TLCSALYVGD	LCGSVFLVGQ	LFTFSPPRHH W
HPCFG	HPGVTTASIR	NHVNMLVAPP	TLCSALYVED	AFGAVSLVGQ	AFTFRPRQHK
HPCGENANTI	NNSVPTATIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HPCGENOM	NATIPTATVR	RHVDLLVGAA	AFSSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HPCHUMR	NVTIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHH W
HPCJ	NTTVPTTTTIR	RHVDLLVGTA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHE
HPCJCG	NSSIPTTTTIR	RHVDLLVGAA	ALCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HPCJK046	NSTVPASGFR	QHIDLMVGAA	ALCSAMYVGD	LCGGLFLVGQ	LFTFRPRIHQ
HPCJK049	RPGAATASLR	THVDMVMGAA	TLCSALYVGD	LCGALFLVGQ	GFSWRHRQHW
HPCJTA	NTSIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HPCJTB	NTSIPTTTTIR	RHVDLLVGAA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRRE
HPCK3A	YVGATTASIR	SHVDLLVGAG	TMCSALYVGD	MCGPVFLVGQ	AFTFRPRRHR
HPCPLYPRE	DGKLPTATQLR	RHIDLLVGSA	TLCSALYVGD	LCGSVFLVGQ	LFTFSPPRHH W
HPCPOLP	QPGALTQGLR	THIDMVMSA	TLCSALYVGD	LCGGVMLAAQ	MFIVSPQH HH
HPCPP	NSSIPTTTTIR	RHVDLLVGAA	ALCSAMYVGD	FCGSVFLVSQ	LFTFSPPRRE
HPCUNKCD	NASVPTTTTLR	RHVDLLVGVA	AFCSAMYVGD	LCGSVFLVSQ	LFTFSPPRHE
MKC1A	NSSIPTTTTIR	RHVDLLVGAA	ALCSAMYVGD	FCGSVFLVSQ	LFTFSPPRRE
NDM59	RPGALTQGLR	AHIDMVMSA	TLCSALYVGD	LCGGVMLAAQ	MFIVSPQH HH
NZLI	YVGATTASIR	SHVDLLVGAA	TMCSALYVGD	MCGAVFLVGQ	AFTFRPRRHH W
SA13	SLGAVTAPLR	RAVDYLAGGA	ALCSALYVGD	ACGAVFLVGQ	MFTYSPRRHN

Th580	NASVPASGFR	KHVDLLAGAA	VVCSSMYIGD	LCGAVFLAQ	LATFSPRIHD
Type_3a_CB	YVGATTASIR	SHVDLLVGAA	TMCSALYVGD	MCGAVFLVGQ	AFTFRPRRHQ
TypeV_D	YVGATTASIR	SHVDLLVGAA	TMCSALYVGD	MCGAVFLVGQ	AFTFRPRRHQ
VN004	NSSVPIHGFR	RHVDLLVGAA	AFCSAMYIGD	LCGSVFLVGQ	LFTFRPKHHQ
VN235	NASIPVRGFR	RHVDLMVGAA	AFCSAMYVGD	LCGGIFLVGQ	LFSFNPRRHW
VN405	NASVPIRGFR	SHVDLLVGSA	AACSALYIGD	LCGGVFLVGQ	LFTFRPRQHT

	301			350
BEBE1	FVQECNCSIY	PGKITGHRMA	WDMMMNWSPT	TTMLLAYLVR
D89815	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	AALVVSQLLR
ED43type_4	TTQDCNCSIY	TGHITGHRMA	WDMMMNWSPT	TTLVLAQVMR
HC_C2	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	TALVVSQLLR
HC_G9	TTQDCNCSIY	PGHVTGHRMA	WDMMMNWSPT	GALVVAQLLR
HCU16326	TVQDCNCSIY	PGRVSGHRMA	WDMMMNWSPT	TALVVSQLLR
HCV_H_CMR	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVAQLLR
HCV_J1	TTQGCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVMAQLLR
HCV_J483	TVQDCNCSIY	PGHLSGHRMA	WDMMMNWSPT	TALVVSQLLR
HCV_J8	FTQECNCSIY	QGHITGHRMA	WDMMLWSPT	LTMILAYAAR
HCV_JK1	TVQDCNCSLY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HCV_JS	TVQDCNCSLY	PGHVSghRMA	WDMMMNWSPT	AALVVSQLLR
HCV_K1_R1	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HCV_K1_R2	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HCV_K1_R3	TVQDCNCSLY	PGHITGHRMA	WDMMMNWSPT	TALVVSQLLR
HCV_K1_S1	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HCV_K1_S2	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HCV_K1_S3	TVQDCNCSLY	PGHITGHRMA	WDMMMNWSPT	TALVVSQLLR
HCV_L2	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVSQLLR
HCV_N	TLQDCNCSIY	PGHASGHRMA	WDMMMNWSPT	TALVVSQLLR
HCV12083	TVQDCNCSIY	TGHVTGHRMA	WDMMMNWSPT	TTLVLSILR
HCV1480	TVQDCNCSIY	SGHITGHRMA	WDMMMKWSPT	TALLMAQLLR
HCVPOLYP	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVSQLLR
HD_1	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	AALVVSQLLR
HPCCGAA	TTQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	AALVVAQLLR
HPCFG	TVQTCNCSIY	PGHVSghRMA	WDMMMNWSPT	IGLVISHLMR
HPCGENANTI	TVQDCNCSIY	PGHVTGHRMA	WDMMMNWSPT	TALVVSQLLR
HPCGENOM	TIQDCNCSIY	PGHVTGHRMA	WDMMMNWSPT	TALVVSQLLR
HPCHUMR	TLQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HPCJ	TVQDCNCSIY	PGHLSGHRMA	WDMMMNWSPT	AALVVSQLLR
HPCJCG	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HPCJK046	TVQDCNCSIY	TGHVTGHRMA	WDMMMNWSPT	ATFVVSALR
HPCJK049	TVQDCNCSIY	PGHITGHRMA	WDMMMNWSPT	MTLIVSQVLR
HPCJTA	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HPCJTB	TVQDCNCSIY	PGHVSghRMA	WDMMMNWSPT	TALVVSQLLR
HPCK3A	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	VGMVVAHILR
HPCPLYPRE	TTQGCNCSIY	PGHITGHRMA	WDMMMNWSPT	TALVMAQLLR
HPCPOLP	FVQDCNCSIY	PGTITGHRMA	WDMMMNWSPT	ATMILAYAMR
HPCPP	TVQDCNCSIY	PGHVSghRMA	WDMIMNWSPT	TALVVSQLLR
HPCUNKCD	TVQDCNCSIY	PGRVSGHRMA	WDMMMNWSPT	TALVVSQLLR
MKC1A	TVQDCNCSIY	PGHVSghRMA	WDMIMNWSPT	TALVVSQLLR
NDM59	FVQECNCSIY	PGAITGHRMA	WDMMMNWSPT	ATMILAYAMR
NZLI	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	VGMVVAHVLR
SA13	VVQDCNCSIY	SGHITGHRMA	WDMMMNWSPT	TALVMAQLLR
Th580	ITQDCNCSVY	TGHVTGHRMA	WDMMMNWSPT	TTLVLSILR
Type_3a_CB	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	LGMAVAHVLR
TypeV_D	TVQTCNCSLY	PGHLSGHRMA	WDMMMNWSPT	VGMVVS HVLR
VN004	TVQDCNCSIY	AGHITGHRMA	WDMMLNWSPT	VSYVVSALR
VN235	VVQDCNCSIY	VGHITGHRMA	WDMMMNWSPT	ATLVLSYVMR
VN405	TVQECNCSIY	TGHITGHRMA	WDMMMNWSPT	VTFITSSLLR

	351		400
BEBE1	GGHWGVMFGL	AYFSMQGAWA	KVVVILLTA GVEASTYTTG
D89815	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGHTRVTG
ED43type_4	GGHWGVLVGV	AYFSMQANWA	KVILVFLFA GVDATHVSG
HC_C2	GAHWGVLAGL	AYYSMVGNWA	KVLIVLLLFA GVDGNTYVTG
HC_G9	GAHWGVLAGL	AYYSMVGNWA	KVVVVLLLFA GVDAETRVTG
HCU16326	GSHWGILAGL	AYYSMVGNWA	KVLIAMLLFA GVDGTHVTG
HCV_H_CMR	GAHWGVLAGI	AYFSMVGNWA	KVLVLLLFA GVDAETHVTG
HCV_J1	GAHWGVLAGI	AYFSMVGNWA	KVLVLLLFA GVDATIVSG
HCV_J483	GAHWGVLAGL	AYYSMVGNWA	KVLIVALLFA GVDGETYTS
HCV_J8	GGHWGVVFG	AYFSMQGAWA	KVIAILLVA GVDATTYSSG
HCV_JK1	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGTTYVSV
HCV_JS	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GADGTHVTG
HCV_K1_R1	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGNTYTTG
HCV_K1_R2	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGNTYVSG
HCV_K1_R3	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGTHVSG
HCV_K1_S1	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGDTYTTG
HCV_K1_S2	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGRTTVTG
HCV_K1_S3	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGSTRVSG
HCV_L2	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGTTVTMG
HCV_N	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGHTLTG
HCV12083	GGHWGILLAV	AYFGMAGNWL	KVLAVLFLFA GVEAQT.MIA
HCV1480	GGHWGVLLAA	AYFASTANWA	KVILVFLFA GVDGRTHVTG
HCVPOLYP	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGDTHTTG
HD_1	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGTTTVTG
HPCCGAA	GAHWGVLAGI	KYFSMVGNWA	KVLVLLLFA GVDATHVTG
HPCFG	GAHWGVMAGL	AYFSMQGNWA	KVVIVLIMFS GVDATHTTG
HPCGENANTI	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGSTIVSG
HPCGENOM	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGDTYASG
HPCHUMR	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGDTHVTG
HPCJ	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGQTYTTG
HPCJCG	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGHTVTG
HPCJK046	GGHWGIIGAL	LYYSTAANWA	KVIVLLLFA GVDAST.YVA
HPCJK049	GAHWGVMAGV	AYYSMQGNWA	KVFLVLCFLS GVDASTTITG
HPCJTA	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGVTYTTG
HPCJTB	GAHWGVLAGL	AYYSMVGNWA	KVLIVMLLFA GVDGVTYTTG
HPC3A	GAHWGIAGL	AYYSMQGNWA	KVAIIMVMFS GVDASTHVTG
HPCPLYPRE	GAHWGVLAGI	AYFSMVGNWA	KVLVLLLFA GVDATHVTG
HPCPOLP	GAHWGVMFGL	AYFSMQGAWA	KVVVILLAA GVDATHTVTG
HPCPP	GAHWGVLAGL	AYYSMVGNWA	KVLVMLLFA GVDGGTHVTG
HPCUNKCD	GSHWGILAGL	AYYSMVGNWA	KVLIAMLLFA GVDGTHVTG
MKC1A	GAHWGVLAGL	AYYSMVGNWA	KVLVMLLFA GVDGGTHVTG
NDM59	GAHWGVMFGL	AYFSMQGAWA	KVVVILLTA GVDATHRSIA
NZLI	GAHWGILAGL	AYYSMQGNWA	KVAIIMVMFS GVDATHTYTTG
SA13	GAHWGVLFAL	AYYASAAANWA	KVVLVFLFA GVDANTRVTG
Th580	GGHWGVLFAL	AYFGMSGNWL	KVIAVFLFA GVEATT.TVG
Type_3a_CB	GAHWGILAGL	AYYSMQGNWA	KVAIIMVMFS GVDATHTYTTG
TypeV_D	GAHWGILAGL	AYYSMQGNWA	KVAIIMVMFS GVDATHTYTTG
VN004	GAHWGVLAGL	LYFSMVANWA	KVIAVFLFA GADATT.YTG
VN235	GGHWGILAGI	LYYSMVANWA	KVLCILFLFA GVDATTRTTG
VN405	EGHWGVIGAL	LYYSMVANWA	KVFAVLLLFA GVDATT.HIG
	401		450
BEBE1	TSMFSLGSQ	RVQLIHTNGS	WHINRTALNC NDSLETGFLA
D89815	TSLFRPGASQ	KIQLVNTNGS	WHINRTALNC NDSLKTGFLA
ED43type_4	ANLFSSGSQ	NLQLINSNGS	WHINRTALNC NDSLNTGFLA
HC_C2	TSLFSRGPQ	KIQLVNTNGS	WHINRTALNC NDSFNTGFLA
HC_G9	ASFLAPGAKQ	KIQLINTNGS	WHINRTALNC NESLDTGWLA
HCU16326	TSLFSPGPVQ	HLQLINTNGS	WHINRTALNC NDSLNTGFVA
HCV_H_CMR	VGLLTPGAKQ	NIQLINTNGS	WHINSTALNC NDSLTTGWLA

HCV_J1 VSLFTPGAKQ NIQLINTNGS WHINSTALNC NESLNTGWLA GLIYQHKFNS
 HCV_J483 ASLFTSPGASQ RIQLVNTNGS WHINRTALNC NDSLHTGFLA ALFYTHRFNS
 HCV_J8 AGLFTTGAKQ NLYLINTNGS WHINRTALNC NDSLQTGFIA SLFYTHKFNS
 HCV_JK1 ASFFSPGSAQ KIQLVNTNGS WHINRTALNC NESINTGFFA ALFYVKKFNS
 HCV_JS ASLFNVGPHQ KIQLVNTNGS WHINRTALNC NDTLQTGFIA ALFYKHFNA
 HCV_K1_R1 TSIFTPGASQ NIQLINTNGS WHINRTALNC NDSLQTGFIA ALFYARFNS
 HCV_K1_R2 VSLFAPGAQQ KIQLVNTNGS WHINRTALNC NDSLNTGFLA ALFYTHRFNS
 HCV_K1_R3 TSLFSSGAQQ KIQLVNTNGS WHINRTALNC NDTLQTGFIA ALFYTHRFND
 HCV_K1_S1 ASLFTSGASQ NIQLINTNGS WHINRTALNC NDSLQTGFIA ALFYAHFNS
 HCV_K1_S2 ASLFTFGAQQ RIQLVNTNGS WHINRTALNC NDSLNTGFLA ALFYTHRFNS
 HCV_K1_S3 TSLFSSGAQQ KIQLVNTNGS WHINRTALNC NDTLQTGFIA ALFYTHRFND
 HCV_L2 TGLFRPGASQ KIQLINTNGS WHINRTALNC NDSLNTGFLA ALFYTHRFNA
 HCV_N AGLFTPGPSQ RIQLINTNGS WHINRTALNC NDSLQTGFIA ALSYTYRFNS
 HCV12083 ASLLTPGAKQ NIQLINTNGS WHINRTALNC NDSLQTGFIA SLFYTHKFNS
 HCV1480 TSFFNPGPQR QLQFVNTNGS WHINSTALNC NDSLQTGFIA GLMYAHKFNS
 HCVPOLYP TGFFSLGPKQ KIQLVNTNGS WHINRTALNC NDSLNTGWLA ALFYTHSFNA
 HD_1 TSLYTRGPSQ RIQLVNTNGS WHINRTALNC NDSLQTGFIA ALFYTRSFNS
 HPCCGAA VGLLTPGAKQ NIQLINTNGS WHINSTALNC NESLNTGWLA GLFYQHKFNS
 HPCFG TSFFTRGPSQ NLQLVNSNGS WHINSTALNC NDSLNTGFIA GLFYHKKFNS
 HPCGENANTI ASLFTQASQ KIQLINTNGS WHINRTALNC NDSLQTGFIA SLFYAHFNA
 HPCGENOM TSLFTPGASQ KIQLINTNGS WHINRTALNC NDSLNTGFLA ALFYTHRFNA
 HPCHUMR VSMFASGPSQ KIQLINTNGS WHINRTALNC NDSLQTGFIA ALFYTHSFNS
 HPCJ ASLFSAGSQ NIQLINTNGS WHINRTALNC NDSLNTGFLA ALFYTHKFNS
 HPCJCG VSWLSQGPSQ KIQLVNTNGS WHINRTALNC NDSLQTGFIA ALFYAHFNA
 HPCJK046 VSLFSAGARQ NLQLINTNGS WHINRTALNC NDSLQTGFIA SLFYRNKFNA
 HPCJK049 TSLFSTGAKQ PLHLVNTNGS WHINRTALNC NDSLNTGFIA GLLYYHKFNS
 HPCJTA TSFFTPGPAQ RIQLINTNGS WHINRTALNC NESLNTGFFA ALFYAHKFNS
 HPCJTB ASFFTPGPAQ KIQLINTNGS WHINRTALNC NESLNTGFFA ALFYAHKFNS
 HPC3A TSLFSVGAQ NIQLINTNGS WHINRTALNC NESINTGFIA GLFYHKKFNS
 HPCPLYPRE VSLLAPGAKQ NVQLINTNGS WHINSTALNC NDSLNTGWLA GLFYHKKFNS
 HPCPOLP TGMFSLGARQ KIQLINTNGS WHINRTALNC NDSLHTGFLA SLFYTHSFNS
 HPCPP TSFFSRGPSQ KIQLVNTNGS WHINRTALNC NDSLNTGFLA ALFYTHSFNA
 HPCUNKCD TSLFSPGPVQ HLQLINTNGS WHINRTALNC NDSLNTGFVA ALFYKYRFNA
 MKC1A TSFFSRGPSQ KIQLVNTNGS WHINRTALNC NDSLNTGFIA ALFYTHSFNA
 NDM59 AGLFTSGAKQ NIQLINTNGS WHINRTALNC NDSLNTGFIA SLFYTYRFNS
 NZLI AGLFDIGPQQ KLQLVNTNGS WHINSTALNC NESINTGFIA GLFYHKKFNS
 SA13 ASLFTPGPQQ NLQLINTNGS WHINRTALNC NDSLQTGFVA GLLYYHKFNS
 Th580 TSIFSSGPNQ KIQLINTNGS WHINRTALNC IDSLQTGFIA ALFYRSNFNS
 Type_3a_CB TSLFSVGAQQ KLQLVNTNGS WHINSTALNC NESINTGFIA GLFYHKKFNS
 TypeV_D TSLFSSGPNQ KLQLVNTNGS WHINSTALNC NESINTGFIA GLFYHKKFNS
 VN004 VSLFSPGPTQ NLQLVNSNGS WHINRTALNC NDSLQTGFIA GLFYHKKFNS
 VN235 TGLFQTGAKQ NIHLINTNGS WHINRTALNC NDSLNTGFMA ALFYHKKFNS
 VN405 TSFFSPGSKQ NVQLIKTNGS WHINRTALNC NDSLHTGFIA GLLYAHFNS

451

500

BEBE1 SGCPERLAAC RSIESFRIGW GSLEYEESVT NDADMRPYCW HYPPRPGCIV
 D89815 SGCPERMASC RSIDKFDQGW GPITYAQPD. .NSDQRPYCW HYAPRQCGIV
 ED43type_4 SGCSERLACC KSLDSYGQGW GPLGVANISG. .SSDDRYPYCW HYAPRPGCIV
 HC_C2 SGCPERMASC RSIDKFDQGW GPITYYQGD. .SPDQRPYCW HYPPRPGCIV
 HC_G9 SGCPERMASC QPLTAFDQGW GPITHEGNA. .SDDQRPYCW HYALRPGCIV
 HCU16326 SGCPERLASC RPIDTFAQGW GPITYTEPH. .GLDQRPYCW HYAPQPCGIV
 HCV_H_CMR SGCPERLASC RRLTDFDQGW GPISYANGS. .GPDQRPYCW HYPPRPGCIV
 HCV_J1 SGCPERLASC RRLTDFDQGW GPISHANGS. .SPDQRPYCW HYAPRPGCIV
 HCV_J483 SGCPERMASC RPIDWFAQGW GPITYTEPD. .SPDQRPYCW HYAPRPGCIV
 HCV_J8 SGCPERLSSC RGLDDFRIGW GTLEYETNVT NDGDMRPYCW HYPPRPGCIV
 HCV_JK1 SGCSERMASC RPIDRFAQGW GPITHAESR. .SSDQRPYCW HYAPQPCGIV
 HCV_JS SGCPERMASC RPIDKFAQGW GPITYAEPD. .RLDQRPYCW HYPPRPGCIV
 HCV_K1_R1 SGCPORLASC RSIDKFAQGW GPITYAEGH. .SSDQRPYCW HYAPRPGCIV
 HCV_K1_R2 SGCPERIAASC RSIDAFQGW GPITYAEPG. .SSDQRPYCW HYAPRPGCIV
 HCV_K1_R3 SGCPERMASC RPIDKFAQGW GPITYVKPD. .ILDQRPYCW HYAPRPGCIV

HCV_K1_S1	SGCPQRLASC	RSIDKFAQGW	GPITYTEGH.	.NSDQRPYCW	HYAPRPGIV
HCV_K1_S2	SGCPERIASC	RSIDAFQGW	GPITYAEPG.	.SSDQRPYCW	HYAPRPGIV
HCV_K1_S3	SGCPERMASC	RPIDKFAQGW	GPITYAKPD.	.ILDQRPYCW	HYAPRPGIV
HCV_L2	SGCPERMASC	QSIDKFVQGW	GPITYAENG.	.SSDQRPYCW	HYAPRRCGIV
HCV_N	SGCPGRMASC	RSIDKFDQGW	GPITYADPK.	.DPDQRPYCW	HYAPQCGII
HCV12083	SGCPERMAAC	KPLAEFRQGW	GQITHKN.VS	GPSDDRYPYCW	HYAPRPEVV
HCV1480	SGCPERMSSC	RPLAAFDQGW	GTISYATISG	.PSDDKPYCW	HYPPRPGV
HCVPOLYP	SGCPERMASC	HPIDBFAQGW	GPITYAEHS.	.SSDQRPYCW	HYAPQPCGIV
HD_1	SGCPERMASC	RSIDQFDQGW	GPITYAEPR.	.DLDQRPYCW	HYAPRPGIV
HPCCGAA	SGCPERLASC	RRLTDFQGW	GPISYANGS.	.GLDERPYCW	HYPPRPGIV
HPCFG	SGCPERMSSC	KPITYFNQGW	GPLTDANING	.PSEDRPYCW	HYPPRPNIT
HPCGENANTI	SGCPERMASC	RSIDKFDQGW	GPITYTEAD.	.IQDQRPYCW	HYAPRPGIV
HPCGENOM	SGCAERMASC	RPIDTFDQGW	GPITYTEPD.	.SSDQRPYCW	HYAPRKCIV
HPCHUMR	SGCPERMAQC	RTIDKFDQGW	GPITYAESS.	.RSDQRPYCW	HYPPPOCTIV
HPCJ	SRAESVLASC	RFIDEFDQGW	GPITYTERN.	.SSDQRPYCW	HYPPRQCGII
HPCJCG	SGCPERMASC	RPIDEFAQGW	GPITHDMPE.	.SSDQRPYCW	HYAPRPGIV
HPCJK046	TGCPERLSAC	KTLDSDQGW	GPITYAN.IS	GPAVEKPYCW	HYPPRPEVV
HPCJK049	SGCVERMSAC	SPLDRFAQGW	GPLGPANISG	.PSSEKPYCW	HYAPRCDTV
HPCJTA	SGCPERMASC	SSIDKFAQGW	GPITYTEPR.	.DLDQRPYCW	HYAPRQCGIV
HPCJTB	SGCPERMASC	SSIDKFAQGW	GPITYTEPG.	.DLDQRPYCW	HYAPRQCGIV
HPCK3A	TGCPQRLSSC	KPITFFKQGW	GPLTDANITG	.PSDDKPYCW	HYAPRPGIV
HPCPLYPRE	SGCPERLASC	RPLTDFDQGW	GPISYANGS.	.GPDQRPYCW	HYPPKPCGIV
HPCPOLP	SGCPERMSAC	RSIEAFRVGW	GALQYEDNVT	NPEDMRPYCW	HYPPRQCGV
HPCPP	SGCPERMAGC	RPIDEFAQGW	GPITHVVPN.	.ISDQRPYCW	HYAPRPGIV
HPCUNKCD	SGCPERLATC	RPIDTFAQGW	GPITYTEPH.	.DLDQRPYCW	HYAPQPCGIV
MKC1A	SGCPERMAGC	RPIDEFAQGW	GPITHVVPN.	.ISDQRPYCW	HYAPRPGIV
NDM59	SGCPERLSAC	RGIOAFRIGW	GTLRYEDNVT	NPEDMRPYCW	HYPPKQCGIV
NZLI	TGCPQRLSSC	KPITFFRQGW	GPLTDANITG	.PSDDRYPYCW	HYAPRCDIV
SA13	TGCPQRMASC	RPLAAFDQGW	GTISYAAVSG	.PSDDKPYCW	HYPPRPGIV
Th580	TGCSERLGAC	KPLEHFQQGW	GPITHKSNIT	GPSEDRPYCW	HYAPRECSV
Type_3a_CB	TGCPQRLSSC	KPITFFKQGW	GPLTDANISG	.PSDDKPYCW	HYAPRCKV
TypeV_D	TGCPQRLSSC	KPITFFRQGW	GSLTDANVTG	.ASADKPYCW	HYAPRCDV
VN004	TGCPERMASK	RPLHSFEQGW	GPISYVN.IS	GSSDKPYCW	HYAPRPGIV
VN235	TGCPERLSAC	KSITQFAQGW	GPVTYAN.VS	GSSEDRPYCW	HYAPRPGV
VN405	SGCBERLSSC	RPLHAFEQGW	GPLTYAN.IS	GPSNDKPYCW	HYPPRCDIV

501

550

BEBE1	PARTVCGPVY	CFTSPVVVG	TTDRAGAPTY	NWGENETDVF	LLNSTRPPKG
D89815	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGDNETDVL	LLNNTRPPHG
ED43type_4	PASSVCGPVY	CFTSPVVVG	TTDHVGVPTY	TWGENETDVF	LLNSTRPPHG
HC_C2	PASEVCGPVY	CFTSPVVVG	TTDRLGVPY	NWGENETDVL	LLNNTRPPQG
HC_G9	PAKVCGPVY	CFTSPVVVG	TTDRAGVPTY	RWGANETDVL	LLNNSRPPMG
HCU16326	PTLVCGPVY	CFTSPVAVG	TTDRFGAPTY	RWGANETDVL	LLNNAGPPQG
HCV_H_CMR	PAKSVCVPY	CFTSPVVVG	TTDRSGAPTY	SWGANDTDVF	VLNNTTRPPLG
HCV_J1	PAKSVCVPY	CFTSPVVVG	TTDRSGAPTY	NWGANETDVF	VLNNTTRPPLG
HCV_J483	PASQVCGPVY	CFTSPVVVG	TTDRSGVPTY	SWGENETDVM	LLNNTRPPQG
HCV_J8	PARTVCGPVY	CFTSPVVVG	TTDKQGVPTY	TWGENETDVF	LLNSTRPPRG
HCV_JK1	PALQVCGPVY	CFTSPVVVG	TTDRFGVPTY	NWGDNETDVL	LLNNTRPPQG
HCV_JS	PALEVCGPVY	CFTSPVVVG	TTDRFGVPTY	SWGENETDVL	LLNNTRPPQG
HCV_K1_R1	PAQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGANETDVL	LLNNTRPPQG
HCV_K1_R2	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGENETDVL	LLNNTRAPQG
HCV_K1_R3	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	NWGGNETDVL	LLNNTRPPQG
HCV_K1_S1	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGANETDVL	LLNNTRPPQG
HCV_K1_S2	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGENETDVL	LLNNTRAPQG
HCV_K1_S3	PASEVCGPVY	CFTSPVVVG	TTDRSGAPTY	NWGGNETDVL	LLNNTRPPQG
HCV_L2	PASQVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGENETDVL	LLNNTRPPQG
HCV_N	PRSEACGPVY	CSTSPVVVG	TTDRFGAPTY	NWGDNETDVL	LLNNTRPPQG
HCV12083	PARSVCGPVY	CFTSPVVVG	TTDKRGNPTY	TWGENETDVF	MLESRLPPTG
HCV1480	PARDVCGPVY	CFTSPVVVG	TTDRRGCPY	NWGSNETDIL	LLNNIRPPAG
HCVPOLYP	PASEVCGPVY	CFTSPVVVG	TTDRHGVPTY	SWGENGTDL	LLNNTRPPQG

HD_1	PASQVCGPVY	CFTSPVVVG	TTDRSGVPTY	SWGENETDVL	LLNNTRPPQG
HPCCGAA	PAKSVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGANDTDVF	VLNNTRPPQG
HPCFG	KPLNVCBPVY	CFTSPVVVG	TTDIKGLPTY	RFGVNESDVF	LLTSLRPPQG
HPCGENANTI	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	SWGENETDVL	ILNNTRPPQG
HPCGENOM	PASEVCGPVY	CFTSPVVVG	TTDRFGVPTY	SWGENETDVL	LLNNTRPPQG
HPCHUMR	PASEVCGPVY	CFTSPVVVG	TTDRFGVPTY	RWGENETDVL	LLNNTRPPQG
HPCJ	PASEVCGPVY	CFTSPVVVG	TTDRFGVPTY	SWGENETDVL	VLNNTRPPQG
HPCJCG	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	SWGNETDVL	LLSNTTRPPQG
HPCJK046	SALNVCBPVY	CFTSPVVLG	TTDRRGNTY	TWGANETDVF	MMSSLRPPAG
HPCJK049	PAQSVCGPVY	CFTSPVVVG	ATDKRGAPTY	TWGENESDVF	LLESARPPTE
HPCJTA	PASQVCGPVY	CFTSPVVVG	TTDRSGAPTY	NWGANETDVL	LLNNTRPPQG
HPCJTB	PASQVCGPVY	CFTSPVVVG	TTDRSGAPTY	NWGANETDVL	LLNNTRPPQG
HPCK3A	PALNVCBPVY	CFTSPVVVG	TTDAKGAPTY	TWGANETDVF	LLESARPPSG
HPCPLYPRE	PAKSVCGPVY	CFTSPVVVG	TTDRSGAPTY	SWGNETDVF	VLNNTRPPQG
HPCPOLP	SASSVCGPVY	CFTSPVVVG	TTDRLGAPTY	TWGENETDVF	LLNSTRPPQG
HPCPP	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGNNETDVL	LLNNTRPPQG
HPCUNKCD	PTLQVCGPVY	CFTSPVAVG	TTDRFGAPTY	RWGANETDVL	LLNAGPPQG
MKC1A	PASQVCGPVY	CFTSPVVVG	TTDRFGAPTY	NWGNNETDVL	LLNNTRPPQG
NDM59	SARSVCGPVY	CFTSPVVVG	TTDRLGVPY	TWGENETDVF	ILNSTRPPQG
NZLI	PASSVCGPVY	CFTSPVVVG	TTDARGVPTY	TWGENEKDVF	LLKSQRPPSG
SA13	PARGVCGPVY	CFTSPVVVG	TTDRKGNPTY	SWGENETDIF	LLNNTRPPQG
Th580	PASSVCGPVY	CFTSPVVVG	TTDRKGNPTY	NWGENETDVF	MLESARPPQG
Type_3a_CB	PASVCGPVY	CFTSPVVVG	TTDAKGVPY	TWGANETDVF	LLESARPPQG
TypeV_D	PALNVCBPVY	CFTSPVVVG	TTDRKGVPTY	NWGENESDVF	LLESARPPSG
VN004	PARNVCBPVY	CFTSPVVVG	TTDRGIPY	TWGENVSDVF	LLHSARPPQG
VN235	SARSVCGPVY	CFTSPVVVG	TTDRRGVPTY	TWGENESDVF	LLESARPPAG
VN405	PASVCGPVY	CFTSPVVVG	TTDRKGLPTY	TWGANESDVF	LLRSTRPPRG

551

600

BEBE1	AWFGCTWMNG	TGFTKTCGAP	PCRIRKDFN.	.A..SEDLLC	PTDCFRKHG
D89815	NWFGCTWMNS	TGFTKTCGGP	PCNIRG....	VG..NNTLTC	PTDCFRKHDP
ED43type_4	AWFGCTWMNS	TGFTKTCGAP	PCEVN.....	TN..NGTWHC	PTDCFRKHPE
HC_C2	NWFGCTWMNT	TGFTKTCGGP	PCNIGG....	AG..NNTLTC	PTDCFRKHPE
HC_G9	NWFGCTWMNS	SGFTKTCGAP	ACNIGG....	SG..NNTLLC	PTDCFRKHDP
HCU16326	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHG
HCV_H_CMR	NWFGCTWMNS	TGFTKVC GAP	PCVIGG....	VG..NNTLLC	PTDCFRKHPE
HCV_J1	NWFGCTWMNS	TGFTKVC GAP	PCVIGG....	GG..NNTLHC	PTDCFRKHPE
HCV_J483	NWFGCTWMNS	TGFTKTCGAP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HCV_J8	AWFGCTWMNG	TGFTKTCGAP	PCRIRKDFN.	.S..TIDLLC	PTDCFRKHDP
HCV_JK1	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	AG..NNTLTC	PTDCFRKHPE
HCV_JS	NWFGCTWMNS	TGYTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HCV_K1_R1	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	AG..NNTLTC	PTDCFRKHPE
HCV_K1_R2	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HCV_K1_R3	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	AG..NNTFTC	PTDCFRKHPE
HCV_K1_S1	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	AG..NDTLTC	PTDCFRKHPE
HCV_K1_S2	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HCV_K1_S3	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	AG..NNTLTC	PTDCFRKHPE
HCV_L2	NWFGCTWMSS	TGFTKTCGGP	PCNIGG....	AG..NNTLTC	PTDCFRKHPE
HCV_N	NWFGCTWMNS	TGFTKTCGAP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HCV12083	GWFGCTWMNS	TGFTKTCGAP	PCQIVPGNYN	SS..ANELLC	PTDCFRKHPE
HCV1480	NWFGCTWMNS	TGFVKNC GAP	PCNLGP....	TG..NNSLKC	PTDCFRKHDP
HCVPOLYP	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HD_1	NWFGCTWMNS	TGFTKTCGGP	PCGIGG....	VG..NNTLIC	PTDCFRKHPE
HPCCGAA	NWFGCTWMNS	TGFTKVC GAP	PCVIGG....	VG..NNTLLC	PTDCFRKHPE
HPCFG	RWFGCTWMNS	TGFVKTCGAP	PCNIYGGMKD	IEANQTHLKC	PTDCFRKHHD
HPCGENANTI	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	GG..NNTLVC	PTDCFRKHPE
HPCGENOM	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HPCHUMR	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HPCJ	NWFGCTWMNG	TGFTKTCGGP	PCHIGG....	RG..NNTLTC	PTDCFRKHPE
HPCJCG	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	VG..NNTLVC	PTDCFRKHPE

HPCJK046	GWYGCTWMNT	SGFVKTCGAP	PCNIRPNPEE	NR..TETLRC	PTDCFRKHPP
HPCJK049	PWFGCTWMNG	SGYVKTGCGAP	PCHIYGGREG	KS..NNSLVC	PTDCFRKHPP
HPCJTA	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	VG..NLTLTC	PTDCFRKHPE
HPCJTB	NWFGCTWMNS	TGFTKTCGGP	PCNIGG....	VG..NLTLTC	PTDCFRKHPE
HPCK3A	RWFGCTWMNS	TGFVKTCGAP	PCNIYGDGRD	AQ.NESDLFC	PTDCFRKHPE
HPCPLYPRE	NWFGCTWMNS	TGFTKVC GAP	PCVIGG....	AG..NNTLHC	PTDCFRKHPP
HPCPOLP	SWFGCTWMNS	TGYTKTCGAP	PCRIRADFN.	.A..SMDLLC	PTDCFRKHPP
HPCPP	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
HPCUNKCD	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPP
MKC1A	NWFGCTWMNG	TGFTKTCGGP	PCNIGG....	VG..NNTLTC	PTDCFRKHPE
NDM59	SWFGCTWMNS	TGFTKTCGAP	PCRIRADFN.	.A..SMDLLC	PTDCFRKHPP
NZLI	RWFGCSWMNS	TCFLKTCGAP	PCNIYGGEGN	PH.NESDLFC	PTDCFRKHPE
SA13	NWFGCTWMNS	TGFVKTCGAP	PCNLGP....	TG..NNSLKC	PTDCFRKHPP
Th580	GWFGCTWMNS	TGFTKTCGAP	PCQLIPGDYN	SS..SNQLLC	PTDCFRKHPE
Type_3a_CB	RWFGCTWMNS	TGFVKTCGAS	PCDIYGGGGN	SG.NESDLFC	PTDCFRKHPE
TypeV_D	RWFGCAWMNS	TGFLKTCGAP	PCNIYGGCGN	PN.NESHLFC	PTDCFRKHPP
VN004	AWFGCTWMNS	SGFVKTCGAP	PCRIKPTIN.ETDLVC	PTDCFRKHPP
VN235	AWYGCTWMNS	TGYTKTCGAP	PCHIGP.PDQFC	PTDCFRKHPE
VN405	SWFGCTWMNS	TGFVKTCGAP	PCNTRPVGSGNDTLVC	PTDCFRKHPE

601

650

BEBE1	ATYIKCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIYKVRM	FVGGIEHRLQ
D89815	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLD
ED43type_4	TTYAKCGSGP	WITPRCLIDY	PYRLWHFPCT	ANFSVFNIRT	FVGGIEHRMQ
HC_C2	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLD
HC_G9	ATYSRCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIFKIRM	FVGGVEHRLD
HCU16326	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGAEHRLD
HCV_H_CMR	ATYSRCGSGP	WITPRCMVDY	PYRLWHYPCT	INVTIFKVRM	YVGGVEHRLD
HCV_J1	ATYSRCGSGP	WITPRCLVDY	PYRLWHYPCT	INVTIFKVRM	YVGGVEHRLD
HCV_J483	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	FNFSIFKVRM	YVGGVEHRLN
HCV_J8	ATYIKCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNFTIFKARM	YVGGVEHRFS
HCV_JK1	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	FNFTIFKIRM	YVGGVEHRLN
HCV_JS	ATYTKCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNFTIFKVRM	YVGGIEHRLD
HCV_K1_R1	ATYAKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFSIFKVRM	YVGGVEHRLT
HCV_K1_R2	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HCV_K1_R3	ATYTKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFTIFTIRM	YVGGVEHRLK
HCV_K1_S1	ATYAKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFSIFKVRM	YVGGVEHRLT
HCV_K1_S2	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HCV_K1_S3	ATYTKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFTIFTIRM	YVGGVEHRLK
HCV_L2	ATYTKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFTTFKVRM	YVGGVEHRLI
HCV_N	ATYSKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFSIFKVRM	YVGGVEHRLN
HCV12083	ATYQRCGSGP	WVTPRCLVDY	AYRLWHYPCT	VNFTLHKVRM	FVGGTEHRFD
HCV1480	ATYTRCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNYTIFKVRM	FIGGLEHRLD
HCVPOLYP	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLS
HD_1	ATYTRCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HPCCGAA	ATYSRCGSGP	RITPRCMVDY	PYRLWHYPCT	INVTIFKVRM	YVGGVEHRLD
HPCFG	ATFTRCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFSIFKVRM	FVGGHEHRFS
HPCGENANTI	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HPCGENOM	ATYTRCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNFAIFKVRM	YVGGVEHRLD
HPCHUMR	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLN
HPCJ	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTTFKVRM	YVGGVEHRLI
HPCJCG	ATYTKCGSGP	WLTPRCMVDY	PYRLWHYPCT	VNFTVFKVRM	YVGGVEHRLN
HPCJK046	ATYAKCGSGP	WLTPRCLVDY	PYRLWHYPCT	VNYTLHKVRM	YIAGSEHRFT
HPCJK049	ATYNRCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNYTIFKVRM	FVGGLEHRLF
HPCJTA	ATYTKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLS
HPCJTB	ATYTKCGSGP	WLTPRCIVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLS
HPCK3A	ATYSRCGAGP	WLTPRCLVDY	PYRLWHYPCT	VNFTLHKVRM	FVGGFEHRFT
HPCPLYPRE	ATYSRCGSGP	WITPRCLVDY	PYRLWHYPCT	INVTIFKIRM	YVGGVEHRLD
HPCPOLP	TTYIKCGSGP	WLTPRCLIDY	PYRLWHYPCT	VNYTIFKIRM	YVGGVEHRLT
HPCPP	ATYTKCGSGP	WLTPRCLVHY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLD

HPCUNKCD	ATYTKCGSGP	WLTTPRCLVDY	PYRLWHYPCT	VNFTIFKVRM	YVGGAEHRLD
MKC1A	ATYTKCGSGP	WLTTPRCLVHY	PYRLWHYPCT	VNFTIFKVRM	YVGGVEHRLE
NDM59	ATYIKCGSGP	WLTTPRCLVDY	PYRLWHYPCT	INYTIFKIRM	YVGGVEHRLT
NZLI	TTYSRCGAGP	WLTTPRCMVDY	PYRLWHYPCT	VDFRLFKVRM	FVGGFEHRFT
SA13	ATYTKCGSGP	WLTTPRCLVHY	PYRLWHYPCT	LNFTIFKVRM	YIGGLEHRLE
Th580	ATYQKCGSGP	WLTTPRCLVDY	PYRLWHYPCT	VNYTIHKVRM	FIGGVEHRFD
Type_3a_CB	ATYSRCGAGP	WLTTPRCMVDY	PYRLWHYPCT	VNFTLKFVRM	FVGGFEHRFT
TypeV_D	ATYSRCGAGP	WLTTPRCMVDY	PYRLWHYPCT	VNFTLKFVRM	FVGGFEHRFT
VN004	ASFVKCGSGP	WLTTPRCMVDY	PYRLWHYPCT	VNFTIHKVRV	FVGGVEHRFN
VN235	ATYRKCGSGP	WLTTPRCLVDY	PYRLWHYPCT	VNYTIHKVRL	FINGLEHRFD
VN405	ATYARCGSGP	WLTTPRCLVNY	PYRLWHYPCT	VNYTIHKVRM	FVGGIEHRFE

651

700

BEBE1	AACNFTRGDR	CNLEDRDRSQ	LSPLLHSTTE	WAILPCSYTD	LPALSTGLLH
D89815	AACNWTRGER	CDLEDRDRAE	LSPLLLSTTE	WQILPCSITT	LPALSTGLIH
ED43type_4	AACNWTRGEV	CGLEHRDRVE	LSPLLLTTTA	WQILPCSFTT	LPALSTGLIH
HC_C2	AACNWTRGER	CALEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HC_G9	AACNWTRGER	CDLEDRDRAE	LSPLLLSTTQ	WQVLPSCFTT	LPALSTGLIH
HCU16326	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
HCV_H_CMR	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTQ	WQVLPSCFTT	LPALSTGLIH
HCV_J1	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTQ	WQVLPSCFTT	LPALSTGLIH
HCV_J483	AACNWTRGER	CNLEDRDRSE	LSPLLLSTTE	WQILPCAFTT	LPALSTGLIH
HCV_J8	AACNFTRGDR	CRLEDRDRGQ	QSPLLHSTTE	WAVLPCSFSD	LPALSTGLLH
HCV_JK1	AACNWTRGER	CNLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_JS	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_R1	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_R2	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_R3	AACNWTRGER	CNLEDRDRAE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_S1	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_S2	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_K1_S3	AACNWTRGER	CNLEDRDRAE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_L2	AACNWTRGER	CNLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV_N	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HCV12083	VACNWTRGER	CELHDRNRIE	MSPLLFSTTQ	LSILPCSFST	MPALSTGLIH
HCV1480	AACNWTYGER	CDLEDRDRAE	LSPLLLSTTE	WAILPCSFTT	TPALSTGLIH
HCVPOLYP	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
HD_1	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
HPCCGAA	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTQ	WQVLPSCFTT	LPALSTGLIH
HPCFG	AACNWTRGER	CDLEDRDRSE	QOPLHSTTD	SLILPCSFTT	MPALSTGLIH
HPCGENANTI	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPCGENOM	AACNWTRGER	CNLEDRDRSE	LSPLLLSTTE	WQILPCAFTT	LPALSTGLIH
HPCHUMR	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
HPCJ	AACNWTRGER	CNLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPCJCG	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPCJK046	AACNWTRGER	CDLADRDRSE	MSPLLFSTTE	LAILPCSFTT	MPALSTGLIH
HPCJK049	AACNWTRGER	CNLEDRDRSE	MYPLHSTTE	QAILPCSFTT	IPALSTGLIH
HPCJTA	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPCJTB	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQILPCSFTT	LPALSTGLIH
HPC3A	AACNWTRGER	CDLEDRDRSE	QHPLHSTTE	LAILPCSFTT	MPALSTGLIH
HPCPLYPRE	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTQ	WQVLPSCFTT	LPALSTGLIH
HPCPOLP	AACNFTRGDR	CNLEDRDRSQ	LSPLLHSTTE	WAILPCTYSD	LPALSTGLLH
HPCPP	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
HPCUNKCD	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
MKC1A	AACNWTRGER	CDLEDRDRSE	LSPLLLSTTE	WQVLPSCFTT	LPALSTGLIH
NDM59	AACNFTRGDP	CNLEDRDRSQ	LSPLLHSTTE	WAILPCSYSD	LPALSTGLLH
NZLI	AACNWTRGER	CDLEDRDRSE	QHPLHSTTE	LAILPCSFTT	MPALSTGLIH
SA13	VACNWTRGER	CDLEDRDRAE	LSPLLLSTTQ	WAILPCSFTT	TPALSTGLIH
Th580	AACNWTRGER	CDLYDRDRSE	MSPLLFSTTQ	LAILPCSFTT	MPALSTGLIH
Type_3a_CB	AACNWTRGER	CDLEDRDRSE	QHPLHSTTE	LAILPCSFTT	MPALSTGLIH
TypeV_D	AACNWTRGER	CNLEDRDRSE	QHPLHSTTE	LAILPCSFTT	MPALSTGLIH

VN004	AACNWTRGDR	CELDDRRDFE	MSPLLFTTQ	LAILPCSFTT	MPALSTGLIH
VN235	AACNWTRGER	CELEDRDRIE	MSPLLFTTE	LAILPCSFTT	MPALSTGLVH
VN405	AACNWTRGER	CELDDRRDVE	MSPLLFTTQ	LSILPCSFTT	MPALSTGLIH

701

750

BEBE1	LHQNVIVDVQY	LYGLSPAITH	YVVKWEVVVL	LFLLLADARV	CACLWMLLLL
D89815	LHQNVIDIQY	LYGIGSAVVS	IAIKWEYVVL	LFLLLADARV	CACLWMLLLL
ED43type_4	LHQNVIVDVQY	LYGVGSAVVS	WALKWEYVVL	AFLLLADARV	SAYLWMMFLV
HC_C2	LHRNIVDVQY	LYGIGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMLLLI
HC_G9	LHQNVIVDVQY	LYGLSSAVTS	WVIKWEYVVL	LFLLLADARI	CACLWMLLLI
HCU16326	LHQNVIDIQY	LYGIGSAVVS	FAIKWEYIVL	LFLLLADARV	CACLWMLLLV
HCV_H_CMR	LHQNVIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMLLLI
HCV_J1	LHQNVIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMLLLI
HCV_J483	LHQNVIVDVQY	LYGVGSAFVS	FAIKWEYILL	LFLLLADARV	CACLWMLLLI
HCV_J8	LHQNVIVDVQY	LYGLSPALTR	YIVKWEYVIL	LFLLLADARI	CACLWMLIIL
HCV_JK1	LHQNVIVDVQY	LYGVGSAVVS	IVIKWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_JS	LHRNIVDVQY	LYGIGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_K1_R1	LHQNVIVDVQY	LYGVGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_K1_R2	LHQNVIVDVQY	LYGVGSAVVS	FVIKWEYILL	LFLLLADARV	CACLWMLLLV
HCV_K1_R3	LHQNVIVDVQY	LYGVGSAVVS	VVIRWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_K1_S1	LHQNVIVDVQY	LYGVGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_K1_S2	LHQNVIVDVQY	LYGVGSAVVS	FVIKWEYILL	LFLLLADARV	CACLWMLLLV
HCV_K1_S3	LHQNVIVDVQY	LYGVGSAVVS	VVIRWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_L2	LHQNVIVDVQY	LYGIGSAVVS	FVIKWEYVLL	LFLLLADARV	CACLWMLLLI
HCV_N	LHQNVIVDVQY	LYGIGSAVVS	FAIKWEYVVL	LFLLLADARV	CACLWMLLLI
HCV12083	LHQNVIVDVQY	LYGVSTNVTS	WVVKWEYIVL	MFLVLADARI	CTCLWMLLLI
HCV1480	LHQNVIVDTQY	LYGLSSSIIVS	WAVKWEYIML	VFLLLADARI	CTCLLILLLI
HCVPOLYP	LHQNVIVDVQY	LYGIGSVVVS	FAIKWEYVVL	LFLLLADARV	CACLWMLLLI
HD_1	LHQNVVDVQY	LYGIGSVVVS	FAIKWEYILL	LFLLLADARV	CACLWMLLLI
HPCCGAA	LHQNVIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CACLWMLLLI
HPCFG	LHQNVIVDVQY	LYGVGSAVVG	WALKWEFVVL	VFLLLADARV	CVALWMLLLI
HPCGENANTI	LHQNVVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLLLADARV	CACLWMLLLI
HPCGENOM	LHQNVIVDVQY	LYGIGSAVAS	FAIKWEYVLL	LFLLLADARV	CACLWMLLLI
HPCHUMR	LHQNVIVDVQY	LYGIGSAVVS	FAIKWEYVLL	LFLLLADARV	CACLWMLLLI
HPCJ	LHQNVIVDVQY	LYGIGSAVVS	IAIRWEYVLL	LFLLLADARV	CACLWMLLLI
HPCJCG	LHRNIVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLLLADARV	CACLWMLLLI
HPCJK046	LHQNVVDVQY	LYGLSTSIVN	WAIKWEYVVL	LFLVLADSRI	CLALWMLLLI
HPCJK049	LHQNVIVDVQY	LYGISSGLVG	WAIKWEFVIL	IFLLLLADARV	CVVLWMMMLI
HPCJTA	LHQNVIVDVQY	LYGIGSAVVS	FVIKWEYIVL	LFLLLADARV	CACLWMLLLI
HPCJTB	LHQNVIVDVQY	LYGIGSAVVS	FVIKWEYIVL	LFLLLADARV	CACLWMLLLI
HPCK3A	LHQNVIVDVQY	LYGIGSGMVG	WALKWEFVIL	IFLLLLADARV	CVALWLILTI
HPCLYPRE	LHQNVIVDVQY	LYGVGSSIAS	WAIKWEYVVL	LFLLLADARV	CSCLWMLLLI
HPCPOLP	LHQNVIVDVQF	MYGLSPALTK	YIVRWEWVVL	LFLLLADARV	CACLWMLILL
HPCPP	LHQNVIVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLPLADARV	CAWLWMLLLI
HPCUNCKD	LHQNVIDIQY	LYGIGSAVVS	FAIKWEYIVL	LFLPLADARV	CAWLWMLLLI
MKC1A	LHQNVIVDVQY	LYGIGSAVVS	FAIKWEYILL	LFLPLADARV	CACLWMLILL
NDM59	LHQNVIVDVQY	MYGLSPALTK	YIVRWEWVVL	LFLLLADARV	CVALWMLLMI
NZLI	LHQNVIVDVQY	LYGVGSGMVG	WALKWEFVIL	VFLLLADARV	CVALWMLLMI
SA13	LHQNVIVDTQY	LYGLSSSIIVS	WAVKWEYIVL	AFLLLADARI	CTCLWMLLLV
Th580	LHQNVIVDVQY	LYGVSSSIIVS	WAVKWEYVVL	MFLVLADARI	CTCLWMLLLV
Type_3a_CB	LHQNVIVDVQY	LYGVGSGMVG	WALKWEFVIL	IFLLLLADRRV	CVALWMLLMI
TypeV_D	LHQNVIVDVQY	LYGVGSGMVG	WALKWEFVIL	IFLLLLADARV	CVALWMLLMI
VN004	LHQNVIVDTQY	LYGVSTAVVS	WAMKWEYVVL	AFLVLADARV	CACLWMLFLV
VN235	LHQNVIDIQY	LYGLAPALVS	WAVRWEYVVL	AFLLLADARI	CACLWMLVLI
VN405	LHQNVIVDVQY	LYGVSSAVVS	WAVKWEYIVL	AFLVLAVARV	CACLWMLFLV

751

800

BEBE1	800
D89815	
ED43type_4	

HC_C2	AQAEAALENL	VVLNAASVAG	VHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HC_G9	SQVEAALENL	IVLNAASLVG	THGIVPFFIF	FCAAWYLKGR	WAPGLAYSVY
HCU16326	AQAEAALENL	VVLNAASVAG	AHGILSFIVF	FCAAWYIKGR	LVPGAAYALY
HCV_H_CMR	SQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYAFY
HCV_J1	SQAEAALENL	VILNAASLAG	TRGLVSFLVF	FCFAWYLKGR	WVPGAAAYALY
HCV_J483	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LAPGAAYAFY
HCV_J8	GQAEAALEKL	IILHSASAAS	ANGPLWFFIF	FTAAWYLKGR	VVPVATYSVL
HCV_JK1	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_JS	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_R1	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_R2	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HCV_K1_R3	AQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_S1	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HCV_K1_S2	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_K1_S3	AQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_L2	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HCV_N	ARAEAALENL	VALNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYASY
HCV12083	STVEAAVERL	VVLNAASAAG	TAGWWWAVLF	LCCVWYVKGR	LVPACTYMAL
HCV1480	CQAEATCKNV	IVLNAASVAG	NHGFFWGLLV	VCLAWHVKGR	LVPGATYLCCL
HCVPOLYP	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYATY
HD_1	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCCGAA	SQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYALY
HPCFG	SQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYALY
HPCGENANTI	AQAEAALENL	VILNAASLAG	THGLVSFLVF	FCFAWYLKGR	WVPGAVYALY
HPCGENOM	AQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCUMR	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HPCJ	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJCG	AQAEATLENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJK046	GQAEAALENL	IVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJK049	SQAEAALENL	IVLNAASAAG	TRGWEFCLLF	MCWAWYVRGR	VVPAVITYGLL
HPCJTA	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCJTB	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCK3A	SQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCPLYPRE	SQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
HPCPOLP	GQAEAALEKL	VVLHAASAAS	CNGFLYFVIF	FVAAWYIKGR	AVPLAAYSLT
HPCPP	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
HPCUNKCD	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
MKC1A	AQAEAALENL	VVLNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYAFY
NDM59	GQAEAALEKL	VVLHAASAAS	CNGFLYFVIF	FVAAWYIKGR	AVPLAAYSLT
NZLI	SQTEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
SA13	CQAEAALENV	IVLNAASAAG	THGIGWYLVA	FCAAWYVRGR	LVPLVTYSLT
Th580	GKVEAALERL	VVLNAASAAG	TAGWCWTLIF	LCCVWYVKGR	LVPACTYTAL
Type_3a_CB	TQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
TypeV_D	SQAEAALENL	VILNAASVAG	AHGILSFLVF	FCAAWYIKGR	LVPGAAYALY
VN004	GQAEAALENV	IVLNAASAAS	CQGLLWGLIF	ICCAWHVRGR	AVPVTYALL
VN235	SQVEAALENL	IVLNAASAAS	SQGWYICLVF	ICCAWYIKGR	VVPGATYAIL
VN405	GQAEAALENL	IVLNATSAAG	SQGWVGVVVF	ICCAWYIRGR	AAPITTYAIL

801

BEBE1	GCWSFVLLLM	ALPHQAYALD	AAEQQGIGMA	LLIAITAFTI	TPAYKILLSR
D89815	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLALLTL	SPHYKVLAR
ED43type_4	GLWPCFLLLL	MLPERAYAYD	QEVAGSLGGA	IVVMLTILTL	SPHYKLWLAR
HC_C2	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLALLTL	SPHYKVLAR
HC_G9	GMWPLLLLLL	ALPQRAYALD	TEVAASCGGV	VLVGLMALTL	SPHYKRYISW
HCU16326	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLALLTL	SPHYKVLAR
HCV_H_CMR	GMWPLLLLLL	ALPQRAYALD	TEVAASCGGV	VLVGLMALTL	SPHYKRYISW
HCV_J1	GMWPLLLLLL	ALPQRAYALD	TEVAASCGGV	VLVGLMALTL	SPHYKRYISW
HCV_J483	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLALLTL	SPHYKVLAR
HCV_J8	GLWSFLLLV	ALPQRAYALD	AAEQGELGLA	ILVIISIFTL	TPAYKILLSR
HCV_JK1	GVWPLLLLLL	ALPPRAYAMD	REMAASCGGA	VFVGLALLTL	SPHYKVLAR

850

HCV_JS GVWPLLLLLL ALPPRAFAMD REMAASCGGA VFVGLALLTL SPHYKVFLAR
 HCV_K1_R1 GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLALLTL SPYKVFLLAK
 HCV_K1_R2 GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLALLTL SPHYKVFLAR
 HCV_K1_R3 GVWPLLLLLL SLPPRAYAMD REMAASCGGA VFVGLALLTL SPHYKAFLLAK
 HCV_K1_S1 GVWPLLLLLL ALPPRAYAMD REMAASCGGV VFVGLALLTL SPYKVFLLAR
 HCV_K1_S2 GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLALLTL SPHYKVFLAR
 HCV_K1_S3 GVWPLLLLLL SLPPRAYAMD REMAASCGGA VFVGLALLTL SPHYKAFLLAK
 HCV_L2 GVWPLLLLLL ALPPRAYAMD QGMAASSGGT VLVGLMLLTL SPYKVFLLAR
 HCV_N GAWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLALLTL SPYKVFLLAR
 HCV12083 GMWPLLLTIL ALPPRAYAMD NEQAASLGAV GLLVITIFSI TPKYKLLNC
 HCV1480 GVWPLLLVRL LRPRLALALD SSDGGTVGCL VLVLTIFTTL TPKYKLLNC
 HCVPOLYP GVWPLLLLLL ALPPRAYALD REMAASCGGA VFVGLVLLTL SPHYKFLAR
 HD_1 GVWPLLLLLL ALPPRAYALD REMAASCGGA VFVGLIILTL SPHYKAFLLAR
 HPCCGAA GMWPLLLLLL ALPQRAYALD TEVAASCGGV VLVGLMALTL SPYKRYISW
 HPCFG GLWPLALLDL LLPRAYAWT GEDDATIGAG VLLLLGFFTL SPYKHWIGR
 HPCGENANTI GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLVLLTL SPHYKFLAR
 HPCGENOM GVWPLLLLLL TLPPRAYAMD REMAASCGGA VFVGLVFTL SPYKVFLLAR
 HPCHUMR GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLVLLTL SPYKVFLLAR
 HPCJ GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLVLLTL SPYKVFLLAR
 HPCJCG GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLVLLTL SPYKVFLLAR
 HPCJK046 NLWPLLLVL LLPRAYAYD GVQAGSIGAA VIAALTIFSL TPAYKTLLAH
 HPCJK049 GLWPLLLVL MLPYRAYAWT GTDTSTLGAG VLSLFALFTL SPYKHWIAR
 HPCJTA GVWPLLLLLL ALPPRAYAMD REMAASCGGV VFVGLIILTL SPHYKFLAR
 HPCJTB GVWPLLLLLL ALPPRAYAMD REMAASCGGV VFVGLIILTL SPHYKFLAR
 HPC3A GLWSLALLVL LLPQRAYAWS GEDSATLGAG ILVLFGFFTL SPYKHWIAR
 HPCPLYPRE GMWPLLLLLL ALPQRAYALD TEVAASCGGV VLVGLMALTL SPYKRYISW
 HPCPOLP GLWSFGLLL LLPQAYAYD ASVHCQIGAA LLVLTIFTL TPYKTLISR
 HPCPP GVWPLLLLLL ALPARAYAMD REMAASCGGA VFVGLVLLTL SPYKVFLLAK
 HPCUNKCD GVWPLLLLLL ALPPRAYAMD REMAASCGGA VFVGLVLLTL SPHYKFLAR
 MKC1A GVWPLLLLLL ALPARAYAMD REMAASCGGA VFVGLVLLTL SPYKVFLLAK
 NDM59 GLWPFCLLL ALPQAYAYD ASVHGQTGVA LLILITLFTL TPYKILLSR
 NZLI GLWSLALLVL LLPQRAYAWS GEDSATLGAG VLVLFGFFTL SPYKHWIGR
 SA13 GIWPLLLLF LLPQALALD SSDGGTVGCL VLTILTIFTL TPYKMMVVL
 Th580 GMWPILLVIL ALPQRAYAWD NSQAASLGAV ALLVLTIFTL SPYKQLLTH
 Type_3a_CB GLWPLALLVL MLPQRAYAWS GEDSATLGAG VLVLFGFFTL SPYKHWIGR
 TypeV_D GLWSLALLVL LLPQRAYAWS GEDSATLGAG VLVLFGFFTL SPYKHWIGR
 VN004 QLWPLLLIL ALPRRAYAFD SEQAASAGLL VLGLITIFTL TPAYKQLIS
 VN235 HLWPLLLVL ALPQRAYAQD REQASIGVV VIAAITIFTL TPAYKTMVH
 VN405 QLWPLLLVL ALPRRAYAYN GEEAASLGML AIVITIFTL TPAYKTLIS

851

900

BEBE1 CLWWTCTMLV LAEALIQDWI PPLQARGGRD GVIWAMTMFY PGVVFDTKW
 D89815 LIWWLQYFIT KAEHLQVSL PPLNVRGGRD AIILLMCAVH PELIFDITKL
 ED43type_4 GLWWLQYFIA RTEAVLHVYI PSFNVGRPRD SVIVLAVLVC PDLVFDITKY
 HC_C2 LIWWLQYFIT RAEHLQVWI PPLNVRGGRD AIILLTCAAH PELIFDITKL
 HC_G9 GIWWLQYMLT RAEALLQVWV PPLNARGGRD GVVLLTCVLH PHLLFEITKI
 HCU16326 FIWWLQYLIT RTEAHLQVWV PPLNVRGGRD AIILLTCVH PELIFDITKY
 HCV_H_CMR CMWWLQYFLT RVEAQLHVWV PPLNVRGGRD AVILLMCAVH PTLVFDITKL
 HCV_J1 CLWWLQYFLT RVEAQLHVWV PPLNVRGGRD AVILLMCAVH PTLVFDITKL
 HCV_J483 LIWWLQYFIT RAEAHMQVWV PPLNVRGGRD AIILLTCAVH PELIFDITKL
 HCV_J8 SVWWSYMLV LAEALIQQVW PPLEVRGGRD GIIWVAVILH PRLVFEVTKW
 HCV_JK1 LIWWLQYFIT RVEACLQVWV PPLNVRGGRD AIILLTCAVH SELIFDITKI
 HCV_JS LMWRLLQYLIT RAEHLQIWW PPLNIRGGRD AIILLMCAVH PELIFDITKL
 HCV_K1_R1 LIWWLQYLIT RAEALQVWI PPLNVRGGRD AIILLTCAVH PELIFDITKI
 HCV_K1_R2 LIWWLQYFIT RAEACLQVWI PPLNVRGGRD AIILLTCAVH PELIFDITKI
 HCV_K1_R3 LIWWLQYFIT RAEHLQVWI PPLNVRGGRD AIILLTCAVH SELVFEITKI
 HCV_K1_S1 LIWWLQYLIT RAEALQVWI PPLNVRGGRD AIILLTCVH PELIFDITKI
 HCV_K1_S2 LIWWLQYFIT RAEACLQVWI PPLNVRGGRD AIILLTCAVH PELIFDITKI
 HCV_K1_S3 LIWWLQYFIT RAEHLQVWI PPLNVRGGRD AIILLTCAVH SELVFEITKI
 HCV_L2 LIWWLQYFIT RAEHLQVWV PPLNVRGGRD AVILLTCAVH PELVFDITKL

HCV_N	LIWWLQYLIA	RAEAHLHVWV	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HCV12083	FIWWNQYFLA	RAEAMVHEWV	PDLRVRGGRD	SIILLTCLLH	PQLGFEVTKI
HCV1480	VMWWLQYFIA	RVEAIIHVWV	PPLQVKGGRD	AVIMLTCLFH	PALGFEITKI
HCVPOLYP	LIWWLQYYIT	RAEALLQVWI	PPLNVRGGRD	AIILLTCVVH	PELIFDITKL
HD_1	LIWWLQYFIT	RAEALLQVWI	PPLNVRGGRD	AIILLTCAVH	PGLIFDITRL
HPCCGAA	CMWWLQYFLT	RVEAQLHVWV	PPLNVRGGRD	AVILLTCVVH	PALVFDITKL
HPCFG	LIWWNQYAIC	RGEAALQVWV	PPLLVRGSRD	SVILLASLLY	PSLIFDITKL
HPCGENANTI	LIWWLQYFIT	RAEAHLQVWI	PPLNVRGGRD	AIILLTCAAY	PELIFDITKI
HPCGENOM	LIWWLQYFLT	IAEAHLQVWI	PPLNIRGGRD	AIILLTCAIH	PESIFDITKL
HPCCHUMR	LIWWLQYFTT	RAEADLHVWI	PPLNARGGRD	AIILLMCAVH	PELIFDITKL
HPCJ	LIWWLQYLLT	RAEAHLHMWI	PPLNVRGGRD	AIILLACAAH	PELIFDITKL
HPCJCG	LIWWLQYFIT	RAEAHLQVWV	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HPCJK046	FLWWTQYFIA	HIEAKLHVWV	PFLRVRGGRD	AIILLTCVFH	PSLGFEVTKI
HPCJK049	LIWWNQYTIA	RCEAALQIWW	PPLLARGARD	GIILLAGLFY	PALVFDITKL
HPCJTA	LIWWLQYFIT	RAEAHLQVWV	PPLNVRGGRD	AIILLTCAAH	PELIFDITKL
HPCJTB	LIWWLQYFIT	RAEAHLQVWV	PPLNVRGGRD	AIILLTCAAH	PELIFDITKL
HPCK3A	LIWWNQYTIC	RCEAHLQVWV	PPLLARGGRD	GVILLTSLLY	PSLIFDITKL
HPCPLYPRE	CLWWLQYFLT	RVEAQLHVWI	PPLNVRGGRD	AVILLMCAVH	PTLVFDITKL
HPCPOLP	FLWWLCYLLT	LAEAMVQEWV	PPMQVRGGRD	GIIWAVAIFC	PGVVFDTKW
HPCPP	LIWWLQYLIT	RAEAHLQVWI	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
HPCUNKCD	FIWWLQYLIT	RTEAHLQVWV	PPLNVRGGRD	AIILLTCVVH	PELIFDITKY
MKC1A	LIWWLQYLIT	RAEAHLQVWI	PPLNVRGGRD	AIILLTCAVH	PELIFDITKL
NDM59	SLWWLCYLLT	LGEAMIQEWV	PPMQARGGRD	GIIWAATMFC	PGVVFDTKW
NZLI	LMWWNQYTIC	RCEAHLQVWV	PPLLARGSRD	GVILLTSLLY	PSLIFDITKL
SA13	VIWWLQYFIA	RVEAFIHVWV	PPLQVRGGRD	AIIMLTCLFH	PALGFEVTKI
Th580	AIWWNQYMLA	RAEAMIHDWV	PDLRVRGGRD	AIILLTCLLH	PHLGFEVTKI
Type_3a_CB	LIWWNQYTIC	RCEAHLQVWV	PPLLARGSRD	GVILLTSLLY	PSLIFDITKL
TypeV_D	LIWWNQYTIC	RCEAHLQVWV	PPLLARGSRD	GVILLTSLLY	PSLIFDITKL
VN004	MLWWIQYFIA	LTEAQLHQWV	PSLLVRGGRD	AVILLACLH	PQLGFEVTKI
VN235	FLWWNQYFIA	RSEALIQQWV	PSLRVRGGRD	AVILLTCLLH	PSLGFDITKM
VN405	TLWWIQYYIA	RAEAMLYVWV	PSLQVRGGRD	AVILLTCLLH	PQLGFEVTKA

901

950

BEBE1	LLAILGPGYL	FRAAVMRTRY	FVRANALLRM	CALVKQLAGG	KYVQVALITL
D89815	LLSILGPLMV	LQASLIRVPY	FVRAQGLIRA	CMLVRKAAGG	HYVQMAFVKL
ED43type_4	LLAILGPLHI	LQASLLRIPY	FVRAQALVKI	CSLLRGVVYV	KYFQMVVLKS
HC_C2	LLAIFGPIMV	LQAGITKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HC_G9	MLAILGPLWI	LQASLLKVPI	FVRAHGLIRL	CMLVRKTAGG	QYVQMALLKL
HCU16326	LLAIFGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLARKVVGG	HYVQMVFMKL
HCV_H_CMR	LLAIFGPLWI	LQASLLKVPI	FVRVQGLLRI	CALARKIAGG	HYVQMAI IKL
HCV_J1	LLAVLGPLWI	LQASLLKVPI	FVRVQGLLRI	CALARKMVGG	HYVQMAI IKL
HCV_J483	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_J8	LLAILGPAYL	LKASLLRIPY	FVRAHALLRV	CTLVKHLAGA	RYIQMLLITI
HCV_JK1	LLAIFGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMALMKL
HCV_JS	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFVKL
HCV_K1_R1	VLAILGPLMV	LQAGIAKVPD	FVRAQGVIRE	CILVRKVGGG	QYVQMAFMKL
HCV_K1_R2	LVAILGPLMV	LQAGITKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_K1_R3	LLAIFGPLMV	LQAGITKVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFVKL
HCV_K1_S1	MLAILGPLMV	LQAGIAKVPD	FVRAQGVIRE	CILVRKVGGG	QYVQMAFMKL
HCV_K1_S2	LVAILGPLMV	LQAGITKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_K1_S3	LLAIFGPLMV	LQAGLIRVPY	FVRAQGLIRV	CMLVRKVAGG	HYVQMAFVKL
HCV_L2	LLAIFGPLMV	LQAGI IKMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV_N	LIAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HCV12083	LLAVLAPLYI	LQYSLLKVPI	FVRAHILLRA	CLLVRRLAGG	KYVQACLRL
HCV1480	LFCILGPLYL	LQHSLLTKVPY	FLRARALLRL	CLLAKHLVYG	KYVQAALLHL
HCVPOLYP	LLAMLGPPMV	LQAVITKVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMALMKL
HD_1	LLAILGPLMV	LQAGITRVPY	FVRAHGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCCGAA	LLAIFGPLWI	LQASLLKVPI	FVRVQGLLRI	CALARKIAGG	HYVQMAI IKL
HPCFG	LIIVLGPLYL	IQAALTSTPY	FVRAHVLIRI	CMLVRSAMGG	KYVQMAVLT
HPCGENANTI	LLAILGPLMV	LQAGLIRIPY	FVRAQGLIRA	CMLVRKAAGG	HYVQMALMKL

HPCGENOM	LLATLGPLL	LQAGITRVPY	FVRAHGLIRA	CMLLRKVAGG	HYVQMAFMKL
HPCHUMR	LLAILGPLMV	LQAGITRVPY	FVRAQGLIHA	CMLVRKVAGG	HYVQMAFMKL
HPCJ	LLAILGPLYM	LQAGITAVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCJCG	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCJK046	LLAILGPLYL	LHASLLRVPY	YVRAHALIRI	CALVQNVAGG	KYVQAAILRA
HPCJK049	LLAILGPLYI	LQASLVRVPY	FVRAHAVVRL	CILVRNITGG	KYVQMVLAL
HPCJTA	LLAILGPLMV	LQAAITAMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCJTB	LLAILGPLMV	LQAAITAMPY	FVRAQGLIRA	CMLVRKVAGG	HYVQMAFMKL
HPCK3A	LIAALGPLYL	IQATITATPY	FVRAHVLVRL	CMLVRSVMGG	KYFQMIILSL
HPCPLYPRE	LLAVFGPLWI	LQASLLKVPY	FVRVQGLLRF	CALARKMIGG	HYVQMVIIKL
HPCPOLP	LLAVLGPAYL	LKGALTRVPY	FVRAHALLRM	CTMVRHLAGG	RYVQMVLLAL
HPCPP	LLAILGPLMV	LQAGLTQMPY	FVRAQGLIRM	CMLVRKAAGG	HYVQMALMKL
HPCUNKCD	LLAIFGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLARKVVG	HYVQMVFMKL
MKC1A	LLAILGPLMV	LQAGITRVPY	FVRAQGLIRA	CMLVWKAAGG	HYVQMAFVKL
NDM59	LLAMLGPAYL	LRDALTRVPY	FVRAHALLRL	CTMVRHLAGG	RYVQMAALLAL
NZLI	LMAVLGPLYL	IQATITATPY	FVRAHVLVRL	CMLVRSVIGG	KYFQMIILSI
SA13	LLGILGPLYL	LQYSLIKLPY	FIRARALLRA	CLLAKHLACG	RYVQAALLHL
Th580	LLAILAPLYI	LQHSLLKVPY	FVRAHILLRA	CMFFRKVAAG	KYVQACLLRL
Type_3a_CB	LIAVLGPLYL	IQAAVTTTPY	FVRAQVLVRL	CMLVRSVMGG	KYFQMIILSI
TypeV_D	LIAVLGPLYL	IQASITATPY	FVRAHVLVRL	CMLVRSMMGG	KYFQMIILSV
VN004	LLALLGPLYL	LQYSLKTPY	FVRAHILLRA	CMFFRGMARG	RYAQAILLRI
VN235	LLALLGPLYL	LQVSLLRVPY	YVRAHALLRV	CILVRRVAGG	KYIQAALLKL
VN405	ILALLGPLYI	LQYSLKTPY	FVRAHILLRV	CMFLRGVAGG	KYVQAALLRL

951

1000

BEBE1	GKWTGTYYID	HLSPMSDWAA	DGLRDLAVAV	EPVIFSPMER	KVIVWGAETT
D89815	AALTGTYYVD	HLTPLQDWAH	VGLRDLAVAV	EPVVFSAFET	KVITWGADTA
ED43type_4	RGLTGTYYID	HLTPMSDWPP	YGLRDLAVAL	EPVVFPTMEK	KVIVWGADTA
HC_C2	AALTGTYYVD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HC_G9	GAFAGTYIYN	HLSPLODWAH	SGLRDLAVAT	EPVIFSRMEI	KTITWGADTA
HCU16326	AALAGTYVYD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KVITWGADTA
HCV_H_CMR	GALTGTYYVN	HLTPLRDWAH	NGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HCV_J1	CALTGTYYVN	HLTPLRDWAH	NGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HCV_J483	GALTGTYYVN	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KVITWGADTA
HCV_J8	GRWTGTYYID	HLSPSTWAA	QGLRDLAIAV	EPVVFSPMEK	KVIVWGAETV
HCV_JK1	AALTGTYYVD	HLTPLRDWAH	SGLRDLVAV	EPVVFSDMET	KIITWGADTA
HCV_JS	AALTGTYYVD	HLAPLQHWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_R1	AELKGTSVYD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_R2	AALTGTYYVD	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_R3	AALTGTYYVN	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_S1	AELKGTSVYD	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_S2	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_K1_S3	AALTGTYYVN	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_L2	AALTCTYYVD	HLTPLRDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV_N	GALTGTYYVN	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HCV12083	GAWTGTFFVD	HLAPLSDWAA	DGLRDLAVAV	EPVIFSPMEK	KIITWGADTA
HCV1480	GRLTGTYYID	HLAPMKDWAA	SGLRELTVAT	EPVIFSAFET	KVITWGADTA
HCVPOLYP	AGLTSTYYVD	HLTPLQDWAH	GGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HD_1	AALTGTYYVD	HLTPLRDCRH	AGLRDLAVAV	EPVVFSAFET	KIITWGADTA
HPCCGAA	GALTGTCTVYN	HLAPLRDWAH	NGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HPCFG	GRWFNTYLYD	HLSPIDWAA	EGLKGLAVAT	EPVIFSPMEI	KVITWGADTA
HPCGENANTI	AALTGTYYVD	HLTPLQDWAH	TGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCGENOM	GALTGTYYVN	HLTPLQYWR	AGLRELAVAV	EPVIFSDMET	KIITWGADTA
HPCHUMR	GALTGTYYIN	HLTPLRDWR	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCJ	AALTGTYYVD	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCJCG	AALTGTYYVD	HLTPLRDWAH	AGLRDLAVAV	EPVVFSDMET	KLITWGADTA
HPCJK046	GSWTGTYYID	HLVPLRTWAS	DGLRDLAVAV	EPVVFSPMEK	KVITWGADTA
HPCJK049	ARGFNTYLYD	HLSPMTDWAA	EGLKDLAVAV	EPVIFSPMEV	KVITWGADTT
HPCJTA	AALTCTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA
HPCJTB	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	EPVVFSDMET	KIITWGADTA

HPCK3A	ADGSNTYLYD	HLAPMQHWAA	AGLKDLAVAT	BPVIFSPMEI	KVITWGADTA
HPCPLYPRE	GALTGTYYVN	HLTPLRDWAH	NGLRDLAVAV	BPVVFSQMET	KLITWGADTA
HPCPOLP	GRWTGTYYID	HLTPMSDWAA	NGLRDLAVAV	EPIIFSPMEK	KVIVWGAETA
HPCPP	AALTGTYYVD	HLTPLQDWAH	AGLRDLAVAV	BPVVFSQMET	KIITWGAETA
HPCUNKCD	AALAGTYVYD	HLTPLRDWAH	TGLRDLAVAV	BPVVFSQMET	KVITWGADTA
MKC1A	AALTGTYYID	HLTPLRDWAH	AGLRDLAVAV	BPVVFSQMET	KIITWGADTA
NDM59	GRWTGTYYID	HLSPMSDWAA	SGLRDLAVAV	EPIIFSPMEK	KVIVWGAETA
NZLI	GRWFNTYLYD	HLAPMQHWAA	AGLKDLAVAT	BPVIFSPMEI	KVITWGADTA
SA13	GRLTGTYYID	HLAPMKDWAA	SGLRDLAVAT	EPIIFSPMET	KVITWGADTA
Th580	GAWTGTYYID	HLAPLSEWAS	DGLRDLAVAV	BPVIFSPMEK	KIITWGADTA
Type_3a_CB	GRWFNTYLYD	HLAPMQHWAA	AGLKDLAVAT	BPVIFSPMEI	KVITWGADTA
TypeV_D	GRWFNTYLYD	HLAPMQHWAA	AGLKDLAVAT	BPVIFSPMEI	KVITWGADTA
VN004	GAWTGTYYID	HLAPLSDWAC	DGLRDLAVAV	BPVVFSQMET	KVITWGADTA
VN235	GAWTGTYYID	HLAPLSTWAS	DGLRDLAVAV	BPVTFSPMEK	KIITWGADTA
VN405	GAWTGTYYID	HLTPLSDWAC	DGLRDLAVAV	BPVVFSQMET	KVITWGADTV

1001

1050

BEBE1	ACGDIHGLP	VSARLGQEV	LGPADGYTSK	GWRLAPITA	YAQQTRGLLS
D89815	ACGDIISGLP	VSARRGKEIL	LGPADSFEGQ	GWRLAPITA	YSQQTRGLLG
ED43type_4	ACGDIIRGLP	VSARLGNEIL	LGPADTETSK	GWRLAPITA	YAQQTRGLFS
HC_C2	ACGDIILGLP	VSARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
HC_G9	ACGDIINGLP	VSARRGREVL	LGPADALTDK	GWRLAPITA	YAQQTRGLLG
HCU16326	ACGDIILACP	ASARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
HCV_H_CMR	ACGDIINGLP	VSARRGQEIL	LGPADGMVSK	GWRLAPITA	YAQQTRGLLG
HCV_J1	ACGDIINGLP	VSARRGREIL	LGPADGMVSK	GWRLAPITA	YAQQTRGLLG
HCV_J483	ACGDIILGLP	VSARRGKEIF	LGPADSLEGQ	GWRLAPITA	YSQQTRGLVG
HCV_J8	ACGDILHGLP	VSARRGREVL	LGPADGYTSK	GWRLAPITA	YTQQTRGLLG
HCV_JK1	ACGDIILGLP	VSARRGREIL	LGPADGFREQ	GWRLAPITA	YSQQTRGLFG
HCV_JS	ACGDIILGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
HCV_K1_R1	ACGDIIMGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLFG
HCV_K1_R2	ACGDIILGLA	VSARRGKEIF	LGPADSLEGS	GWRLAPITA	YSQQTRGLLG
HCV_K1_R3	ACGDIISGLA	VSARRGREIL	LGPADSFEGQ	GWRLAPITA	YSQQTRGLLG
HCV_K1_S1	ACGDIIMGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLFG
HCV_K1_S2	ACGDIILGLA	VSARRGKEIF	LGPADSLEGS	GWRLAPITA	YSQQTRGLLG
HCV_K1_S3	ACGDIISGLP	VSARRGREIL	LGPADSFEGQ	GWRLAPITA	YSQQTRGLLG
HCV_L2	ECGDIILGYR	SSARRGREIL	LGPADSLEGQ	GWRLAPITA	YAQQTRGLLG
HCV_N	ACGDIILGLP	VSARRGREIL	LGPADSLVGQ	GWRLAPITA	YSRQTRGLLG
HCV12083	ACGDILSGLP	VSARLGNLVL	LGPADDMQRG	GWRLAPITA	YAQQTRGLVG
HCV1480	ACGNILAVLP	VSARRGREIF	LGPADDIKTS	GWRLAPITA	YAQQTRGLVG
HCVPOLYP	ACGDIISGLP	VSARRGREIL	LGPADSLKEQ	GWRLAPITA	YSQQTRGLLG
HD_1	ACGDIILGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YAQQTRGLLG
HPCCGAA	ACGDIINGLP	VSARRGQEIL	LGPADGMVSK	GWRLAPITA	YAQQTRGLLG
HPCFG	ACGDILCGLP	VSARRGRELL	LGPADDYKMM	GWRLSPISA	YAQQTRGLFG
HPCGENANTI	ACGDIILCLP	VSARRGREIL	LGPADSLEGR	GWRLAPITA	YAQQTRGLFG
HPCGENOM	ACGDIILGLP	VSARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
HPCHUMR	ACGDIILGLP	VSARRGKEIL	LGPADSLEGR	GLRLAPITA	YSQQTRGLLG
HPCJ	ACGDIILGLP	VSARRGREIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
HPCJCG	ACGDIISGLP	VSARRGKEIL	LGPADSFEGQ	GWRLAPITA	YSQQTRGLLG
HPCJK046	ACGDILAGLP	VSARRGNLIL	LGPADDVKDK	GWRLAPITA	YAQQTRGLLG
HPCJK049	ACGDILCGLP	VSARLGKEVL	LGPADDYRSM	GWRLAPITA	HAQQTRGLFG
HPCJTA	ACGDIILGLP	VSARRGREIL	LGPADSIEGQ	GWRLAPITA	YAQQTRGLLG
HPCJTB	ACGDIILGLP	VSARREREIL	LGPADSIEGQ	GWRLAPITA	YXQQTRGLLG
HPCK3A	ACGDILCGLP	VSARRGREVL	LGPADDYREM	GWRLAPITA	YAQQTRGLLG
HPCPLYPRE	ACGDIINGLP	VSARRGREIL	LGPADGMVSK	GWRLAPITA	YAQQTRGLLG
HPCPOLP	ACGDILHGLP	VSARRGREVL	LGPADGYTSK	GWRLAPITA	YAQQTRGLLG
HPCPP	ACGDIISLPL	VSARRGRELL	LGPADSFEGQ	GWRLAPITA	YSQQTRGLLG
HPCUNKCD	ACGDIILALP	ASARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
MKC1A	ACGDIILGLP	VSARRGKEIL	LGPADSLEGQ	GWRLAPITA	YSQQTRGLLG
NDM59	ACGDVLHGLP	VSARRGREIL	LGPADGYTSK	GWRLAPITA	YAQQTRGLLG
NZLI	ACGDILCGLP	VSARRGREVL	LGPADDYREM	GWRLAPITA	YAQQTRGLLG

SA13	ACGDILAGLP	VSARRGHEIF	LGPADDIREA	GWRLAPITA	YAQQTRGVLG
Th580	ACGDILRGLP	VSARLGDLVL	LGPADDMRHG	GWKLLAPITA	YAQQTRGLVG
Type_3a_CB	ACGDILCGLP	VSARLGREVL	LGPADDYREM	GWRLAPITA	YAQQTRGLLG
TypeV_D	ACGDILCGLP	VSARLGREVL	LGPADDYREM	GWRLAPITA	YAQQTRGLLG
VN004	ACGDI IAGLP	VAARRGNLLF	LGPADDVKGK	GWRLAPITA	YAQQTRGIVG
VN235	ACGDILAGLP	VSARLGHLF	LGPADDMKSM	GWRLAPITA	YCQQTRGLLG
VN405	ACGDIISGLP	VSARRGNLIF	LGPADDIRDG	GWRLAPITA	YAQQTRGLVG
1051					
BEBE1	AIVVSM TGRD	KTDQAGEIQV	LSTVTQSFLG	TSISGVLWTV	FHGAGNKT LA
D89815	CIITSLTGRD	KNQVEGEVQV	VSTAKQSFLA	TCVNGACWTV	FHGAGSKT LA
ED43type_4	TIVTSLTGRD	TNENCGEVQV	LSTATQSFLG	TAVNGVMWTV	YHGAGAKT IS
HC_C2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HC_G9	CIITSLTGRD	KNQVEGEVQI	VSTATQTFLA	TCVNGVCWTV	YHGAGSRT IA
HCU16326	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	FHGAGSKT LA
HCV_H_CMR	CIITSLTGRD	KNQVEGEVQI	VSTATQTFLA	TCINGVCWTV	YHGAGTRT IA
HCV_J1	CIITSLTGRD	KNQVEGEVQI	VSTAAQTFLA	TCINGVCWTV	YHGAGTRT IA
HCV_J483	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	YHGAGSKT LA
HCV_J8	AIVVSLTGRD	KNEQAGQVQV	LSSVTQTFLG	TSISGVLWTV	YHGAGNKT LA
HCV_JK1	CIVTSLTGRD	KNQVEGEAQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HCV_JS	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	FHGAGSKT LA
HCV_K1_R1	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HCV_K1_R2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCTNGVCWTV	YHGAGSKT LA
HCV_K1_R3	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HCV_K1_S1	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HCV_K1_S2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCTNGVCWTV	YHGAGSKT LA
HCV_K1_S3	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HCV_L2	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	FHGAGSKT LA
HCV_N	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HCV12083	TIVTSLTGRD	KNEVEGEVQV	VSDTQSFLA	TSINGVMWTV	YHGPFGKT LA
HCV1480	AIVLSLTGRD	KNEAEGEVQF	LSTATQTFLG	ICINGVMWTV	FHGAGSKT LA
HCPOLYP	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HD_1	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HPCCGAA	CIITSLTGRD	KNQVEGEVQI	VSTATQTFLA	TCINGVCWTV	YHGAGTRT IA
HPCFG	TIVTSLTGRD	KNVVTGEVQV	LSTATQTFLG	TTVGGVMWTV	YHGAGSRT LA
HPCGENANTI	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	YHGAGSKT LA
HPCGENOM	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	YHGAGSKT LA
HPCUMR	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HPCJ	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	YHGAGSKT LA
HPCJCG	CIITSLTGRD	KNQVDGEVQV	LSTATQSFLA	TCVNGVCWTV	YHGAGSKT LA
HPCJK046	TIVTSLTGRD	KNEAAGEIQI	LSTATQTFLA	TCVNGVCWTV	YHGAGSKT LA
HPCJK049	TIVTSLTGRD	KNIVTGEIQV	LSTSTQTFLG	TSVGGVMWTV	YHGAGSRT LA
HPCJTA	CIVTSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	FHGAGSKT LA
HPCJTB	CIVTSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCVNGVCWTV	FHGAGSKT LA
HPCK3A	TIVTSLTGRD	KNV VAGEVQV	LSTATQTFLG	TTVGGVMWTV	YHGAGSRT LA
HPCPLYPRE	CIITSLTGRD	KNQVEGEVQI	VSTAAQTFLA	TCINGVCWTV	YHGAGTRT IA
HPCPOLP	TIVVSM TGRD	KTEQAGEIQV	LSTVTQSFLG	TTISGVLWTV	YHGAGNKT LA
HPCPP	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	FHGAGSKT LA
HPCUNKCD	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	FHGAGSKT LA
MKC1A	CIITSLTGRD	KNQVEGEVQV	VSTATQSFLA	TCINGVCWTV	YHGAGSKT LA
NDM59	AIVVSM TGRD	KTEQAGEIQV	LSTVTQSFLG	TSISGVLWTV	YHGAGNKT LA
NZLI	TIVTSLTGRD	KNVVTGEVQV	LSTATQTFLG	TTVGGVIWTV	YHGAGSRT LA
SA13	AIVVSLTGRD	KNEAEGEVQV	LSTATQTFLG	TCINGVMWTV	FHGAGAKT LA
Th580	TIVTSLTGRD	KNEAEGEVQV	VSTATQSFLA	TTINGVLWTV	YHGAGSKN LA
Type_3a_CB	TIVTSLTGRD	KNVVTGEVQV	LSTATQTFLG	TTVGGVTWTV	YHGAGSRT LA
TypeV_D	TIVTGLTGRD	KNVVTGEVQV	LSTATQTFLG	TTVGGVMWTV	YHGAGSRT LA
VN004	TIVTSLTGRD	KNEVEGEIQV	VSTATQSFLA	TAVNGVLWTV	YHGAGSKT LA
VN235	TIVTSLTGRD	RNVVEGEIQV	LSTATQSFLG	TAINGVMWTV	YHGAGSKT LA
VN405	TIVTSLTGRD	KNEVEGEIQV	VSTATQSFLA	TTVNGVLWTV	YHGAGSKT LA

	1101				1150
BEBE1	GSRGPVVTQMY	SSAEGDLVGW	PSPPGTRSLE	PCTCGAVDLY	LVTRNADVIP
D89815	AAKGPIITQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
ED43type_4	GPKGPIVQMY	TNVDQDLVGW	PAPPGVRSLS	PCTCGSADLY	LVTRHADVIP
HC_C2	GPKGPIITQMY	TNVDQDLVGW	PAPSGARSLT	PCTCGSSDLY	LVTRYADVIP
HC_G9	SASGPVIQMY	TNVDQDLVGW	PAPQGARSLT	PCTCGASDLY	LVTRHADVIP
HCU16326	GPKGPIITQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_H_CMR	SPKGPVIQMY	TNVDQDLVGW	PAPQGSRSLS	PCTCGSSDLY	LVTRHADVIP
HCV_J1	SPKGPVIQMY	TNVDQDLVGW	PAPQGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_J483	GPKGPIITQMY	TNVDLDLVGW	QAPPGARSMT	PCTCGSSDLY	LVTRHADVIP
HCV_J8	GPKGPIVQMY	TSAEGDLVGW	PSPPGTKSLD	PCTCGAVDLY	LVTRNADVIP
HCV_JK1	GPKGPIITQMY	TNVDQDLVGW	QAPSGAASLT	PCTYGSDDLY	LVTRHADVIP
HCV_JS	GPKGPIITQMY	TNVDQDLVGW	QAPPGARSMT	PCTCGSSDLY	LVTRHADVIP
HCV_K1_R1	GPKGPIITQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_K1_R2	GPKGPIITQMY	TNVDQDLVGW	QAPSGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_K1_R3	GPKGPIITQMY	TNVDQDLVGW	QAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_K1_S1	GPKGPIITQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_K1_S2	GSKGPITQMY	TNVDQDLVGW	QAPSGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_K1_S3	GPKGPIITQMY	TNVDQDLVGW	QAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV_L2	GPKGPIITQMY	TNVDQDLVGW	QAAPGMRSLT	PCTCGSSDLY	LVTRHADVIP
HCV_N	GPKGPIAQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HCV12083	GPKGPIVQMY	TNVDLDLVGW	PSPPGARSLT	PCNCGSSDLY	LVTRHADVIP
HCV1480	GPKGPIVQMY	TNVDKDLVGW	PSPPGKGSLS	RCTCGSADLY	LVTRHADVIP
HCVPOLYP	GPKGPIVQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HD_1	GPKGPIVQMY	TNVDQDLVGW	QAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HPCCGAA	SPKGPVIQTY	TNVDQDLVGW	PAPQGSRSLS	PCTCGSSDLY	LVTRHADVIP
HPCFG	GNKRPAQMY	TNVDQDLVGW	PAPAGTKSLD	PCTCGSSDLY	LVTRHADVIP
HPCGENANTI	GPKGPIITQMY	TNVDQDLVGW	HAPQGARSLT	PCTCGSSDLY	LVTRHADVIP
HPCGENOM	GPKGPIITQMY	TNVDQDLVGW	HRPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HPCHUMR	APKGPITQMY	TNVDQDLVGW	PKPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HPCJ	GPKGPIITQMY	TNVDQDLVGW	QAPPGARSMT	PCTCGSSDLY	LVTRHADVIP
HPCJCG	GPKGPIITQMY	TNVDQDLVGW	PAPPGARSMT	PCTCGSSDLY	LVTRHADVIP
HPCJK046	GPRGPVQMY	TNVDQDMVGW	PAPAGTRSYT	PCTCGASDLY	LVTRHADVIP
HPCJK049	GNKRPAQMY	TNVDQDLVGW	PSPPGAKSLV	PCTCGSADLY	LVTRHADVIP
HPCJTA	GPKGPIITQMY	TNVDQDLVGW	HAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HPCJTB	GPKGPIITQMY	TNVDQDLVGW	HAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HPC3A	GVKHPALQMY	TNVDQDLVGW	PAPPGAKSLE	PCTCGSADLY	LVTRHADVIP
HPCPLYPRE	SPKGPVIQMY	TNVDQDLVGW	PAPQGSRSLS	PCTCGSSDLY	LVTRHADVIP
HPCPOLP	GSRGPVVTQMY	SSAEGDLVGW	PSPPGTKSLE	PCTCGAVDLY	LVTRNADVIP
HPCPP	GPKGPIITQMY	TNVDQDLVGW	SAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
HPCUNKCD	GPKGPIITQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
MKC1A	GPKGPIITQMY	TNVDQDLVGW	PAPPGARSMT	PCTCGSSDLY	LVTRHADVIP
NDM59	GSRGPVVTQMY	SSAEGDLVGW	PSPPGTKSLE	PCTCGAVDLY	LVTRNADVIP
NZLI	GAKHAPALQMY	TNVDQDLVGW	PAPPGAKSLE	PCACGSADLY	LVTRHADVIP
SA13	GPKGPIVQMY	TNVDKDLVGW	PTPPGTRSLT	PCTCGSADLY	LVTRHADVIP
Th580	GPKGPIVQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
Type_3a_CB	GAKHAPALQMY	TNVDQDLVGW	PAPPGAKSLE	PCACGSADLY	LVTRHADVIP
TypeV_D	GAKHAPALQMY	TNVDQDLVGW	PAPPGAKSLE	PCACGSADLY	LVTRHADVIP
VN004	GPKGPIVQMY	TNVDQDLVGW	PAPAGARSLT	PCSCGSADLY	LVTRHADVIP
VN235	GPKGPIVQMY	TNVDQDMVGW	PAPPGTRSLT	PCTCGASDLY	LVTRHADVIP
VN405	GPKGPIQMY	TNVDQDLVGW	PAPPGARSLT	PCTCGSSDLY	LVTRHADVIP
	1151				1200
BEBE1	ARRRGDRRGA	LLSPRPLSSL	KGSSGGPVLC	PRGHAVGIFR	AAVCSRGVAK
D89815	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
ED43type_4	VRRRGDTRGA	LLSPRPISIL	KGSSGGPLLC	PMGHRAGIFR	AAVCTRGVAK
HC_C2	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAAGIFR	AAVCTRGVAK
HC_G9	VRRRGDNRRGS	LLSPRPISYL	KGSSGGPLLC	PMGHAVGIFR	AAVCTRGVAK
HCU16326	VRRRGDSRGS	LLPPRPVSYL	KGSSGGPLLC	PSGHAVGILP	AAVCTRGVAM
HCV_H_CMR	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PAGHAVGLFR	AAVCTRGVTK

HCV_J1	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PAGHVVGIFR	AAVCTRGVAK
HCV_J483	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
HCV_J8	VRRKDDRRGA	LLSPRPLSTL	KGSSGGPVLC	SRGHAVGLFR	AAVCARGVAK
HCV_JK1	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HCV_JS	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLPC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_R1	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
HCV_K1_R2	VRRRGDGRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_R3	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_S1	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
HCV_K1_S2	VRRRGDGRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HCV_K1_S3	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HCV_L2	VRRRGDGRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HCV_N	VRRRGDNRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGVFR	AAVCTRGVAK
HCV12083	ARRRGDSRAA	LLSPRPISYL	KGSSGGPIMC	PSGHVVGIFR	AAVCTRGVAK
HCV1480	ARRRGDTRAS	LLSPRPISYL	KGSSGGPIMC	PSGHVVGIFR	AAVCTRGVAK
HCVPOLYP	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HD_1	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HPCCGAA	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PTGHAVGLFR	AAVCTRGVAK
HPCFG	ARRRGDSTAS	LLSTRPLSCL	KGSSGGPVMC	PSGHVVGIFR	AAVCTRGVAK
HPCGENANTI	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
HPCGENOM	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PFGHVAGIFR	AAVCTRGVAK
HPCHUMR	VRRRGDSRGS	LLSPRPVSYL	KGSSGGPLLC	PFGHVAGIFR	AAVCTRGVAK
HPCJ	VRRRGDGRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HPCJCG	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
HPCJK046	ARRRGDNRAG	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
HPCJK049	ARRRGDSTAS	LLSPRPLACL	KGSSGGPIMC	PSGHVAGIFR	AAVCTRGVAK
HPCJTA	VRRRGDGRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HPCJTB	VRRRGDGRGS	LLSPRPVSYL	KGSSGGPLLC	PSGHAVGIFR	AAVCTRGVAK
HPCK3A	ARRRGDSTAS	LLSPRPLARL	KGSSGGPVMC	PSGHVAGIFR	AAVCTRGVAK
HPCPLYPRE	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PAGHAVGIFR	AAVCTRGVAK
HPCPOLP	ARRRGDKRGA	LLSPRPLSTL	KGSSGGPVLC	PRGHAVGVFR	AAVCSRGVAK
HPCPP	VRRRGDSRGS	LLSPGPISYL	KGSSGGPLPC	PSGRVVGIFR	AAVCTRGVAK
HPCUNKCD	VRRRGDGRGS	LLPPRPVSYL	KGSSGGPLLC	PSGHAVGILP	AAVCTRGVAM
MKC1A	VRRRGDSRGS	LLSPRPISYL	KGSSGGPLLC	PSGHVVGIFR	AAVCTRGVAK
NDM59	ARRRGDKRGA	LLSPRPLSTL	KGSSGGPVLC	PRGHAVGIFR	AAVCSRGVAK
NZLI	ARRRGDSTAS	LLSPRPLACL	KGSSGGPVMC	PSGHVAGIFR	AAVCTRGVAK
SA13	ARRRGDTRAS	LLSPRPISYL	KGSSGGPVMC	PSGHVVGIFR	AAVCTRGVAK
Th580	ARRRGDTRAA	LLSPRPISYL	KGSSGGPLMC	PSGHVVGIFR	AAVCTRGVAK
Type_3a_CB	ARRRGDSTAS	LLSPRPLACL	KGSSGGPVMC	PSGHVAGIFR	AAVCTRGVAK
TypeV_D	ARRRGDSTAS	LLSPRPLACL	KGSSGGPVMC	PSGHVAGIFR	AAVCTRGVAK
VN004	ARRRGDNRAA	LLSPRPISYL	KGSSGGPMLC	PSGHVAGIFR	AAVCTRGVAK
VN235	ARRRGDTRAG	LLSPRPLSTL	KGSSGGPLMC	PSDHVVGIFR	AAVCTRGVAK
VN405	ARRRGDTRAA	LLSPRPISYL	KGSSGGPMLC	PSGHVAGIFR	AAVCTRGVAK

1201

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BEBE1	SIDFIPVESL	DVTRSPNFT	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
D89815	AVDFIPVESM	ETTMRSPVFT	DNSTPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
ED43type_4	AVDFVPVESL	ETTMRSPVFT	DNSTPPAVPQ	TYQVAHLHAP	TGSGKSTKVP
HC_C2	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HC_G9	AVDFVPVESL	ETTMRSPVFT	DNSSPPTVPQ	SYQVAHLHAP	TGSGKSTKVP
HCU16326	AVEFIPVESM	ETTMRSPVFT	DNPSPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
HCV_H_CMR	AVDFIPVENL	ETTMRSPVFT	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HCV_J1	AVDFIPVESL	ETTMRSPVFT	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HCV_J483	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_J8	SIDFIPVESL	DVATRTPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
HCV_JK1	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_JS	AVDFIPVESM	ETTMRAPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_R1	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_R2	AVDFIPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_R3	AVDFVPVESM	ETTMRSPVFT	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSNKVP
				TFQVAHLHAP	TGSGKSTKVP

HCV_K1_S1	AVDFVPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_K1_S2	AVDFIPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSNKVP
HCV_K1_S3	AVDFVPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_L2	AVDFVPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HCV_N	AVDFVPVESH	ETTMRSVF	DTSSPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
HCV12083	SLDFIPVENM	ETTMRSVF	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTRVP
HCV1480	ALEFVPVENL	ETTMRSVF	DNSTPPAVPH	EFQVGHHLHAP	TGSGKSTKVP
HCVPOLYP	AVDFVPVESH	ETTMRSVF	DNSSPPAVPE	TFQVAHLHAP	TGSGKSTKVP
HD_1	AVDFVPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCCGAA	AVDFIPVENL	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKTTKVP
HPCFG	ALQFIPVETL	STQVRSPSFS	DNSTPPAVPE	SFQVAHLHAP	TGSGKSTKVP
HPCGENANTI	AVDFVPVESH	ETTMRSVF	DNSSPPAVPQ	AFQVAHLHAP	TGSGKSTKVP
HPCGENOM	AVDFIPVETM	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCHUMR	AVDFVPVESH	ETTMRSVF	DNSSPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
HPCJ	AVDFIPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCJCG	AVDFIPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCJK046	ALDFVPCEAM	DATTRSPTFT	DNSTPPAVPQ	AYQVGYLHAP	TGSGKSTKVP
HPCJK049	ALQFIPVESL	SAQTRSPSFS	DNSTPPAVPQ	TFQVGYLHAP	TGSGESTKVP
HPCJTA	AVDFIPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCJTB	AVDFIPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTKVP
HPCK3A	ALQFIPVETL	STQARSPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
HPCPLYPRE	AVDFIPVENL	ETTMRSVF	DNSSPPVVPQ	SFQVAHLHAP	TGSGKSTKVP
HPCPOLP	SIDFIPVETL	DIVTRSPTFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
HPCPP	AVDFVPVESH	ETTMRSVF	DNSTPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
HPCUNKCD	AVEFIPVESH	ETTMRSVF	DNSSPPAVPQ	TFQVAHLHAP	TGSGKSTRVP
MKC1A	AVDFVPVESH	ETTMRSVF	DNSTPPAVPQ	SFQVAHLHAP	TGSGKSTKVP
NDM59	SIDFIPVEAL	DVVTRSPTFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
NZLI	SLQFIPVETL	STQARSPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
SA13	ALDFIPVENL	ETTMRSVF	DNSTPPAVPH	EFQVGHHLHAP	TGSGKSTKVP
Th580	ALDFIPVENM	ETTMRSVF	DNSSPPAVPQ	TYQVGYLHAP	TGSGKSTRVP
Type_3a_CB	ALQFIPVETL	STQTRSPSFS	DNSTPPAVPQ	SYQVGYLHAP	TGSGKSTKVP
TypeV_D	ALQFIPVETL	STQARSPSFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
VN004	SLDFAPVESH	QSSQSPSFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
VN235	ALDFVPVENM	ETTMRSVF	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP
VN405	SLDFVPVENM	QSTARSPSFS	DNSTPPAVPQ	TYQVGYLHAP	TGSGKSTKVP

1251

1300

BEBE1	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	YGINPNIRTG	VRTVTTGDAI
D89815	AAYAAQGYMV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGAPI
ED43type_4	AAHAAQGYKV	LVLNPSVAAT	LGFGVYMSKA	YGIDPNIRSG	VRTITTGAPI
HC_C2	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNTRTG	VRTITTGAPI
HC_G9	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNVRTG	VRTITTGSPI
HCU16326	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNLRTG	VRTITTGAPI
HCV_H_CMR	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGSPI
HCV_J1	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGSPI
HCV_J483	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMPKA	HGIDPNIRTG	VRTITTGGPI
HCV_J8	AAYASQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGINPNIRTG	VRTVTTGDSI
HCV_JK1	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNISTG	VRTITTGAPI
HCV_JS	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	YGTDPNIRTG	VRTITTGAPI
HCV_K1_R1	AAYAAQGYKV	LVLNPSVTAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_R2	VEYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_R3	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	ARTITTGAPI
HCV_K1_S1	AAYAAQGYKV	LVLNPSVTAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_S2	VEYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HCV_K1_S3	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	ARTITTGAPI
HCV_L2	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	ARTITTGAPI
HCV_N	AAYATQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGAPI
HCV12083	AAYASQGYKV	LVLNPSVAAT	LSFGSYMRQA	YGVEPNIRTG	VRTVTTGGAI
HCV1480	AAYAAQGYKV	LVLNPSVAAT	FGFGAYMSRA	YGVDPNIRTG	VRTVTTGAGI
HCVPOLYP	AAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGAPI

HD_1	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGAPI
HPCCGAA	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGSPI
HPCFG	AAAYVAQGYSV	LVLNPSVAAT	LGFGTYMSKA	YGIDPNIRTG	TRTITTGAKL
HPCGENANTI	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HPCGENOM	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HPCHUMR	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGAPV
HPCJ	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	YGTDPNVRTG	VRTITTGSPI
HPCJCG	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIEPNIRTG	VRTITTGGPI
HPCJK046	VAYASQGYKV	LVLNPSVAAT	LSFGSYLSRA	HGIDPNIRTG	VRTITTGAPI
HPCJK049	ASYVAQGYTV	LVLNPSVAAT	LGFGRFMSHA	YGIDPNVRTG	TRTITTGAKL
HPCJTA	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGAPI
HPCJTB	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGTDPNIRTG	VRTITTGGPI
HPCK3A	AAAYVAQGYNV	LVLNPSVAAT	LGFGSFSMSRA	YGIDPNIRTG	NRTVTTGAKL
HPCPLYPRE	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNIRTG	VRTITTGSPI
HPCPOLP	VAYAAQGYKV	LVLNPSVAAT	LGFGAYLSKA	HGINPNIRTG	VRTVTTGAPI
HPCPP	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
HPCUNKCD	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGIDPNLRTG	VRTITTGAPI
MKC1A	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSKA	HGVDPNIRTG	VRTITTGAPI
NDM59	VAYAAQGYKV	LVLNPSVAAT	LGFGAYLSKA	HGINPNIRTG	VRTVTTGESI
NZLI	AAAYVAQGYNV	LVLNPSVAAT	LGFGSFSMSRA	YGIDPNIRTG	NRTVTTGAKL
SA13	AAAYAAQGYKV	LVLNPSVAAT	LGFGAYMSRA	YGVDPNIRTG	VRTVTTGAAI
Th580	AAAYATQGYKV	LVLNPSVAAT	LSFGAYMSKA	HGIDPNIRTG	VRTITTGGPV
Type_3a_CB	AAAYVAQGYTV	LVLNPSVAAT	LGFGSFSMSRA	YGIDPNIRTG	NRTVTTGAKL
TypeV_D	AAAYVAQGYNV	LVLNPSVAAT	LGFGSFSMSRA	YGTDPNIRTG	NRTVTTGAKL
VN004	AAAYAAQGYKV	LVLNPSVAAT	LGFGSYMSTS	HGIDPNIRTG	VRTITTGGAI
VN235	AAAYASQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGPI
VN405	AAAYAAQGYKV	LVLNPSVAAT	LGFGSYMSTA	HGIDPNIRTG	VRTITTGGAI

1301

1350

BEBE1	TYSTYKFLA	DGGCSGGAYD	VIICDECHSV	DSTTILGIGT	VLDQAETAGV
D89815	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETVGA
ED43type_4	TYSTYKFLA	DGGCSGGAYD	IIICDECYST	DSTTILGIGT	VLDQAETAGV
HC_C2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HC_G9	THSTYKFLA	DGGCSGGAYD	IIICDECHSV	DATSILGIGT	VLDQAETAGV
HCU16326	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTIYGIGT	VLDQAETAGA
HCV_H_CMR	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSILGIGT	VLDQAETAGA
HCV_J1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSVLGIGT	VLDQAETAGA
HCV_J483	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HCV_J8	TYSTYKFLA	DGGCAAGAYD	IIICDECHSV	DATILGIGT	VLDQAETAGV
HCV_JK1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_JS	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	ALDQAETAGA
HCV_K1_R1	TYSTYKFLA	DGGCSGGAYD	IIMCDECHSI	DSTSILGIGT	VLDQAETAGA
HCV_K1_R2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_R3	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_S1	TYSTYKFLA	DGGCSGGAYD	IIMCDECHSI	DSTSILGIGT	VLDQAETAGA
HCV_K1_S2	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_K1_S3	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HCV_L2	TYSTYKFFA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HCV_N	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	VLDQAETAGA
HCV12083	TYSTYGEFLA	DGGCSGGAYD	IIICDECHST	DPTTVLVGT	VLDQAETAGV
HCV1480	TYSTYKFFA	DGGCSGGAYD	VIICDECHSQ	DATILGIGT	VLDQAETAGA
HCVPOLYP	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HD_1	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HPCCGAA	TYSTYKFLA	DAGCSGGAYD	IIICDECHST	DATSISGIGT	VLDQAETAGA
HPCFG	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
HPCGENANTI	TYSTYKFLA	DGGCSGGAYD	IIMCDECHST	DSTTILGIGT	VLDQAETAGA
HPCGENOM	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCHUMR	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJ	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJCG	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA

HPCJK046	TYSTYKFLA	DGGCSGGAYD	VIICDECHST	DPTTVLGIGT	VLDQAETAGC
HPCJK049	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGA
HPCJTA	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCJTB	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTTILGIGT	VLDQAETAGA
HPCK3A	TYSTYKFLA	GGGCSGGAYD	VIICDDCHAQ	DATSILGIGT	VLDQAETAGV
HPCPLYPRE	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DATSILGIGT	VLDQAETAGA
HPCPOLP	TYSTYKFLA	DGGCAGGAYD	IIICDECHAV	DSTTILGIGT	VLDQAETAGV
HPCPP	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
HPCUNKCD	TYSTYKFLA	DGGSGGGAYD	IIMCDECHST	DSTTIYGIGT	VLDQAETAGA
MKC1A	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DSTSILGIGT	VLDQAETAGA
NDM59	TYSTYKFLA	DGGCAGGAYD	IIICDECHAV	DATTILGVGT	VLDQAETAGV
NZLI	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
SA13	TYSTYKFLA	DGGCSGGAYD	VIICDECHSQ	DATTILGIGT	VLDQAETAGA
Th580	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
Type_3a_CB	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
TypeV_D	TYSTYKFLA	DGGCSGGAYD	VIICDECHAQ	DATSILGIGT	VLDQAETAGV
VN004	TYSTYKFLA	DGGCSGGAYD	VIICDECHST	DPTTVSGIGT	VLDQAETSGV
VN235	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV
VN405	TYSTYKFLA	DGGCSGGAYD	IIICDECHST	DPTTVLGIGT	VLDQAETAGV

1351

1400

BEBE1	RLTVLATATP	PGSVTTTPHPN	IEEVALGHEG	EIPFYGKAIP	LSAIKGRHL
D89815	RFVVLATATP	PGSITPFPHPN	IEEVPLANTG	EIPFYAKTIP	IEVIRGGRHL
ED43type_4	RLTVLATATP	PGSVTTPHSN	IEEVALPTTG	EIPFYGKAIP	LELIKGRHL
HC_C2	RLVVLATATP	PGSVTVPHSN	IEEVALSTTG	EIPFYGKAIP	IETIKGRHL
HC_G9	RLTILATATP	PGSVTVPHSN	IEEVALSTEG	EIPFYGKAIP	LNYIKGRHL
HCU16326	RLVVLSTATP	PGSVTVPHLN	IEEVALSNTG	EIPFYGKAIP	IEAIKGRHL
HCV_H_CMR	RLVVLATATP	PGSVTVSHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGRHL
HCV_J1	RLVVLATATP	PGSITVPHAN	IEEVALSTTG	EIPFYGKAIP	LEAIKGRHL
HCV_J483	RLVVLATATP	PGSVTVPHPN	IEEIGLSNNG	EIPFYGKAIP	IEAIKGRHL
HCV_J8	RLVVLATATP	PGTVTTPHSN	IEEVALGHEG	EIPFYGKAIP	LAFIKGRHL
HCV_JK1	RLVVLAAATP	PGSVTVPHPN	IEEVALPNTG	EIPFYGKAIP	LETIKGRHL
HCV_JS	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEVIKGRHL
HCV_K1_R1	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_R2	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_R3	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LDTIKGRHL
HCV_K1_S1	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_S2	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IETIKGRHL
HCV_K1_S3	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LDTIKGRHL
HCV_L2	RLVVLATATP	PGSTTVPHPN	IEEVALPNTG	EIPFYGRAIP	IEFIKGRHL
HCV_N	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIMGRHL
HCV12083	RLTVLPTATP	PGSVTVPHPN	ITETALPTTG	EIPFYGKAIP	LEYIKGRHL
HCV1480	RLVVLATAIP	PGSVTTTPHPN	IEEVALPSEG	EIPFYGRAIP	LVLIKGRHL
HCVPOLYP	RLVVLATATP	PGSVTVPHPN	IEEVALSNIG	EIPFYGKAIP	IETIKGRHL
HD_1	RLVVLATATP	PGSVTVPHSN	IEEVALSNIG	EIPFYGKAIP	LENIKGRHL
HPCCGAA	RLVVLATATP	PGSVTVSHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGRHL
HPCFG	RLTVLATATP	PGSITVPHPN	IEEVGLTSDG	EIPFYGKALP	LAMIKGRHL
HPCGENANTI	RLVVLATATP	PGSVTVPHPN	IEEIALSNTG	EIPFYGKAIP	IETIKGRHL
HPCGENOM	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIRGRHL
HPCHUMR	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIRGRHL
HPCJ	RLVVLATATP	PGSVTVPHPN	IEEVGLSNTG	EIPFYGKAIP	IEVIKGRHL
HPCJCG	RLVVLATATP	PGSITVPHPN	IEEVALSNTG	EIPFYGKAIP	IEAIKGRHL
HPCJK046	RLTVLATATP	PGSVTVPHPN	IQETALPLTG	EVPPFYGKAIP	LEYIKGRHL
HPCJK049	RLVVLATATP	PGSITVPHSN	IEEVALTPEG	EIPFYGRAIP	LGVIKGRHL
HPCJTA	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGRHL
HPCJTB	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	IEVIKGRHL
HPCK3A	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IACIKGRHL
HPCPLYPRE	RLVVLATATP	PGSVTVPHPN	IEEVALSTTG	EIPFYGKAIP	LEVIKGRHL
HPCPOLP	RLTVLATATP	PGSVTTTPHPN	IEEVALQEG	EIPFYGRAIP	LSYIKGRHL
HPCPP	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGRHL

HPCUNKCD	RLVVLSTATP	PGSVTVPHLN	IEEVALSNTG	BIPFYGKAIP	IEAIKGRHL
MKC1A	RLVVLATATP	PGSVTVPHPN	IEEVALSNTG	EIPFYGKAIP	LEAIKGRHL
NDM59	RLTVLATATP	PGSVTTPHPN	IEEVALGQEG	EIPFYGRAIP	LSYIKGRHL
NZLI	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALLKGRHL
SA13	RLVVLATATP	PGSVTTPHPN	IEEVALPSEG	EIPFYGRAIP	LALIKGRHL
Th580	RLTVLATATP	PGSVTVPHPN	ITETALPTTG	EIPFYGKCIP	LEFIKGRHL
Type_3a_CB	RLTVLATRTP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALLKGRHL
TypeV_D	RLTVLATATP	PGSITVPHSN	IEEVALGSEG	EIPFYGKAIP	IALLKGRHL
VN004	RLTVLATATP	PGSVTVPHPN	ITESALPTTG	EIPFYGKAVP	LEYIKGRHL
VN235	RLTVLATATP	PGSVTVPHPN	ITETALPSTG	EVPFYGKAIP	LECIKGRHL
VN405	RLTVLATATP	PGSVTVPHPN	ITEVALSSTG	EVPFYGKAIP	LEYIKGRHL
1401					
BEBE1	IFCHSKKKCD	ELAVLRGMG	LNAVAYYRGL	DVSIPTQGD	VVVVATDALM
D89815	IFCHSKKKCD	ELPAKLSALG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
ED43type_4	IFCHSKKKCD	ELARQLTSLG	LNAVAYYRGL	DVSVIPTSGD	VVVCATDALM
HC_C2	IFCHSKKKCD	ELAAKLSALG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HC_G9	IFCHSKKKCD	ELAAKLVLGL	VNAVAFYRGL	DVSVIPTTGD	VVVVATDALM
HCU16326	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_H_CMR	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTNGD	VVVVSTDALM
HCV_J1	IFCHSKKKCD	ELAAKLVALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_J483	IFCHSKKKCD	ELAAKLTLGL	LNAVAYYRGL	DVSVIPPIGD	VAVVATDALM
HCV_J8	IFCHSKKKCD	ELAAALRGMG	VNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
HCV_JK1	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_JS	IFCHSKKKCD	ELAAKLSTLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_K1_R1	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_R2	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_R3	IFCHSKKKCD	ELATKLSALG	VNAVAYYRGL	DVSVIPTSGN	VVVVATDALM
HCV_K1_S1	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_S2	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HCV_K1_S3	IFCHSKKKCD	ELATKLSALG	VNAVAYYRGL	DVSVIPTSGN	VVVVATDALM
HCV_L2	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV_N	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HCV12083	IFCHSKKKCD	ELAGKLKSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
HCV1480	IFCHSKKKCD	ELAKQLTSLG	VNAVAYYRGL	DVAVIPATGD	VVVCSTDALM
HCVPOLYP	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HD_1	IFCHSRKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCCGAA	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTSGD	VVVVSTDALM
HPCFG	IFCHSKKKCD	ELASKLRGMG	VNAVAFYRGL	DVSVIPVSGD	VVVCATDALM
HPCGENANTI	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPASGN	VVVVATDALM
HPCGENOM	IFCHSKKKCD	ELAAKLSSLG	LNAVAYYRGL	DVSVIPSSGD	VVVVATDALM
HPCHUMR	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTIGD	VVVVATDALM
HPCJ	IFCHSKKKCD	ELAAKLSALG	INAVAYYRGL	DVSVIPASGD	VVVVATDALM
HPCJCG	IFCHSKKKCD	ELAAKLTLGL	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCJK046	IFCHSKKKCD	ELAAQLRTL	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
HPCJK049	IFCHSKKKCD	ELAKQLTSLG	VNAVAFYRGL	DVSVIPTQGD	VVVCATDALI
HPCJTA	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVIVATDALM
HPCJTB	IFCHSKKKCD	ELAAKLSGLG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCK3A	IFCHSKKKCD	KMASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
HPCPLYPRE	IFCHSKKKCD	ELAAKLVALG	INAVAYYRGL	DVSVIPTSGD	VVVVATDALM
HPCPOLP	IFCHSKKKCD	ELAAALRGMG	LNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
HPCPP	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSIPTSGD	VVVVATDALM
HPCUNKCD	IFCHSKKKCD	ELAAKLSGLG	LNAVAYYRGL	DVSVIPTSGD	VVVVATDALM
MKC1A	IFCHSKKKCD	ELAAKLSALG	VNAVAYYRGL	DVSIPTSGD	VVVVATDALM
NDM59	IFCHSKKKCD	ELSAALRSMG	LNAVAYYRGL	DVSVIPTQGD	VVVVATDALM
NZLI	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
SA13	IFCHSKKKCD	ELAKQLTSQ	VNAVAYYRGL	DVAVIPATGD	VVVCSTDALM
Th580	IFCHSKKKCD	ELSKQLTSLG	LNAVAFYRGV	DVAVIPTSGD	VVVCATDALM
Type_3a_CB	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM
TypeV_D	IFCHSKKKCD	EIASKLRGMG	LNAVAYYRGL	DVSVIPTTGD	VVVCATDALM

VN004	IFCHPKKKCD	ELAKQLVSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM
VN235	IFCHSKKKCD	ELAKQLRTLK	LNAVAFYRGV	DVSVIPTAGD	VVVCATDALM
VN405	IFCHSKKKCD	ELAKQLTSLG	LNAVAFYRGV	DVSVIPTSGD	VVVCATDALM

	1451		1500
BEBE1	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFT ITTQTV PQDS VSR SQRRGRT
D89815	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR TQRRGRT
ED43type_4	TGFTGDFDSV	IDCNTSVIQT	VDFS LDPTFS IEITTV PQDA VSR SQRRGRT
HC_C2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HC_G9	TGYTGDFDSV	IDCNTCVVQT	VDFS LDPTFS IETSTVPQDA VSR SQRRGRT
HCU16326	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_H_CMR	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTLPQDA VSR TQRRGRT
HCV_J1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTLPQDA VSR TQRRGRT
HCV_J483	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_J8	TGYTGDFDSV	IDCNVAVSQI	VDFS LDPTFT ITTQTV PQDA VSR SQRRGRT
HCV_JK1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTLPQDA VSR SQRRGRT
HCV_JS	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_K1_R1	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_K1_R2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_K1_R3	TGYTGDFDSV	IDCNTCVIQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_K1_S1	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_K1_S2	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV_K1_S3	TGYTGDFDSV	IDCNTCVIQT	DDFS LDPTFT IETRTVPQDA VSR SQRRGRT
HCV_L2	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR TQRRGRT
HCV_N	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCV12083	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFS IETTTVPQDA VSR SQRRGRT
HCV1480	TGFTGDFDSV	IDCNSAVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HCVPOLYP	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HD_1	TGYTGDFDSV	IDCNVCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCCGAA	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTLPQDA VSR TQRRGRT
HPCFG	TGYTGDFDTV	IDCNVAVEQY	VDFS LDPTFS IETRTVPQDA VSR SQRRGRT
HPCGENANTI	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTMPQDA VSR SQRRGRT
HPCGENOM	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCHUMR	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCJ	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCJCG	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTLPQDA VSR AQRRGRT
HPCJK046	TGYTGDFDSV	IDCNVAVTQI	VDFS LDPTFS IETTTVPQDA VARSQRRGRT
HPCJK049	TGYTGDFDSV	IDCNVAVEQY	VDFS LDPTFS IETHTV PQDA VSR SQRRGRT
HPCJTA	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCJTB	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCK3A	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS IETCTAPQDA VSR SQRRGRT
HPCPLYPRE	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETITLPQDA VSR TQRRGRT
HPCPOLP	TGFTGDFDSV	IDCNVAVTQV	VDFS LDPTFT ITTQTV PQDA VSR SQRRGRT
HPCPP	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
HPCUNKCD	TGFTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
MKC1A	TGYTGDFDSV	IDCNTCVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
NDM59	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFT ITTQTV PQDA VSR SQRRGRT
NZLI	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS IETRTAPQDA VSR SQRRGRT
SA13	TGFTGDFDSV	IDCNTTVTQT	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
Th580	TGYTGDFDSV	IDCNVAVTQV	VDFS LDPTFS IETTTVPQDA VSR SQRRGRT
Type_3a_CB	TGYTGDFDSV	IDCNVAVEQY	VDFS LDPTFS IETRTAPQDA VSR SQRRGRT
TypeV_D	TGFTGDFDSV	IDCNVAVEQY	VDFS LDPTFS IETRTAPQDA VSR SQRRGRT
VN004	TGYTGDFDSV	IDCNVTVTQV	VDFS LDPTFT IETTTVPQDA VSR SQRRGRT
VN235	TGYTGDFDSV	IDCNVAVTQI	VDFS LDPTFS IETTTVPQDA VARSQRRGRT
VN405	TGYTGDFDSV	IDCNVSVTQV	VDFS LDPTFT IETTTMPQDA VSR SQRRGRT

	1501		1550
BEBE1	GRGRLGIYRY	VSSGERASGM	FDTVVLCECY DAGAAWYELT PAETT VRLRA
D89815	GRGRRGIYRF	VTPGERPSAM	FDSSVLCECY DAGCAWYELT PAETS VRLRA
ED43type_4	GRGRLGTYRY	VTPGERPSGM	FDTAELCECY DAGCAWYELT PAETTT RLKA

HC_C2	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HC_G9	GRGKHGIYRY	VSPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETTVRLRA
HCU16326	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HCV_H_CMV	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELM	PAETTVRLRA
HCV_J1	GRGKPGIYRF	VAPGERPSGM	FDSSILCECY	DTGCAWYELT	PAETTVRLRA
HCV_J483	GRGRSGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_J8	GRGRLGVYRY	VSSGERPSGM	FDSVVLCECY	DAGAAWYELT	PAETTVRLRA
HCV_JK1	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HCV_JS	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R1	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R2	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_R3	GRGRRGIYRF	VTPGERTSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S1	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S2	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_K1_S3	GRGRRGIYRF	VTPGERTSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_L2	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HCV_N	GRGRGGIYRF	VTPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETTVRLRA
HCV12083	GRGKPGVYRF	VSQGERPSGM	FDTVVLCEAY	DTGCAWYELT	PSETTVRLRA
HCV1480	GRGRHGIYRY	VSSGERPSGI	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
HCVPOLYP	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HD_1	GRGRMGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCCGAA	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAEASVRLRA
HPCFG	GRGRPGIYRF	VTPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETTVRLRA
HPCGENANTI	SRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCGENOM	GRGREGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCHUMR	GRGRRGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCJ	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DSGCAWYELT	PAETSVRLRA
HPCJCG	GRGRSGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCJK046	GRGKPGVYRY	VSQGERPSGM	FDTVVLCEAY	DTGAAWYELT	PAETTVRLRA
HPCJK049	GRGKSGTYRY	VSPGERPSGM	FDSVVLCECY	DAGCAWYELT	PSETTVRLRA
HPCJTA	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCJTB	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCK3A	GRGRLGTIYRY	VTPGERPSGM	FDSVVLCECY	DAGCAWYELT	PAETTVRLRA
HPCPLYPRE	GRGKPGIYRF	VAPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETTVRLRA
HPCPOLP	GRGRLGIYRY	VSTGERASGM	FDSVVLCECY	DAGAAWYELT	PAETTVRLRA
HPCPP	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
HPCUNKCD	GRGRAGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
MKC1A	GRGRGGIYRF	VTPGERPSGM	FDSSVLCECY	DAGCAWYELT	PAETSVRLRA
NDM59	GRGRLGIYRY	VSTGERASGM	FDSVVLCECY	DAGAAWYELT	PSETTVRLRA
NZLI	GRGRLGTIYRY	VASGERPSGM	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
SA13	GRGRHGIYRY	VSSGERPSGI	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
Th580	GRGKPGVYRY	VSQGERPSGM	FDSVVLCEAY	DTGCAWYELT	PAETTVRLRA
Type_3a_CB	GRGRLGTIYRY	VAPGERPSGM	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
TypeV_D	GRGRLGTIYRY	VAPGERPSGM	FDSVVLCECY	DAGCAWYDLT	PAETTVRLRA
VN004	GRGKHGVYRY	VSQGERPSGM	FDSVILCEAY	DTGCAWYELT	PAETTVRLRA
VN235	GRGKPGVYRY	VSQGERPSGM	FDTVVLCEAY	DVGCAWYELT	PSETTVRLRA
VN405	GRGKHGVYRY	VSQGERPSGI	FDTVVLCEAY	DTGCAWYELT	PSETTVRLRA

1551

1600

BEBE1	YFNTPLPVC	QDHLEFWFV	FTGLTHIDAH	FLSQTQKAGE	GFPYLVAYQA
D89815	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKAGD	NFPYLVAYQA
ED43type_4	YFDTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HC_C2	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HC_G9	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCU16326	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_H_CMV	YMNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_J1	YMNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_J483	YLNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_J8	YFNTPLPVC	QDHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA
HCV_JK1	YLNTPLPVC	QVHLEFWESV	FTGLTHIDAH	FLSQTQKQSGE	NFPYLVAYQA

HCV_JS	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_R1	YLNTPLPFC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NLPYLVAYQA
HCV_K1_R2	YLNTPLPVW	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_R3	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_S1	YLNTPLPFC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NLPYLVAYQA
HCV_K1_S2	YLNTPLPVW	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_K1_S3	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_L2	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV_N	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HCV12083	YMNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSHTKQAGE	NFAYLVAYQA
HCV1480	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSHTKQAGE	NFAYLVAYQA
HCVPOLYP	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGE	NFPYLTAYQA
HD_1	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCCGAA	YMNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
HPCFG	YLSTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFPYLTAYQA
HPCGENANTI	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCGENOM	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCHUMR	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJ	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJCG	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJK046	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJK049	YLSTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
HPCJTA	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCJTB	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCK3A	YLSTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
HPCPLYPRE	YMNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
HPCPOLP	YFNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
HPCPP	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
HPCUNKCD	YLNTPLPVC	QDHLEFSEV	FTGLTHIDAH	FLSQTQAGE	NFPYLVAYQA
MKC1A	YLNTPLPVC	QDHLEFVESV	FTGLTHIDAH	FLSQTQAGD	NFPYLVAYQA
NDM59	YFNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
NZLI	YLSTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
SA13	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
Th580	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
Type_3a_CB	YLSTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
TypeV_D	YLSTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
VN004	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
VN235	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA
VN405	YLNTPLPVC	QDHLEFWEV	FTGLTHIDAH	FLSQTQAGE	NFAYLVAYQA

1601

BEBE1	TVCARAKAPP	PSWDVMWKCL	IRLKPTLVGP	TPLLYRLGSV	TNEVTLTHPV
D89815	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
ED43type_4	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HC_C2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HC_G9	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCU16326	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_H_CMR	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J483	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_J8	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_JK1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_JS	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_R1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_R2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_R3	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_S1	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_S2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_K1_S3	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV_L2	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI

1650

HCV_N	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HCV12083	TVCARAKAPP	PSWDMMWKCL	IRLKPTLTGP	TPLLYRLGAV	QNGVITTHPI
HCV1480	TVCVRAKAPP	PSWDTMWKCM	ICLKPTLTGP	TPLLYRLGAV	QNEITLTHPI
HCVPOLYP	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVVLTHPI
HD_1	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCCGAA	TVCARQAAPP	PSWDQMRKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCFG	TVCARAKASP	PCWDEMWKCL	IRLKPTLQGP	TPLLYRLGAI	QNDICMTHPI
HPCGENANTI	TVCARQAAPP	PSWDQMWKCL	TRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCGENOM	TVCAKAQAPP	PSWDQMWKCL	TRLKPTLQGP	TPLLYRLGAV	QNEVTLTHPI
HPCCHUMR	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCJ	TVCARSQAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCJCG	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCJK046	TVCARAKAPP	PSWDTMWKCL	LRLKPTLTGP	TPLLYRLGAV	QNEVTPTHPV
HPCJK049	TVCARAAALP	PSWDETWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEICTTHPV
HPCJTA	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPI
HPCJTB	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPI
HPCK3A	TVCARQAAPP	PSWDETWKCL	VRKPTLHGP	TPLLYRLGPV	QNEICLTHPI
HPCPLYPRE	TVCARQAAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEITLTHPV
HPCPOLP	TVCARAKAPP	PSWDVMWKCL	TRLKPTLVGP	TPLLYRLGSV	TNEVTLTHPV
HPCPP	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
HPCUNKCD	TVCARQAAPP	PSWDEMWRCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
MKC1A	TVCARAKAPP	PSWDQMWKCL	IRLKPTLHGP	TPLLYRLGAV	QNEVTLTHPI
NDM59	TVCARAKAPP	PSWDVMWKCL	TRLKPTLVGP	TPLLYRLGPV	TNEVTLTHPV
NZLI	TVCARQAAPP	PSWDEMWKCL	VRKPTLHGP	TPLLYRLGPV	QNETCLTHPI
SA13	TVCVRAKAPP	PSWDTMWKCM	LRLKPTLTGP	TPLLYRLGAV	QNEITLTHPI
Th580	TVCARAKAPP	PSWDVMWKCL	TRLKPTLTGP	TPLLYRLGAV	QNEIVTTHPI
Type_3a_CB	TVCARQAAPP	PSWDETWKCL	VRKPTLHGP	TPLLYRLGPV	QNEICLSHPI
TypeV_D	TVCARQAAPP	PSWDEMWKCL	VRKPTLHGP	TPLLYRLGPV	QNETCLTHPV
VN004	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGPV	QNEVVTTHPI
VN235	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGAV	QNEIITTHPI
VN405	TVCARAKAPP	PSWDTMWKCL	IRLKPMLTGP	TPLLYRLGAV	QNEITTTTHPI

1651

1700

BEBE1	TKYIATCMQA	DLEIMTSTWV	LAGGVLAAVA	AYCLATGCVS	IIGRIHVNQK
D89815	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
ED43type_4	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSVGSVV	IVGRVVLSSQ
HC_C2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIVLSGR
HC_G9	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIILSGK
HCU16326	TKFIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_H_CMR	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGR
HCV_J1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_J483	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIVLSGR
HCV_J8	TKYIATCMQA	DLEIMTSSWV	LAGGVLAAVA	AYCLATGCIS	IIGRIHLNDR
HCV_JK1	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_JS	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_K1_R1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAAL	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_R3	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S1	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAAL	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S2	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_K1_S3	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK
HCV_L2	TKLIMASMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV_N	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HCV12083	TKYIMTCMSA	DLEVITSTWV	LVGGVLAALA	AYCLSVGCVV	ICGRITLTGK
HCV1480	TKYIMACMSA	DLEVITSTWV	LVGGVLAALA	AYCLTVGSA	IVGRIILSGR
HCVPOLYP	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGR
HD_1	TKFIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGCVV	IVGRIILSGR
HPCCGAA	TKYIMTCMSA	DLEVVTSTWV	LVGGVLAALA	AYCLSTGCVV	IVGRIVLSGK
HPCFG	TKYIMACMSA	DLEVTTSAV	LVGGVLAALA	AYCLSVGCVV	IVGRIILSGK
HPCGENANTI	TKYIMACMSA	DLEVVTSTWV	LVGGVLAALA	AYCLTTGSVV	IVGRIILSGK

HPCGENOM TKYIMTCMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIVLSGS
 HPCCHUMR TKYIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 HPCJ TKFIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 HPCJCG TKYIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 HPCJK046 TKYIMACMSA DLEVITSTWV VAGGILAAIA AYCLTVGSV ICGRITSSR
 HPCJK049 TKYIATCMAA DLEVATSAWV LLGGVMAALT AYCLSVGSV IVGHLVLGGK
 HPCJTA TKFIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 HPCJTB TKFIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 HPCJ3A TKYVMACMSA DLEVTTSTWV LLGGVLAAVA AYCLSTGCVV IVGRVVLSSGK
 HPCPLYPRE TKYIMTCMSA DLEVVTSTWV LVGGVLAALA AYCLSTGCVV IVGRVVLSSGK
 HPCPOLP TKYIATCMAA DLEVMTSTWV LAGGVLAAVA AYCLATGCVV IIGRLHVNQR
 HPCPP TKFIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 HPCUNKCD TKFIMTCMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGK
 MKC1A TKFIMACMSA DLEVVTSTWV LVGGVLAALA AYCLTTGSSV IVGRIILSGR
 NDM59 TKYIATCMAA DLEVMTSTWV LAGGVLAAVA AYCLATGCVS IIGRLHVNQR
 NZLI TKYLMACMSA DLEVTTSTWV LLGGVLAALA AYCLSVGCVV IVGHIELEGK
 SA13 TKYIMACMSA DLEVITSTWV LVGGVLAALA AYCLTVGSV IVGRIILSGR
 Th580 TKYIMTCMSA DLEVITSTWV LVGGVLAALA AYCLTVGCVV ICGRIVTSGK
 Type_3a_CB TKYVMACMSA DLEVTTSTWV LLGGVLAALA AYCLSVGCVV IVGHIELGGK
 TypeV_D TKYIMACMSA DLEVTTSTWV LLGGVLAALA AYCLSVGCVV IVGHIELGGK
 VN004 TKYIMTCMSA DLEVITSTWV LVGGVLAALA AYCLSVGCVV ICGRISTSGK
 VN235 TKYIMTCMAA DLEVITSTWV LAGGIVAALA AYCLTVGSV ICGRIVTSGK
 VN405 TKYIMTCMSA DLEVITSTWV LVGGVLAALA AYCLSVGCVV VCGRISTTGGK

1701

BEBE1 TIIAPDKEVL YEAFDEMEEC ASRTALIEEG HRIAEMLKSK IQGLMQQASK
 D89815 PAVIPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 ED43type_4 PAVIPDREVL YQEFDEMEEC SKHLPLVEHG LQLAEQFKQK ALGLLNFAGK
 HC_C2 PAVIPDREVL YQEFDEMEEC GSHLPYIEQG MQLAEQFKQK ALGLLQIATK
 HC_G9 PAVIPDREVL YREFDEMEEC AAHIPYLEQG MHLAEQFKQK ALGLLQTASK
 HCU16326 PAIIPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_H_CMR PAIIPDREVL YQEFDEMEEC SQHLPIYEQG MMLAEQFKQK ALGLLQTASR
 HCV_J1 PAIIPDREVL YREFDEMEEC SQHLPIYEQG MMLAEQFKQK ALGLLQTASR
 HCV_J483 PAVVPDREVL YQEFDEMEEC ASQLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_J8 VVVPDKEIL YEAFDEMEEC ASKAALIEEG QRMALMLKSK IQGLLQQAATK
 HCV_JK1 PAIIPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTASK
 HCV_JS PAVIPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_K1_R1 PAVIPDREAL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATN
 HCV_K1_R2 PAIIPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATN
 HCV_K1_R3 PAVIPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_K1_S1 PAVIPDREAL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_K1_S2 PAIIPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATN
 HCV_K1_S3 PAVIPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_L2 PAVIPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV_N PAVVPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HCV12083 PAVVPDREIL YQEFDEMEEC SRHIPYLAEG QQIAEQFRQK VLGLLQASAK
 HCV1480 PAITPDREVL YQEFDEMEEC SASLPYVDEA RAIAGQFKEK VLGLIGTAGQ
 HCVPOLYP PAIIPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HD_1 PAIIPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HPCCGAA PAIIPDREVL YQEFDEMEEC SQHLPIYEQG MMLAEQFKQK ALGLLQTASR
 HPCFG PALVPDRQVL YQQYDEMEEC SOSAPYIEQA QAIQQQFKDK VLGLLQASQ
 HPCGENANTI PAVVPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HPCGENOM PAIIPDREVL YQDFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HPCCHUMR PAIIPDRELL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HPCJ PAVIPDREVL YREFDEMEEC ASHLPIYEQG MMLAEQFKQK ALGLLQMATK
 HPCJCG PAVIPDREVL YQEFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HPCJK046 PAVIPDREVM YQQYDEMEEC SRHLPYLVG QQLAEQFKQN VLGLIQVTTK
 HPCJK049 PALVPDKEVL YQQYDEMEEC SRAAPYIEQA QGIAQQFKEK VIGLLQQAQDQ
 HPCJTA PAVVPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK
 HPCJTB PAVVPDREVL YREFDEMEEC ASHLPIYEQG MQLAEQFKQK ALGLLQTATK

HPCCK3A	PALVPDKEVL	YQYDEMEEC	SQARPYIEQA	QVIAHQFKEK	VLGLLQRATQ
HPCPLYPRE	PAIIPDREVL	YREFDEMEEC	SQHLPLYIEQG	MMLAEQFKQK	ALGLLQTASR
HPCPOLP	AVVAPDKEVL	YEADEMEEC	ASRAALIEEG	QRIAEMLKSK	IQGLLQQASK
HPCPP	PAVIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
HPCUNKCD	PAIIPDREVL	YQEFDEMEEC	ASHLPYFEQG	MQLAEQFKQK	ALGLLQTATK
MKC1A	PAVIPDREVL	YQEFDEMEEC	ASHLPYIEQG	MQLAEQFKQK	ALGLLQTATK
NDM59	AVVAPDKEVL	YEADEMEEC	ASRAALIEEG	QRIAEMLKSK	IQGLLQQASK
NZLI	PALVPDKEVL	YQYDEMEEC	SQAAPYIEQA	QVIAHQFKEK	ILGLLQRATQ
SA13	PAIIPDREVL	YQYDEMEEC	SASLPYMDEA	RAIAEQFKEK	VLGLLIGTAGQ
Th580	PAVVPDREVL	YQYDEMEEC	SKHIPYLVEG	QOIAEQFKQK	VLGLLQAGTK
Type_3a_CB	PALVPDKEVL	YQYDEMEEC	SQAAPYIEQA	QAIHQFKEK	VLGLLQRATQ
TypeV_D	PALVPDKEVL	YQYDEMEEC	SQAAPYIEQA	QAIHQFKEK	VLGLLQRATQ
VN004	PVLPDREVL	YQYDEMEEC	SRHIPYLAEG	HLIAEQFKQK	VLGLIQSTSK
VN235	PVLPDREVL	YQYDEMEEC	SRHIPYLAEG	QOIAEQFKQK	ILGLLQNTAK
VN405	PVLPDREVL	YQYDEMEEC	SRHIPYLVEG	QHLAEQFKQK	VLGLIQTTR

1751

1800

BEBE1	QAQGVQPAVQ	ATWPKLEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
D89815	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
ED43type_4	QAQEATPVIQ	SNFAKLEQFW	ANDMWNFISG	IQYLAGLSTL	PGNPAIASLM
HC_C2	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	VQYLAGLSTL	PGNPAIASLM
HC_G9	QAETITPAVH	TNWQKLEFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAIASLM
HCU16326	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIRSPM
HCV_H_CMR	HAEVITPAVQ	TNWQKLEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J1	QAEVIAPTQ	TNWQKLEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J483	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_J8	QAQDIQPAIQ	SSWPKLEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
HCV_JK1	QAEAAAPVVE	SKWQALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIVSLM
HCV_JS	QAEAAAPVME	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R1	QAEAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R2	QAEAAAPVVE	SKWQALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_R3	QAEAAAPVVE	SKWRTLEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S1	QAEAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S2	QAEAAAPVVE	SKWQALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_K1_S3	QAEAAAPVVE	SKWRTLEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV_L2	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAALSTL	PGNPAIASLM
HCV_N	QAEAAAPVVG	SKWRAFETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HCV12083	QAEELKPAVH	SAWPRVEDFW	RKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HCV1480	KAETLKPAAT	SMWSKAEQFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAVATLM
HCVPOLYP	QAEAAAPVVE	SKWQALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HD_1	QAEAAAPVVE	SKWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCCGAA	HAEVITPAVQ	TNWQKLEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCFG	QAEAIRPIVQ	SQWQKAEAFW	QOHWWNFVSG	IQYLAGLSTL	PGNPAVASLM
HPCGENANTI	QAEAAAPVVE	SKWRTLEAFW	ANDMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCGENOM	QAEAAAPVVE	SKWRALETFW	EKHMWNFISG	IQYLAGLSTL	PGNPAMASLM
HPCHUMR	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJ	QAEAAAPVVE	TKWQALEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJCG	QAEAAAPVVE	SKWRALEFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJK046	QAEELKPAVH	SAWPKLEQFW	YKHMWNFISG	IQYLAGLSTL	PGNPAVAALM
HPCJK049	KAADIKPIAT	PYWQKLETFW	SKHMWNFVSG	IQYLAGLSTL	PGNPAIASLM
HPCJTA	QAEAAAPVVE	SRWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCJTB	QAEAAAPVVE	SRWRALEAFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCCK3A	QOAVIEPIV	SNWQKLEFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
HPCPLYPRE	QAEVIAPAVQ	TNWQKLETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCPOLP	QAQDIQPAVQ	ASWPKVEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
HPCPP	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
HPCUNKCD	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIRSPM
MKC1A	QAEAAAPVVE	SKWRALETFW	AKHMWNFISG	IQYLAGLSTL	PGNPAIASLM
NDM59	QAQDIQPAVQ	ASWPKVEQFW	AKHMWNFISG	IQYLAGLSTL	PGNPAVASMM
NZLI	QOAVIEPIV	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM

SA13	KAETLKPAAT	SMWNRABQFW	AKHMWNFVSG	IQYLAGLSTL	PGNPAVATLM
Th580	HABELKPAIH	STWPRVEEFW	RKHMWNFVSG	IQYLAGLSTL	PGSPAVASLM
Type_3a_CB	QOAVIEPIVA	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLSTL	PGNPAVASLM
TypeV_D	QOAVIEPIVA	TNWQKLEAFW	HKHMWNFVSG	IQYLAGLPTL	PGNPAVASLM
VN004	QABELKPAVH	AAWPKLEQFW	QKQLWNFVSG	IQYLAGLSTL	PGNPAIASLM
VN235	QAEDLKPAVQ	SAWPKLEQFW	QKHLWNFVSG	VQYLAGLSTL	PGNPAVASLM
VN405	QAEEIEPVVH	SAWPKLEQFW	QKHLWNFVSG	IQYLAGLSTL	PGNPAVASLM

	1801		1850
BEBE1	SFSAALTSPL	STSTTILLNI	MGGWLASQIA
D89815	AFTASITSPL	ATQYTLLFNI	LGGWVAAQLA
ED43type_4	SFTAAVTSPL	TTQQTLLFNI	LGGWVASQIR
HC_C2	AFTASVTSPL	TTQSTLLFNI	LGGWVAAQLA
HC_G9	SFTAAVTSPL	TTQQTLLFNI	LGGWVAAQLA
HCU16326	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HCV_H_CMR	AFTAAVTSPL	TTGQTLLFNI	LGGWVAAQLA
HCV_J1	AFTAAVTSPL	TTSQTLLFNI	LGGWVAAQLA
HCV_J483	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA
HCV_J8	AFTAALTSPL	PTSTTILLNI	MGGWLASQIA
HCV_JK1	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HCV_JS	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA
HCV_K1_R1	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA
HCV_K1_R2	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HCV_K1_R3	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HCV_K1_S1	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA
HCV_K1_S2	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HCV_K1_S3	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HCV_L2	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA
HCV_N	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA
HCV12083	SFTASLTSP	RTSQTLNLI	LGGWIAAQVA
HCV1480	SFTAAVTSPL	TTQHTLLFNI	LGGWVASQIA
HCVPOLYP	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HD_1	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA
HPCCGAA	AFTAAVTSPL	TTGQTLLFNI	LGGWVAAQLA
HPCFG	AFTASVTSPL	TTQNTMFFNI	LGGWVATHLA
HPCGENANTI	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA
HPCGENOM	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
HPCJHUMR	AFTASITSPL	TTQSTLLFNI	LGGWVAAQLA
HPCJ	AFTSSITSPL	TTQSTLLFNI	LGGWVAAQLA
HPCJCG	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA
HPCJK046	SFSASLTSP	TTAQTLNLI	LGGWVASQIA
HPCJK049	AFTASVTSPL	TTQNTLLFNI	LGGWVASNLA
HPCJTA	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA
HPCJTB	AFTASITSPL	TTQNTLLFNI	LGGWVAAQLA
HPCK3A	AFTASVTSPL	TTQNTMFFNI	LGGWVATHLA
HPCPLYPRE	AFTAAVTSPL	TTQSTLLFNI	LGGWVAAQLA
HPCPOLP	AFTAALTSPL	STSTTILLNI	LGGWLASQIA
HPCPP	AFTASITSPL	TTQYTLLFNI	LGGWVAAQLA
HPCUNKCD	AFTASITSPL	TTQHTLLFNI	LGGWVAAQLA
MKC1A	AFTASITSPL	TTQYTLLFNI	LGGWVAAQLA
NDM59	AFTAALTSPL	STSTTILLNI	LGGWLASQIA
NZLI	AFTASVTSPL	TTQNTMFFNI	LGGWVATHLA
SA13	SFTAAVTSPL	TTQQTLLFNI	LGGWVASQIA
Th580	SFTASLTSP	RTSQTLNLI	LGGWIASQVA
Type_3a_CB	AFTASVTSPL	TTQNTMFFNI	LGGWVATHLA
TypeV_D	AFTASVTSPL	TTQNTMFFNI	LGGWVATHLA
VN004	SFSASLTSP	STHQTLNLI	LGGWVASQIA
VN235	SFTAALTSPL	STSTTILLNI	LGGWVASQIA
VN405	SFSASLTSP	STSTTILLNI	LGGWVASQIA

	1851				1900
BEBE1	IGLGKILVDV	LAGYGAGISG	ALVAFKIMSG	EKPSVEDVNVN	LLPAILSPGA
D89815	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	DMPSTEDLVN	LLPAILSPGA
ED43type_4	VGLGKILVDI	LPGYGAGVRG	AVVTFKIMSG	EMPSTEDLVN	LLPAILSPGA
HC_C2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	ETPSAEDLVN	LLPAILSPGA
HC_G9	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPTAEDLVN	LLPAILSPGA
HCU16326	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSAEDMVN	LLPAILSPGA
HCV_H_CMR	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVVSTEDLVN	LLPAILSPGA
HCV_J1	VGLGRVLVDI	LAGYGAGVAG	ALVAFKIMSG	ELPSTEDLVN	LLPAILSPGA
HCV_J483	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EVPSTEDLVN	LLPAILSPGA
HCV_J8	IGLGKILVDV	LAGYGAGISG	ALVAFKIMSG	EKPTVEDVNVN	LLPAILSPGA
HCV_JK1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HCV_JS	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPATEDLVN	LLPAILSPGA
HCV_K1_R1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EMPSTEDLVN	LLPAILSPGA
HCV_K1_R2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	DMPSTEDLVN	LLPAILSPGA
HCV_K1_R3	IGLGKVLVDI	LAGYGAGVAG	ALVDFKVMMSG	EMPSAEDIVN	LLPAILSPGA
HCV_K1_S1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EMPSTEDLVN	LLPAILSPGA
HCV_K1_S2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	DMPSTEDLVN	LLPAILSPGA
HCV_K1_S3	IGLGKVLVDI	LAGYGAGVAG	ALVDFKVMMSG	EMPSAEDIVN	LLPAILSPGA
HCV_L2	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EMPSTEDLVN	LLPAILSPGA
HCV_N	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EAPSAEDLIN	LLPAILSPGA
HCV12083	IRLGRVLVDV	LAGYGAGVSG	ALVAFKIMSG	ECPSTEDMVN	LLPALLSPGV
HCV1480	IGLGRVLIDI	LAGYGTGVAG	ALVAFKIMCG	ERPTAEDLVN	LLPSILCPGA
HCVPOLYP	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HD_1	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EVVSTEDLIN	LLPAILSPGA
HPCCGAA	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVVSTEDLVN	LLPAILSPGA
HPCFG	IGIGRVLLDV	LAGYGAGVSG	ALVAFKIMGG	ELPTTEDMVN	LLPAILSPGA
HPCGENANTI	IGLGKVLVDM	VAGYGAGVAG	ALVAFKVMMSG	EMPSTEDLVN	LLPAILSPGA
HPCGENOM	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EMPSTEDLVN	LLPAILSPGA
HPCHUMR	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSTEDLVN	LLPAILSPGA
HPCJ	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EVVSTEDLVN	LLPAILSPGA
HPCJCG	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	EMPSTEDLVN	LLPAILSPGA
HPCJK046	IGLGKVLVDI	LAGYGAGVSG	ALVAFKIMSG	ETPSVEDMVN	LLPALLSPGA
HPCJK049	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMGG	EMPSTEDMVN	LLPAILSPGA
HPCJTA	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPSAEDLVN	LLPAILSPGA
HPCJTB	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EAPSAEDLVN	LLPAILSPGA
HPCK3A	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	EPPTTEDMVN	LLPAILSPGA
HPCPLYPRE	VGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EVVSTEDLVN	LLPAILSPGA
HPCPOLP	IGLGKVLVDI	LAGYGAGISG	ALVAFKIMSG	EKPSMEDVNVN	LLPGILSPGA
HPCPP	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	DMPSTEDLVN	LLPAILSPGA
HPCUNKCD	IGLGKVLVDI	LAGYGAGVAG	ALVAFKIMSG	EMPSAEDMVN	LLPAILSPGA
MKC1A	IGLGKVLVDI	LAGYGAGVAG	ALVAFKVMMSG	DMPSTEDLVN	LLPAILSPGA
NDM59	IGLGKVLVDI	LAGYGAGISG	ALVAFKIMSG	EKPSMEDVIN	LLPGILSPGA
NZLI	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	ECPTAEDMVN	LLPAILSPGA
SA13	IGLGRVLIDI	LAGYGAGVAG	ALVAFKIMCG	EKPTAEDLVN	LLPSILCPGA
Th580	IGLGRVIVDI	LAGYGAGVAG	ALVAFKIMSG	ECPSTEDMVN	LLPALLSPGA
Type_3a_CB	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	ELPTAEDMVN	LLPAILSPGA
TypeV_D	IGLGRVLLDI	LAGYGAGVSG	ALVAFKIMGG	ELPTTEDLVN	LLPAILSPGA
VN004	IGLGRVIVDV	LAGYGAGVSG	ALVAFKIMCG	ETPSAEDMVN	LLPALLSPGA
VN235	IGLGKVLIDI	LAGYGAGVSG	ALVAFKIMSG	EAPAVEDMVN	LLPALLSPGA
VN405	IGLGRVLVDI	IAGYGAGVSG	ALVAFKIMSG	ETPSAEDMVN	LLPALLSPGA

	1901				1950	
	BEBE1	LVVGVICAAI	LRRHVQGEG	AVQWMNRLIA	FASRGNHVAP	THYVAESDAS
	D89815	LVVGVVCAAI	LRRHVGPGE	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
ED43type_4		LVVEVVCPAI	LRRHVGPGE	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
	HC_C2	LVVGVVCAAI	QRRHVGPGE	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
	HC_G9	LVVGVVCAAI	LRRHVGPGE	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
	HCU16326	LVVGIVCAAI	LRRHVGPGE	AVQWMNRLIA	FASRGNHVSP	RHYVPESEPA
	HCV_H_CMR	LVVGVVCAAI	LRRHVGPGE	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA

HCV_J1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J483	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_J8	LVVGVICAAI	LRRHVGQGEG	AVQWMNRLIA	FASRGNHVAP	THYVVEDSAS
HCV_JK1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_JS	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_R3	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S1	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_K1_S3	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV_L2	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHDS	THYVPESDAA
HCV_N	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HCV12083	ALVGVVCAAI	LRRHVGPAEG	ANQWMNRLIA	FASRGNHVSP	THYVPETDAS
HCV1480	LVVGVICAAV	LRRHIGPGEG	AVQWMNRLIA	FASRGNHGSP	THYVPETDAS
HCVPOLYP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HD_1	LVVGVVCAAI	LRGHVGPGEG	AVQWMNRLIA	FAFAGNHVSP	THYVPESDAA
HPCCGAA	LAVGVVFASI	LRRRVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCFG	LVVGVICAAV	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCGENANTI	LVVGVVCAAI	LRRHVDPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCGENOM	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCHUMR	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJ	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJCG	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJK046	LVVGVVRAAI	LRRHVGPGEG	AAQWMNRLIA	FASRGNHVSP	THYVPETDAS
HPCJK049	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVPESDAA
HPCJTA	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCJTB	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCK3A	LVVGVICAAI	LRRHVGPGEG	PVQWMNRLIA	FASRGNHVSP	AHYVPESDAA
HPCLYPRE	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCPOLP	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVTESDAS
HPCPP	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
HPCUNKCD	LVVGIVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	RHYVPESEPA
MKC1A	LVVGVVCAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
NDM59	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVAP	THYVTESDAS
NZLI	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
SA13	LVVGVICAAV	LRRHIGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPETDAS
Th580	LVVGVVCAAI	LRRHVGPGEG	ANQWMNRLIA	FASRGNHVSP	THYVPETDAS
Type_3a_CB	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
TypeV_D	LVVGVICAAI	LRRHVGPGEG	AVQWMNRLIA	FASRGNHVSP	THYVPESDAA
VN004	LVVGVVCAAI	LRRHAGPSEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDTS
VN235	LVVGVVCAAV	LRRHVGPGEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDAS
VN405	LVVGVVCAAI	LRRHAGPAEG	ATQWMNRLIA	FASRGNHVSP	THYVPETDTS

1951

2000

BEBE1	QRVTQLLGS	TITSLRLRLH	QWITEDCPVP	CSGSWLRDVW	DWVCSILIDF
D89815	ARVTQILSNL	TITQLLKRHL	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
ED43type_4	RRVTTLSS	TVTSLRLRLH	KWINEDCSTP	CAESWLWEVW	DWVLHVLSD
HC_C2	ARVTQILSSL	TITQLLKRHL	QWINEDCSTP	CSGSWLRDIW	DWICSVLTDF
HC_G9	VRVTHTLTS	TVTQLLKRHL	VWISSDCTAP	CAGSWLKDVW	DWICEVLSDF
HCU16326	ARVTQILSSL	TITQLLKRHL	QWINEDCSTP	CSSSWLRDIW	DWICTVLADF
HCV_H_CMR	ARVTAILSSL	TVTQLLRLRLH	QWISSECTTP	CSGSWLRDIW	DWICEVLSDF
HCV_J1	ARVTAILSSL	TVTQLLRLRLH	QWISSECTTP	CSGSWLRDIW	DWICEVLSDF
HCV_J483	ARVTQILSSL	TITQLLKRHL	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HCV_J8	QRVTQVLSSL	TITSLRLRLH	AWITEDCPVP	CSGSWLRDIW	DWVCSILTDF
HCV_JK1	ARVTQILSSL	TITQLLKRHL	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HCV_JS	ARVTQILSSL	TITQLLKRHL	QWINEDCSTP	CSGSWLRDIW	DWICTVLADF
HCV_K1_R1	ARVTQILSSL	TITQLLRLRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HCV_K1_R2	ARVTQILSSL	TITQLLKRHL	QWINEDCSTP	CSGSWLRDVW	DWICTVLADF
HCV_K1_R3	VRVTQILSNL	TITQLLKRHL	QWISSECTTP	CSGSWLRDVW	DWICTVLADF

HCV_K1_S1	ARVTQILSSL	TITQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_K1_S2	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_K1_S3	VRVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_L2	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV_N	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV12083	KNVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCV1480	AKVTQILSSL	TVTSLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HCVPOLYP	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HD_1	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCCGAA	ARVTAILSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCFG	AKVTALLSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCGENANTI	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCGENOM	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCJ	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCJCG	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCJK046	RAVTNILLSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCJK049	AKVTALLSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCJTA	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCJTB	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCK3A	ARVTALLSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCPLYPRE	ARVTAILSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCPOLP	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCPP	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
HPCUNCDC	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
MKC1A	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
NDM59	ARVTQILSSL	TITQLLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
NZLI	ARVTALLSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
SA13	AKVTQILSSL	TVTSLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
Th580	AKVTQILSSL	TVTSLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
Type_3a_CB	ARVTALLSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
TypeV_D	AKVTALLSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
VN004	RQIMTILSSL	TVTSLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
VN235	RAVTAILSSL	TVTQLLRRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF
VN405	RQVMAILSSL	TVTSLKRLH	QWINEDCSTP	CSGSWLRDVW	DWICTVLTF

2001

BEBE1	KNWLSAKLFP	RLPGIPFISC	QKGYRGVWAG	TGIMTTRCPC	GANITGNVRL
D89815	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMYTTCPC	GAQITGHVKN
ED43type_4	KTCLKAKFVP	LMPGIPPLSW	PRGYKGEWRG	DGVMHTTCPC	GADLAGHKN
HC_C2	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMYTTCPC	GAQITGHVKN
HC_G9	KSWLKAKLMP	QLPGIPFVSC	QKGYRGVWAG	EGIMHARCPC	GADITGHVKN
HCU16326	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_H_CMR	KTWLKAKLMP	QLPGIPFVSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_J1	KTWLKTKLMP	HLPGIPFVSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_J483	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_J8	KNWLSKLLP	KMPGIPFISC	QKGYRGVWAG	TGVMTTRCPC	GANISGHVRL
HCV_JK1	KTWLQSKLLP	RLPGDPFFSC	QKGYRGVWAG	DGVMHTTCPC	GAQITGHVKN
HCV_JS	KTWLKSKLMP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_R1	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_R2	KTWLQSRVLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_R3	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_S1	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_S2	KTWLQSRVLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_K1_S3	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_L2	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV_N	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV12083	KVWLQAKLFP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCV1480	KAWLQAKLFP	QLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN
HCVPOLYP	KTWLQSKLLP	RLPGVPFFSC	QKGYRGVWAG	DGIMHTTCPC	GAQITGHVKN

2050

HD_1	KTWLQSKLLP	RLPGVPFLSC	QRGYRGVWRG	DGIMHTTCPC	GAQMAGHVKN
HPCCGAA	KTWLKAKLMP	QLPGIPFVSC	QRGYRGVWRG	DGIMHTRCHC	GABITGHVKN
HPCFG	KTWLSAKIMP	KVPGIPFLSC	QKGYKGVWRG	DGVMTTRCPC	GEDFTGHVRN
HPCGENANTI	KTWLQSKLLP	RLPGVPFFSC	QRGYKGVWRG	DGIMQTTCP	GAQLTGHVKN
HPCGENOM	KTWLQSKLLP	RLPGVPFLSC	QRGYKGVWRG	DGIMQTTCP	GAQITGHVKN
HPCHUMR	KTWLQSKLLP	QLPGVPFFSC	QRGYKGVWRG	DGIMQTTCP	GAQITGHVKN
HPCJ	KTWLQSKLLP	RLPGVPFFSC	QRGYKGVWRG	EGIMQTTCP	GAQIAGHVKN
HPCJCG	KTWLQSKLLP	RLPGLPFLSC	QRGYKGVWRG	DGIMQTTCP	GAQITGHVKN
HPCJK046	RVWLKSKLMP	SLPGVPFFSC	QRGYRGVWRG	DGICNTTCPC	GASIAGHVKN
HPCJK049	KLWLGAKILP	KMPGIPFLSC	QKGYRGVWRG	DGVVSTRCPC	GALLSGHVKN
HPCJTA	KTWLQSKLLP	KLPGVFFSC	QRGYKGVWRG	DGIMQTTCP	GAQITGHVKN
HPCJTB	KTWLQSKLLP	QLPGVPFFSC	QRGYKGVWRG	DGIMQTTCP	GAQITGHVKN
HPCCK3A	KTWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GASIAGHVKN
HPCPLYPRE	KTWLKAKLMP	QLPGIPFVSC	QRGYKGVWRV	DGIMHTRCHC	GABITGHVKN
HPCPOLP	KNWLTSKLFP	KMPGLPFISC	QKGYKGVWAG	TGIMTTRCPC	GANISGNVRL
HPCPP	KTWLQSKLLP	RLPGVPFFSC	QRGYKGVWRG	DGIMYTTCP	GAQITGHVKN
HPCUNKCD	KTWLQSKLLP	RLPGVPFFSC	QRGYKGVWRG	DGIMHTTCPC	GAQITGHVKN
MKC1A	KTWLQSKLLP	RLPGVPFFSC	QRGYKGVWRG	DGIMYTTCP	GAQITGHVKN
NDM59	KNWLTSKLFP	KMPGLPFISC	QKGYRGVWAG	TGIMTTRCPC	GANISGNVRL
NZLI	KAWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GAAITGHVKN
SA13	KAWLOAKLLP	QLPGVPFLSC	QRGYRGVWRG	DGVNSTKCPC	GATISGHVKN
Th580	KTWLKAKITP	RIPGIPFISC	QAGYRGVWAG	DGVCHTTCS	GAQIAGHVKN
Type_3a_CB	KSWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVMSTRCPC	GATITGHVKN
TypeV_D	KTWLSAKIMP	ALPGLPFISC	QKGYKGVWRG	DGVTTTRCPC	GATITGHVKN
VN004	KTWLKAKLVP	ALPGVPFLSC	QRGFRGTWRG	DGICHTTCPC	GSEITGHVKN
VN235	KTWLRACLVP	TLPGIPFISC	QRGFRGVWRG	DGVNYTTCS	GANITGHVKN
VN405	KVWLKSKLVP	ALPGVPFLSC	QRGFRGVWRG	DGICRTTCPC	GADIVGHVKN

2051

2100

BEBE1	GTMRISGPKT	CLNTWQGTFF	INCYTEGSCV	PKPAPNFKTA	IWRVAASEYA
D89815	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
ED43type_4	GSMRITGPKT	CSNTWHGTFF	INAYTTGPGV	PIPAPNYKFA	LWRVSAEDYV
HC_C2	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HC_G9	GSMRIVGPRT	CSNTWRGSFF	INAHTTGPCT	PSPAPNYTFA	LWRVSAEEYV
HCU16326	GSMRIVGPRT	CSNTWYGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
HCV_H_CMR	GTMRIVGPRT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYKFA	LWRVSAEEYV
HCV_J1	GTMRIVGPRT	CRNMWSGTFF	INAYTTGPCT	PLPAPNYTFA	LWRVSAEEYV
HCV_J483	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_J8	GTMKITGPKT	CLNLWQGTFF	INCYTEGPCV	PKPPPNYKTA	IWRVAASEYV
HCV_JK1	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_JS	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R1	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R2	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_R3	GSMKIVGPKT	CSNTWDGTFF	INGYTTGSST	PTPASNYSKA	LWRVVFEEYV
HCV_K1_S1	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_S2	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HCV_K1_S3	GSMKIVGPKT	CSNTWDGTFF	INGYTTGSST	PTPASNYSKA	LWRVVFEEYV
HCV_L2	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PAPTPNYSRA	LWRVAAEEYV
HCV_N	GSMRIIGPKT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
HCV12083	GTMKITGPKT	CSNTWHGTFF	INATTTGPST	PRPAPNYQRA	LWRVSAEDYV
HCV1480	GSMRIVGPKL	CSNTWQGTFF	INATTTGPSV	PAPAPNYKFA	LWRVGAADYA
HCVPOLYP	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HD_1	GSMRIVGPRT	CSNTWYGSFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCCGAA	GTMRIVGPRT	CKNMWSGTFF	INAYTTGPCT	PLPAPNYKFA	LWRVSAEEYV
HPCFG	GSMRIAGSGL	CANMWHGTFF	INEYTTGPST	PVPAHNYKFA	LWRVTSDSYV
HPCGENANTI	GSMRIWGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCGENOM	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCCHUMR	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJ	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJCG	GSMRIVGPRT	CSNTWHGTFF	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV

HPCJK046	GTMRIVGPRT	CSNVWNGTFP	INATTTGPSI	PIAPAPNYKKA	LWRVSATEYV
HPCJK049	GTMRLVGPRT	CANTWHGTFP	INGYTTGPST	PAPSYAYSRA	LWRVASDSYV
HPCJTA	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCJTB	GSMRIVGPRT	CSNMWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCK3A	GSMRLAGPRT	CANMCHGTFP	INEYTTGPST	PCPPPNYTRA	LWRVAANSYV
HPCPLYPRE	GTMRIVGPRT	CRNMWSGTFP	INAYTTGPCT	PLPAPNYTFA	LWRVSAEEYV
HPCPOLP	GSMRITGPRT	CMNIWQGTFP	INCYTEGQCV	PKPAPNFKIA	IWRVAASEYA
HPCPP	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
HPCUNKCD	GSMRIVGPRT	CSNTWYGTFP	INAYTTGPCT	PSPAPNYSKA	LWRVAAEEYV
MKC1A	GSMRIVGPRT	CSNTWHGTFP	INAYTTGPCT	PSPAPNYSRA	LWRVAAEEYV
NDM59	GSMRITGPRT	CMNTWQGTFP	INCYTEGQCV	PKPAPNFKTA	IWRVAASEYA
NZLI	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
SA13	GTMRIVGPRT	CSNTWHGTFP	INATTTGPSV	PAPAPNYKFA	LWRVGAADYA
Th580	GSMKITGPRM	CSNTWHGTFP	INATTTSPSV	PVPAPNYKRA	LWRVSAEEYV
Type_3a_CB	GSMRLAGPRT	CANMWHGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
TypeV_D	GSMRLAGPRT	CANMWYGTFP	INEYTTGPST	PCPSPNYTRA	LWRVAANSYV
VN004	GTMKISGPRW	CSNVSHRTFP	INATTTGPSV	PIPEPNYTRA	LWRVSAEEYV
VN235	GSMKIVGPKM	CSNVWNNRFP	INATTTGPSV	PVPEPNYHKA	LWRVSAEDYV
VN405	GSMRISGSRW	CSNIWHGTFP	INATTTGPSV	PIPEPNYKRA	LWRVSAEEYV

	2101				2150
BEBE1	EVTQHDSHAY	VTGLTADNLK	VPCQLPCPEF	FSWVDGVQIH	RFAPTPKAFM
D89815	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL
ED43type_4	EVRRVGDFFHY	VTGVTQDNK	FPCQVPAPPEL	FTEVDGIRIH	RHAPCKKPLL
HC_C2	EVTRVGDFFHY	ITGMTTDNIK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPVL
HC_G9	EVRRRLGDFHY	ITGVTTDKIK	CPCQVPSPPEF	FTEVDGVRLH	RYAPPCKPLL
HCU16326	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HCV_H_CMR	EIRRVGDFFHY	VSGMTTDNLK	CPCQIPSPPEF	FTELDGVRLH	RFAPPCKPLL
HCV_J1	EIRRVGDFFHY	VTGMTTDNLK	CPCQVPSPPEF	FTELDGVRLH	RFAPPCKPLL
HCV_J483	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HCV_J8	EVTQHGSFSY	VTGLTSDNLK	VPCQVPAPPEF	FSWVDGVQIH	RFAPVPGPFF
HCV_JK1	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HCV_JS	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVQLH	RYAPACKPLL
HCV_K1_R1	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPSPPEF	FTEVDGVRLH	RYAPACKPLL
HCV_K1_R2	EVTRVGDFFHY	VTGMTTDNLK	CPCQVPAPPEF	FKELDGVRLLH	RYAPACKPLL
HCV_K1_R3	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPSPPEF	FTELDGVRLH	RYAPVSKPLL
HCV_K1_S1	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPSPPEF	FTEVDGVRLH	RYAPACKPLL
HCV_K1_S2	EVTRVGDFFHY	VTGMTTDNLK	CPCQVPAPPEF	FKELDGVRLLH	RYAPACKPLL
HCV_K1_S3	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPSPPEF	FTELDGVRLH	RYAPVSKPLL
HCV_L2	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HCV_N	EVTRVGDFFHY	VTGITTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HCV12083	EVRRRLGDCY	VVGVTAEGLK	CPCQVPAPPEF	FTEVDGVRIH	RYAPPCKPLL
HCV1480	EVRRVGDYHY	ITGVTQDNK	CPCQVPSPPEF	FTELDGVRIH	RFAPPCKPLL
HCVPOLYP	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HD_1	EVTRVGDFFHY	VTGMTTDNIK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HPCCGAA	EIRRVGDFFHY	VSGMTTDNLK	CPCQIPSPPEF	FTELDGVRLH	RFAPPCKPLL
HPCFG	EVRRVGDTHY	VVGATNDGLK	IPCQVPAPPEF	FTELDGVRLH	RYAPPCKPLL
HPCGENANTI	EVRRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HPCGENOM	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HPCHUMR	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FSEVDGVRLH	RYAPACKPLL
HPCJ	EVTRVGDFFHY	VTGVTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL
HPCJCG	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTEVDGVRLH	RYAPACKPLL
HPCJK046	EVRRVGDSSH	ITGVTAENTK	CPCQVPAPPEF	FTEVDGVRLH	RYAPVCKPLL
HPCJK049	EVRRVGDFFHY	VTGTTDDGLK	CPCQVPAPPEF	FTEVDGVRLH	RYAPVCKPLL
HPCJTA	EITRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL
HPCJTB	EITRVGDFFHY	VTGXTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL
HPCK3A	EVRRVGDFFHY	ITGATEDGLK	CPCQVPATEF	FTEVDGVRIH	RYAPPCKPLL
HPCPLYPRE	EIRRVGDFFHY	VTGMTTDNLK	CPCQVPSPPEF	FTELDGVRLH	RFAPPCKPLL
HPCPOLP	EVTQHGSYHY	ITGLTTDNK	VPCQLPSPEF	FSWVDGVQIH	RFAPVCKPFF
HPCPP	EVTRVGDFFHY	VTGMTTDNVK	CPCQVPAPPEF	FTELDGVRLH	RYAPACKPLL

HPCUNKCD	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPEF	FTEVDGVR LH	RYAPACRPLL
MKC1A	EVTRVGDFHY	VTGMTTDNVK	CPCQVPAPEF	FTELDGVR LH	RYAPACKPLL
NDM59	EVTQHGSYSY	ITGLTTDSLK	VPCQLPSPEF	FSWVDGVQIH	RFAPTPKPPF
NZLI	EVRRVGDFHY	ITGATEDELK	CPCQVPAAEF	FTEVDGVR LH	RYAPPCKPLL
SA13	EVRRVGDFHY	ITGVTQDNLK	CPCQVPSPEF	FTELDGVR LH	RYAPPCNPLL
Th580	EVERHGDHRY	VVGVTADGLK	CPCQVPGPEF	FTEVDGVR LH	RYAPPCKPLL
Type_3a_CB	EVRRVGDFHY	ITGATEDELK	CPCQVPAAEF	FTEVDGVR LH	RYAPPCKPLL
TypeV_D	EVRRVGDFHY	ITGATEDELK	CPCQVPAAEF	FTEVDGVR LH	RYAPPCKPLL
VN004	EVKRVGDSHF	VVGATTNCLK	CPCQVPAPEF	FTEVDGVR LH	RYAPRCKPLL
VN235	EVVRVNDHHY	IVGATADNLK	CPCQVPAPEF	FTEVDGVR LH	RFAPPCRPLM
VN405	EVARVGDSHF	VVGATNQDLK	CPCQVPAPEF	FTEVDGVR LH	RFAPACKPLL
2151					
BEBE1	RDEVSFVGL	NSYVGSQPL	CEPEPDTEVL	ASMLTDPSHI	2200 TAEAAARRLA
D89815	RDEVTFQVGL	NQYTVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAEAAARRLA
ED43type_4	RDEVSFVGL	NSFVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAESARRRLA
HC_C2	REEVDFQVGL	NQYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HC_G9	RDEVTFQVGL	NEYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAARRLN
HCU16326	REEVVFQVGL	HQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_H_CMR	REEVSFRVGL	HEYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV_J1	REEVSFRVGL	HDYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV_J483	REDVAFQVGL	NQYLVSQPL	CEPEPDVTVL	TSMLTDPSHI	TAETAKRRLA
HCV_J8	RDEVTFQVGL	NSFVGSQPL	CDPEPDTEVL	ASMLTDPSHI	TAEAAARRLA
HCV_JK1	RDEVTFQVGL	NQFPVGSQPL	CEPEPDVTVL	TSMLTDPSHI	TAETAKRRLA
HCV_JS	RDEVTFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV_K1_R1	REEVTFQVGL	NQYLVSQPL	CEPEPDVTVL	TSMLTDPSHI	TGEAAKRRLA
HCV_K1_R2	RDEVTFQVGL	NQYVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_K1_R3	RDEVTFQVGL	NRYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HCV_K1_S1	REEVTFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TGETAKRRLA
HCV_K1_S2	RDEVTFQVGL	NQYVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HCV_K1_S3	RDEVTFQVGL	NRYPVGSQPL	CEPEPDVTVI	TSMLTDPSHI	TAETAKRRLA
HCV_L2	REEVTFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
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HCV12083	RDEVTFQVGL	SNYPVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAETAARRLK
HCV1480	REEVTFQVGL	HSYVGSQPL	CEPEPDVTVL	TSMLSDPAHI	TAETAKRRLN
HCVPOLYP	RDEVTFQVGL	NQYVGSQPL	CEPEPDVVV	TSMLTDPSHI	TAETAKRRLD
HD_1	RDEVVFQVGL	NHYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCCGAA	REEVSFRVGL	HEYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HPCFG	RDEITFSVGL	HSYANGSGLS	CEPEPDVAVL	TSMLRDPahi	TAETAARRLA
HPCGENANTI	REEVSFRVGL	NQYVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCGENOM	REEVVFQVGL	NQYLVSQPL	CEPEPDVTVL	TSMLTDPSHI	TAETAKRRLA
HPCHUMR	REEVTFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJ	RDEVVFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJCG	REEVVFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJK046	RDEVTFQVGL	STYVGSQPL	CEPEPDVLV	TSMLRDPDHI	TAEASRRLK
HPCJK049	RDDVTFTVGL	NSYVIGSGLS	CEPEPDVAVV	TSMLQDPshi	TVETAKRRLD
HPCJTA	REDVTFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPCJTB	REDVTFQVGL	NQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
HPC3A	RDEITFMVGL	NSYAIGSGLS	CEPEPDVSVL	TSMLRDPshi	TAETAARRLA
HPCPLYPRE	REEVSFRVGL	HEYPVGSQPL	CEPEPDVAVL	TSMLTDPSHI	TAEAAKRRLA
HPCPOLP	RDEVSFQVGL	NSFVGSQPL	CDPEPDVTVL	TSMLTDPSHI	TAETAARRLA
HPCPP	RDEVTFQVGL	NQYTVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAEAAARRLA
HPCUNKCD	REEVVFQVGL	HQYLVSQPL	CEPEPDVAVL	TSMLTDPSHI	TAETAKRRLA
MKC1A	RDEVTFQVGL	NQYTVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAEAAARRLA
NDM59	RDEVSFQVGL	NSFVGSQPL	CDPEPDADV	TSMLTDPSHI	TAEAAARRLA
NZLI	RDDITFMVGL	HSYIGSGLS	CEPEPDVSVL	TSMLRDPshi	TAETAARRLA
SA13	REEVCFVGL	HSFVGSQPL	CEPEPDVTVL	TSMLSDPAHI	TAETAKRRLD
Th580	RDEVSFVGL	LEFVGSQPL	CEPEPDVTVV	TSMLTDPSHI	TAETASRRLK
Type_3a_CB	REEITFSVGL	NSYIGSGLS	CEPEPDVSVL	TSMLRDPshi	TAETAARRLA
TypeV_D	RDDITFMVGL	NSYAIGSGLS	CEPEPDVSVL	TSMLRDPshi	TAETAARRLA

VN004 RDEVFSVGL SSVAVGSQLP CEPEPDVTVV TSMLIDPSHV TAAAAARRLA
 VN235 RDDITFSVGL STYVVGSQLP CEPEPDVVIL TSMLTDPDHI TAETAARRLA
 VN405 RDEISFLVGL NSYAIGSQLP CEPEPDVTVV TSMLVDPSHL TAAAAARRLA

2201

2250

BEBE1 RGSPPSAASS SASQLSAPSL RATCTTHAK. ...CPDIDMV DANLFCWCTM
 D89815 RGSPPSLAGS SASQLSALS L KATCTTHHG. ...APDTDLI EANLLWRQEM
 ED43type_4 RGSRRPSLASS SASQLSPRL QATCTAPHD. ...SPGTDLL EANLLW....
 HC_C2 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HC_G9 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI TANLLWRQEM
 HCU16326 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_H CMR RGSPPSMASS SASQLSAPSL KATCTANHD. ...SPDAELI EANLLWRQEM
 HCV_J1 RGSPPSSEASS SASQLSAPSL KATCTINHD. ...SPDAELI EANLLWRQEM
 HCV_J483 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_J8 RGSPPSQASS SASQLSAPSL KATCTTHKT. ...AYDCDMV DANLF...M
 HCV_JK1 RGSPPSLASS SASQLSAPSL KATCTTRHD. ...SPDADLI EANLLWRQEM
 HCV_JS RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_K1_R1 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_K1_R2 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_K1_R3 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_K1_S1 RGSPPSLASS SASQLSAPSS KATYITQYD. ...SPDFDLI EANLLWRQEM
 HCV_K1_S2 RGSPPSLASS SASQLSAPSL KATCTTRHD. ...SPDADLI EANLLWRQEM
 HCV_K1_S3 RGSPPSLASS SASQLSAPSL KATCTTCHD. ...SPDADLI EANLLWRQEM
 HCV_L2 RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HCV_N RGSPPSLASS SASQLSAPSL RATCTTHSSY NLDSPDVLDI EANLLWRQEM
 HCV12083 KGSPPSLASS SANQLSAPSL RATCTTSQK. ...HPMEMELL QANLLWKHEM
 HCV1480 RGSPPSLANS SASQLSAPSL KATCTIQGH. ...HPDADLI KANLLWRQCM
 HCVPOLYP RGSPPSLASS SASQLSAPSL KATCTTRHD. ...SPDADLI EANLLWRQEM
 HD_1 RGSPPSLASS SASQLSAPSL KATCTTRHD. ...SPDADLI EAHLLWRQEM
 HPCCGAA RGSPPSMASS SASQLSAPSL KATCTANHD. ...SPDAELI EANLLWRQEM
 HPCFG RGSPPSSEASS SASQLSAPSL KATCQTHRP. ...HPDAELI DANLLWRQEM
 HPCGENANTI RGSPPSLASS SASQLSALS L KAACTTRHT. ...PPDADLI EANLLWRQEM
 HPCGENOM RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HPCHUMR RGSPPSLASS SASQLSAPSL KATCTTHHV. ...SPDADLI EANLLWRQEM
 HPCJ RGSPPSLASS SASQLSAPSL KATCTIHD. ...SPDADLI EANLLWRQEM
 HPCJCG RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HPCJK046 RGSPPSLASS SASQLSAPSL KATCTTHAD. ...HPDAELV EANLLWRQEM
 HPCJK049 RGSPPSLASS SASQLSAPSR KATCTTHGR. ...HPDAELI TANLLWRQEM
 HPCJTA RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HPCJTB RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 HPCK3A RGSPPSSEASS SASQLSAPSL KATCQTHRP. ...HPDAELV DANLLWRQEM
 HPCPLYPRE RGSPPSVASS SASQLSAPSL KATCTANHD. ...SPDAELI EANLLWRQEM
 HPCPOLP RGSPPSSEASS SASQLSAPSL RATCTTHGK. ...AYDVDMV DANLF...M
 HPCPP RGSPPSLASS SASQLSALS L KATCTTHHG. ...APDTDLI EANLLWRQEM
 HPCUNKCD RGSPPSLASS SASQLSAPSL KATCTTHHD. ...SPDADLI EANLLWRQEM
 MKC1A RGSPPSLASS SASQLSALS L KATCTTHHG. ...APDTDLI EANLLWRQEM
 NDM59 RGSPPSSEASS SASQLSAPSL RATCTTHGK. ...AYDVDMV DANLF...M
 NZLI RGSPPSSEASS SASQLSAPSL KATCQTHRP. ...HPDAELV DANLLWRQEM
 SA13 RGSPPSLASS SASQLSAPSL KATCTTQGH. ...HPDADLI EANLLWRQCM
 Th580 RGSPPSLASS SASQLSAPSL KATCTANGD. ...HPDAELI EANLLWRQEM
 Type_3a_CB RGSPPSSEASS SASQLSAPSL KATCQTHRP. ...HPDAELV NANLLWRQEM
 TypeV_D RGSPPSSEASS SASQLSAPSL KATCQTHRP. ...HPDAELV DANLLWRQEM
 VN004 RGSPPSLASS SASQLSAPSL KATCTMHGA. ...HPDAELI EANLLWRQEM
 VN235 RGSPPSLASS SASQLSAPSL KATCTTAGK. ...HPDAELI EANLLWRQEV
 VN405 RGSPPSSEASS SASQLSAPSL KATCTTHCA. ...HPDADLI EANLLWRQEV

2251

2300

BEBE1 GGNMTRIESE SKVLMVDSFD PVVDKE.DER EPSIPSEYLL PKS.RFPAL
 D89815 GGNITRVESE NKVILDSFE PLRABE.DER EVSAAAEILR KTR.KFPAAM
 ED43type_4 GSTATRVETD EKVIILDSFE SCVAEQNDDR EVSVAAEILR PTK.KFPAAM

HC_C2	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSVA AEILR	KTR.RFPPAM
HC_G9	GGNITRVESE	NKIVILDSFD	PLVAEE.DDR	EISVPAEILL	KSK.KFPPAM
HCU16326	GGNITRVESE	NKVVILDSFD	PLRAED.DEG	EISVPAEILR	KSR.KFPPAL
HCV_H_CMR	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EVSVP AEILR	KSR.RFARAL
HCV_J1	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EISVPAEILR	KSR.RFTQAL
HCV_J483	GGNITRVESE	NKVVILDSFE	PLHAEG.DER	EISVAAEILR	KSR.KFPSAL
HCV_J8	GGDVTRIESD	SKVVILDSLD	SMTEVE.DDR	EPSVPSEYLI	KRR.KFPPAL
HCV_JK1	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSVA AEILR	KSR.KFPPAL
HCV_JS	GGNITRVESE	NKVVILDSFD	PLHAEE.DER	EVSVA AEILR	KSR.KFPPAL
HCV_K1_R1	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSIPAEILR	KSK.KFPPAL
HCV_K1_R2	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSLPAEILR	KSR.KFPPAM
HCV_K1_R3	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KTR.KFPPAL
HCV_K1_S1	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSIPAEILR	KSK.KFPSAL
HCV_K1_S2	GGNITRVESE	NKVVILDSFE	PLRAEE.DER	EVSLPAEILR	KSR.KFPPAM
HCV_K1_S3	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KTK.KFPPAL
HCV_L2	GGNITRVESE	SKVVILDSFD	PLRAEE.GEG	EVSVA AEILR	KSK.KFPPAL
HCV_N	GGNITRVESE	NKVVILDSFE	PLRAEG.DEN	EISIA AEILR	KSK.KFPAAI
HCV12083	GSHIPRVQSE	NKVVILDSFE	LYPLEY.EER	EISVSVECHR	QPRCKFPVPF
HCV1480	GGNITRVEAE	NKVEILDCFK	PLKEEE.DDR	EISVSADCFK	KGP.AFPPAL
HCVPOLYP	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSR.RFPPAM
HD_1	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVP AEILR	KSR.KFPPAM
HPCCGAA	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EVSVP AEILR	KSR.RFAPAL
HPCFG	GSNITRVESE	TKVVILDSFE	PLRAEE.DDT	ELSIPAECK	KPP.KYPPAL
HPCGENANTI	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVP AEILR	KSR.KFPPAL
HPCGENOM	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSR.KFPSAL
HPCHUMR	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVP AEILR	KSK.KFPAAM
HPCJ	GGNITRVESE	NKVVILDSFE	PIRAEE.DER	EVSVP AEILR	RSR.KFPAAM
HPCJCG	GGNITRVESE	NKVVILDSFD	PIRAVE.DER	EISVPAEILR	KPR.KFPPAL
HPCJK046	GGNITRVESE	NKIVILDSFE	PLKAEF.DDR	EISVAAECHR	PPRFKYPPAL
HPCJK049	GSNITRVESE	SKVVILDSFE	PLRACD.DED	ELSVA AECK	KPP.KYPPAL
HPCJTA	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSK.KFPPAL
HPCJTB	GGNITRVESE	NKVVILDSFD	PLRAEE.DER	EVSVA AEILR	KSK.KFPPAL
HPCK3A	GSNITRVESE	TKVVILDSFE	PLRAET.DDA	ELSAAECK	KPP.KYPPAL
HPCPLYPRE	GGNITRVESE	NKVVILDSFD	PLVAEE.DER	EISVPAEILR	KSR.RFAQAL
HPCPOLP	GGDVTRIESE	SKVVILDSLD	PMVEER.SDL	EPSIPSEYML	PKK.RFPPAL
HPCPP	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSVA AEILR	KTR.KFPAAM
HPCUNKCD	GGNITRVESE	NKVVILDSFD	PLRAED.DEG	EISVPAEILR	KSR.KFPPAL
MKC1A	GGNITRVESE	NKIVILDSFE	PLRAEE.DER	EVSVA AEILR	KTR.KFPAAM
NDM59	GGDVTRIESE	SKVVILDSLD	PMABER.SDL	EPSIPSEYML	PRN.RFPPAL
NZLI	GSNITRVESE	TKVVILDSFE	PLRAET.DDV	EPSVAAECK	KPP.KYPPAL
SA13	GGNITRVEAE	NKVVILDSFE	PLKADD.DDR	EISVSADCFR	RGP.AFPPAL
Th580	GSNITRVESE	TKVVILDSFD	PLVAEY.DDR	EISVSAECHR	PPRPKFPPAL
Type_3a_CB	GSNITRVESE	TKVVILDSFE	PLRAET.DDA	ELSVA AECK	KPP.KYPPAL
TypeV_D	GSNITRVESE	TKVVILDSFE	PLRAQT.DDA	ELSVA AECK	KPP.KYPPAL
VN004	GGNITRVESE	NKVVILDSFD	PLVPEF.EER	EMSVPAECHR	PPRPKFPPAL
VN235	GGNITRVESE	NKIVILDSFD	PLIAET.DDR	EISVGAECK	PPRPKFPPAL
VN405	GGNITRVESE	NKIVILDSFD	PLVPEY.DDR	EPSVPAECHR	PNRPKFPPAL

2301

2350

BEBE1	PPWARPDYNP	PLLETWKRPD	YQPPVVAGCA	LPPPGTTPVP	PPRRRR.AVV
D89815	PVWARPDYNP	PLLESWKNDP	YVPPVVHGCP	LPPTKAPPVP	PPRRKR.TVV
ED43type_4	PIWARPDYNP	PLTETWKQD	YQAPT VHGCA	LPPAKQPPVP	SPRRKR.TVQ
HC_C2	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPVP	PPRRKR.TVV
HC_G9	PIWARPDYNP	PLVEPWKRPD	YEPPLVHGCP	LPPPKPTPVP	PPRRKR.TVV
HCU16326	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPVP	PPRRKR.TVV
HCV_H_CMR	PVWARPDYNP	PLVETWKKPD	YEPVVHGCP	LPPPSPPVP	PPRRKR.TVV
HCV_J1	PIWARPDYNP	PLIETWKKNP	YEPVVHGCP	LPPQSPPVP	PPRRKR.TVV
HCV_J483	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPVP	PPRRKR.TVV
HCV_J8	PPWARPDYNP	VLIETWKRPD	YEPPTVLGCA	LPPTPQTVP	PPRRRR.AKV
HCV_JK1	PIWARPSYNP	PLLESWKDPD	YVPPVVHGCP	LPPTMAPPVP	PPRRKR.TVV

HCV_JS	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
HCV_K1_R1	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPAKAPPPI	PPRRKR.TVV
HCV_K1_R2	PIWARPDYNP	PLIESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
HCV_K1_R3	PIWARPDYNP	PLLEPWKDPD	YAPPVVHGCP	LPPAKDPPI	PPRRKR.TVV
HCV_K1_S1	PIWARPDYNP	PLLEPWKDPD	YVPPVVHGCP	LPPAKAPPPI	PPRRKR.TVV
HCV_K1_S2	PIWARPDYNP	PLIESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
HCV_K1_S3	PIWARPDYNP	PLLESWRAPD	YAPPVVHGCP	LPPAKDPPI	PPRRKR.TVV
HCV_L2	PEWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPAKAPPPI	PPRRKR.TVV
HCV_N	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPVKAPPPI	PPRRKR.TVV
HCV12083	PVWARPDNNP	PFIQAWQMPG	YEPPVVS GCA	VAPPKPAPVP	PPRRKR.LVH
HCV1480	PVWARPGYDP	PLLETWKRPD	YDPPQVWGCP	IPPAGPPPPVP	LPRRKRKPME
HCVPOLYP	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
HD_1	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
HPCCGAA	PVWARPDYNP	LLVETWKKPD	YEPPVVHGCP	LPPRSPPVP	PPRRKR.TVV
HPCFG	PIWARPDYNP	PLLPWKDPD	YEPPAVHGCA	LPPTRPAPVP	PPRRKR.TIK
HPCGENANTI	PVWARPDYNP	PLLEPWKDPD	YVPPVVHGCP	LPPVKAPPPI	PPRRKR.TVV
HPCGENOM	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTTAPPVP	PPRRKR.TVV
HPCHEUMR	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPIKAPPPI	PPRRKR.TVV
HPCJ	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAAPI	PPRRKR.TIV
HPCJCG	PIWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPSTKAPPPI	PPRRKR.TVV
HPCJK046	PVWARPDYNP	PLLETWKAPD	YDPPVVS GCA	LPPQGLPPVP	PPRRKR.LVQ
HPCJK049	PIWARPDYNP	PLVEPWKDPD	YVPPTVHGCA	LPPQKLPPVP	PPRRKR.TIV
HPCJTA	PIWARPDYNP	PLLESWKSPD	YVPPAVHGCP	LPPTTGPPPI	PPRRKR.TVV
HPCJTB	PIWARPDYNP	PLLESWKSPD	YVPPAVHGCP	LPPTTGPPPI	PPRRKR.TVV
HPCK3A	PIWARPDYNP	PLLDWKSPD	YVPPTVHGCA	LPPKGAPPVP	PPRRKR.TIQ
HPCPLYPRE	PVWARPDYNP	PLVETWKKPD	YEPPVVHGCP	LPPPKSPPVP	PPRRKR.TVV
HPCPOLP	PAWARPDYNP	PLVESWKRPD	YQPATVAGCA	LPPPKKTPT	PPRRKR.TVG
HPCPP	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
HPCUNKCD	PIWAPPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
MKC1A	PVWARPDYNP	PLLESWKDPD	YVPPVVHGCP	LPPTKAPPPI	PPRRKR.TVV
NDM59	PAWARPDYNP	PLVESWKRPD	YQPATVAGCA	LPPPKKTPT	PPRRKR.TVG
NZLI	PIWARPDYNP	PLLDWKAPD	YVPPTVHGCA	LPPRGAPPVP	PPRRKR.TIQ
SA13	PIWARPGYDP	PLLETWKQPD	YDPPQVSGCP	LPPAGLPPVP	PPRRKRKPVV
Th580	PIWARPDYNP	PLLDWKQMPG	YEPPVVS GCA	LPPAKPTPI	PPRRKR.LIQ
Type_3a_CB	PIWARPDYNP	PLLDWKAPD	YVPPTVHGCA	LPPRGAPPVP	PPRRKR.TIQ
TypeV_D	PIWARPDYNP	PLLDWKTPD	YVPPTVHGCA	LPPRGAPPVP	PPRRKR.TIQ
VN004	PIWATPGYNP	PVLETWKSPT	YEPPVVHGCA	LPPSGPPPI	PPRRKR.VVQ
VN235	PVWARPDYNP	PLLDWKAPD	YEPPVHGCA	LPPKGLPPVP	PPRRKR.VVQ
VN405	PIWARPDYNP	PLLETWKKPD	YAPPLVHGCA	LPPSPQPPVP	PPRRKR.VVH

2351

2400

BEBE1	LDQSNVGEAL	KELAIKSFGC	PPPSGDPGHS	TGGGTTGETS	KSPPD.EPDD
D89815	LTESTVSSAL	AELATKTFGG	SGS.SAVDSG	TATGPPDQAS	AE...GDAG
ED43type_4	LTESTVSTAL	AELAAKTFGQ	SEP.SSDRDT	DLTTPTETTD	SGPIV.VDDA
HC_C2	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	ND...GDRE
HC_G9	LDESTVSSAL	AELATKTFGS	STT.SGVTSG	EAAESSPAPS	CD...GELD
HCU16326	LTESTVSSAL	AELATKTFGS	SGS.SAIDSG	TATAPPDQAS	GD...GDRE
HCV_H_CMR	LTESTLPTAL	AELATKSFGS	SST.SGITGD	NMTTSSEPAP	SG...CPPD
HCV_J1	LTESTLSTAL	AELAAKSFGS	SST.SGITGD	NTTTSSEPAP	SG...CSPD
HCV_J483	LTESTVSSAL	AELATKTFSS	SGS.SAVDSG	TATAPPDQAS	DD...GDKG
HCV_J8	LTQDNVEGVL	REMADKVLSP	LQDNNDSGHS	TGADTGGDIV	QQPSD.ETAA
HCV_JK1	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQPS	DD...GDRG
HCV_JS	LTESTVSSAL	AELATKTFGS	SGS.SAADSG	TATAPPDQAS	DD...GDKG
HCV_K1_R1	LTESTVSSAL	AELATKTFGS	SGS.SAADRG	TATAPPDQAS	ND...GDAG
HCV_K1_R2	LTESTVSSAL	AELATKTFGS	SES.SAADSG	TATAPPDQPS	SD...GDAG
HCV_K1_R3	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	ND...GDTG
HCV_K1_S1	LTESTVSSAL	AELATKTFGS	SES.SAADRG	TATAPPDQTS	ND...GDAG
HCV_K1_S2	LTESTVSSAL	AELATKTFGS	SES.SAADSG	TATAPPDQPS	ND...GDAG
HCV_K1_S3	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQPS	ND...GDTG
HCV_L2	LTESTVSSAL	AELAVKTFGS	SES.SAVDSG	TATAPPDQVS	DN...GDKG

HCV_N	LTDSTVSSVL	AELATKTFGS	SEL.SAADSG	TATAPPDQTS	DN....GGKD
HCV12083	LDESTVSHAL	AQLADKVFE	SSNDPGPSSD	SGLSITSPVP	PDPTTPEDAG
HCV1480	LSDSTVSQVM	ADLADARFKV	DTP.SIEGQD	SALGTSSQHD	SGPEEKRDDN
HCVPOLYP	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPDQPP	DN....DDTG
HD_1	LTESTVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPGQSS	DD....VDTG
HPCCGAA	LTESTLPTAL	AELATKSFGS	SST.SGITGD	NTTTSSEPAP	SG....CPPD
HPCFG	LDGSNVSAAL	LALAERSFPS	TKPEGTGTSS	SGVGTESTAE	SGDSPETGEE
HPCGENANTI	LTESTVSSAL	AELATKTFGS	SES.SAAGSG	TATAPPDQPS	DD....GDAG
HPCGENOM	LTESSVSSAL	AELATKTFGS	SES.SAVDSG	TATAPPDEAS	GG....GDKG
HPCHUMR	LTESSVSSAL	AELATKTFGS	SES.SAVDSG	TATALPDQAS	DD....GDKG
HPCJ	LTESTVSSAL	AELATKTFGG	SGS.SAADSG	TATAPPDQTS	DD....GDKE
HPCJCG	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	DD....GDKG
HPCJK046	LDDSVVGHVL	AQLAEKSFPA	TPDQPQTNSD	SGHGTNGAAS	LPSAE.DDDA
HPCJK049	LSESTVSKAL	ASLAEKSFPQ	PTCSAEDEST	SGVGTQSGSL	TGPVQLDDDD
HPCJTA	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	DD....GDKE
HPCJTB	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATAPPDQTS	DD....GDKE
HPCK3A	LDGSNVSAAL	AALAEKSFPS	SKPQEENSSS	SGVDTQSSTA	SKVLPSPGEE
HPCPLYPRE	LTESTLSTAL	AELATRSFGS	SST.SGITGD	NTTTSSEPAP	SG....CPPD
HPCPOLP	LSESSIADAL	QQLAIKSFGQ	PPPSGDSGLS	TGADAADSGS	RTPPD.ELAL
HPCPP	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
HPCUNKCD	LTESTVSSAL	AELATKTFGS	SGS.SAIDSG	TATAPPDQAS	GD....GDRE
MKC1A	LTESTVSSAL	AELATKTFGS	SGS.SAVDSG	TATGPPDQAS	AE....GDAG
NDM59	LNENTIGDAL	QQLAIKAFGQ	PPLSGDSGLS	TGADAADSGS	RTPPD.ESAL
NZLI	LDGSNVSAAL	AALAEKSFPS	SKPQEENSSS	SGVDTQSSTT	SKVPPSPGGE
SA13	LSDSNVSQVL	ADLAHARFKA	DTQ.SIEGQD	SAVGTSSQPD	SGPEEKRDDD
Th580	LDESAVSQAL	QQLADKVFE	DTSTSEPSSG	LGGSIAGPSS	PDPTTADDTC
Type_3a_CB	LDGSNVSAAL	RALAEKSFPS	LKPQEENSSS	SGVDTQSSTT	SKVPPSPGGE
TypeV_D	LDGSNVSAAL	AALAKKSFPS	VNPQDENSSS	SGVDTQSSTT	SKVPPSPGGE
VN004	LDSSNVSAAL	AQLAAKTFET	PSS.PTTGYG	SDQPDHSTES	SEHDRDDGVA
VN235	LDEGSAKRAL	AELAQTSFPP	STATLSEDSG	RETSTLSSDM	TPPREADRA
VN405	LDDSTVATAL	AELAEKSFPT	QPA.STPDS	SGHPTTSKSS	DQADEGEDTP

2401

2450

BEBE1	SEAGSVSSMP	PLEGEPGDPD	LEPEQVEHPA	PPQEGGAAPG	SDSGSWSTCS
D89815	SDAESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
BD43type_4	SDDGSYSSMP	PLEGEPGDPD	LT.....SDSWSTVS
HC_C2	SDAESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HC_G9	SEAESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCU16326	SDVESFSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_H_CMR	SDVESYSSMP	PLEGEPGDPD	FS.....DGSWSTVS
HCV_J1	SDAESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_J483	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_J8	SEAGSLSSMP	PLEGEPGDPD	LEFEPVGSAP	PSEGECEVID	SDSKSWSTVS
HCV_JK1	SDDESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_JS	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_K1_R1	SDVGSYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_K1_R2	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_K1_R3	SDVGSYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_K1_S1	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_K1_S2	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_K1_S3	SDVGSYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_L2	SDAESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV_N	SDAESCSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HCV12083	SEAESYSSMP	PLEGEPGDPD	LS.....SGSWSTVS
HCV1480	SDAASYSSMP	PLEGEPGDPD	LS.....SGSWSTVS
HCVPOLYP	SDVESCSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HD_1	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HPCCGAA	SDVESYSSMP	PLEGEPGDPD	LS.....DGSWSTVS
HPCFG	SDVESYSSMP	PLEGEPGDPD	LD.....ADSWSTVS
HPCGENANTI	SDVESCSSMP	PLEGEPGDPD	LS.....DGSWSTVS

HPCGENOM	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCHUMR	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJ	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJCG	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJK046	SDADSYSSMP	PLEGEPGDPD	LSDG.....	GGSGSWSTVS
HPCJK049	SDNESHSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
HPCJTA	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCJTB	SDVESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCK3A	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
HPCPLYPRE	SDAESYSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
HPCPOLP	SETGSISSMP	PLEGEPGDPD	LEPEQVELQP	PPQGGVVTPG
HPCPP	SDAESYSSMP	PLEGEPGDPD	LN.....	..DGSWSTVS
HPCUNKCD	SDVESFSSMP	PLEGEPGDPD	LS.....	..DGSWSTVS
MKC1A	SDAESYSSMP	PLEGEPGDPD	LN.....	..DGSWSTVS
NDM59	SETGSISSMP	PLEGEPGDPD	LEPEQVELQP	PPQGEVVPG
NZLI	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
SA13	SDAASYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
Th580	SDAGSFSSMP	PLEGEPGDPD	LS.....	..TGSWSTVS
Type_3a_CB	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
TypeV_D	SDSESCSSMP	PLEGEPGDPD	LS.....	..CDSWSTVS
VN004	SEABSYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
VN235	SDDGSYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS
VN405	SEAGSYSSMP	PLEGEPGDPD	LS.....	..SGSWSTVS

2451

2500

BEBE1	DVD..DSVVC	CSMSYSWTGA	LITPCSPREE	KLPINPLSNS	LLRYHNKVYC
D89815	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYS
ED43type_4	GSE...DVVC	CSMSYSWTGA	LVTPCAAEES	KLPISPLSNS	LLRHHNMVYA
HC_C2	EEA.SGDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HC_G9	SDGGTEDVVC	CSMSYSWTGA	LITPCAAEET	KLPINALSNS	LLRHHNLVYS
HCU16326	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_H_CMR	SGADTEDVVC	CSMSYWTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HCV_J1	SEAGTEDVVC	CSMSYWTGA	LITPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HCV_J483	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_J8	DQE..DSVIC	CSMSYSWTGA	LITPCGPEEE	KLPINPLSNS	LMRFHNKVYS
HCV_JK1	EEA.SEDVAC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_JS	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HCV_K1_R1	EEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_R2	EEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_R3	EEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S1	EEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S2	EEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_K1_S3	EEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_L2	EEA.SEDVVC	CSMSYSWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV_N	EEA.GESVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HCV12083	DEDD...VVC	CSMSYSWTGA	LITPCAAEEE	KLPINPLSNS	LVRHHNMVYS
HCV1480	GED...NVVC	CSMSYWTGA	LITPCSAEEE	KLPINPLSNT	LLRHHNLVYS
HCVPOLYP	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HD_1	EEA.NEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCCGAA	SGADTEDVVC	CSMSYSWTGA	LVTPCAAEEQ	KLPINALSNS	LLRHHNLVYS
HPCFG	DSE.BQSVVC	CSMSYSWTGA	IITPCSAEEE	KLPISPLSNS	LLRHHNLVYS
HPCGENANTI	EED.GEGVIC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCGENOM	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HPCHUMR	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCJ	EEA.SEDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHHNMVYA
HPCJCG	GEA.GEDVVC	CSMSYWTGA	LITPCAAEES	KLPINPLSNS	LLRHSMVYS
HPCJK046	SEETS...VVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNT	LIRHHNMVYS
HPCJK049	.GE.BQSVVC	CSMSYSWTGA	LITPCAAEEE	KLPISPLSNS	LLRHHNLVYS
HPCJTA	GEA.SDDIVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA
HPCJTB	GEA.SDDIVC	CSMSYWTGA	LITPCAAEES	KLPINALSNS	LLRHHNMVYA

HPCCK3A	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEE	KLPISPLSNS	LLRHHNLVYS
HPCPLYPRE	SEANAEDVVC	CSMSYSWTGA	LVTPCAAREEQ	KLPINALSNS	LLRHHNLVYS
HPCPOLP	EED..DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
HPCPP	EEA.SEDVVC	CSMSYTWGTA	LITPCAAREES	KLPINALSNP	LLRHHNMVYA
HPCUNKCD	EEA.SEDVVC	CSMSYTWGTA	LITPCAAREES	KLPINPLSNS	LLRHHNMVYA
MKC1A	EEA.SEDVVC	CSMSYTWGTA	LITPCAAREES	KLPINALSNP	LLRHHNMVYA
NDM59	EED..DSVVC	CSMSYSWTGA	LITPCSPEEE	KLPINPLSNS	LLRYHNKVYC
NZLI	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEE	KLPISPLSNS	LLRHHNLVYS
SA13	DED...SVVC	CSMSYSWTGA	LITPCSAEEE	KLPINPLSNT	LLRHHNLVYS
Th580	EEDD...VVC	CSMSYTWGTA	LITPCAAREEE	KLPINPLSNS	LIRHHNMVYS
Type_3a_CB	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEE	KLPISPLSNS	LLRHHNLVYS
TypeV_D	DSE.EQSVVC	CSMSYSWTGA	LITPCSAEEE	KLPISPLSNS	LLRHHNLVYS
VN004	EEGDS..VVC	CSYSYSWTGA	LVTPCAAREEE	KLPINPLSNS	LIRHHNLVYS
VN235	EDHDS..VVC	CSMSYSWTGA	LITPCAAREEE	KLPISPLSNA	LIRHHNLVYS
VN405	EEGDS..VVC	CSMSYSWTGA	LVTPCAAREEE	KLPINPLSNS	LIRHHNLVYS

2501

2550

BEBE1	TTSRASQRA	KKVTFDRVQL	LDSHYESVLK	DVKQAATKVS	AKLLSIEEAC
D89815	TTSRASLRQ	KKVTFDRMQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
ED43type_4	TTTSAVTRQ	KKVTFDRLQV	VDSTYNEVLK	EIKARASRVK	PRLLTTEEAC
HC_C2	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HC_G9	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	BAKAKASTVK	AKLLSVEEAC
HCU16326	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_H_CMR	TTSRASQORQ	KKVTFDRLQV	LDSHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HCV_J1	TTSRASQORQ	KKVTFDRLQV	LDSHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HCV_J483	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV_J8	TTSRASLRA	KKVTFDRVQV	LDAHYSVLQ	DVKRAASKVS	ARLLTVEEAC
HCV_JK1	TTSRASGLRQ	KKVTFDRLQV	PDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_JS	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV_K1_R1	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_R2	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HCV_K1_R3	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_S1	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_K1_S2	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HCV_K1_S3	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_L2	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HCV_N	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HCV12083	TTSRASLRQ	KKVTFDRVQV	FDQHYQDVLK	EIKLRASVQ	AKLLSIEEAC
HCV1480	TSSRSAGLRQ	KKVTFDRLQV	LDDHYREVVD	EMKRLASKVK	ARLLPLEEAC
HCVPOLYP	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HD_1	TTSRASQORQ	KKVTFDRQQV	QDDHYRDVLK	EMKAKASTVK	ARLLSVEEAC
HPCCGAA	TTSRASQORQ	KKVTFDRLQV	LDSHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HPCFG	TSSRSAAARQ	KKVTFDRLQV	LDDHYKNVLK	EVKERASGVK	GRLLSFEEAC
HPCGENANTI	TTSRASQORQ	KKVTIDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCGENOM	TTSRASLRQ	KKVAFDRMQV	LDDHYRDVLK	EMKAKASTVK	AKLLSIEEAC
HPCHUMR	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJ	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJCG	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	ARLLSIEEAC
HPCJK046	TTSRASALRQ	KKVTFDRQQV	VDQHYDITLK	EMKARASTVS	AKLLSVEEAC
HPCJK049	TSSRSAAQORQ	KKVTFDRLQV	LDDHYNTTLK	EIKELASGVK	AELLSVEEAC
HPCJTA	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
HPCJTB	TTSRASLRQ	KKVTFDRLQV	LDDHYRDVLK	EVKAKASTVK	AKLLSVEEAC
HPCCK3A	TSSRSASQORQ	KKVTFDRLQV	LDDHYKTALQ	EVKERASRVK	ARMLSIEEAC
HPCPLYPRE	TTSRASQORQ	KKVTFDRLQV	LDSHYQDVLK	EVKAAASKVK	ANLLSVEEAC
HPCPOLP	TTSKASLRA	KKVTFDRMQA	LDAHYSVLK	DIKLAASKVT	ARLLTLEEAC
HPCPP	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	DMKAKASTVK	AKLLSVEEAC
HPCUNKCD	TTSRASGLRQ	KKVTFDRLQV	LDDHYRDVLK	EMKAKASTVK	AKLLSVEEAC
MKC1A	TTSRASQORQ	KKVTFDRLQV	LDDHYRDVLK	DMKAKASTVK	AKLLSVEEAC
NDM59	TTSKASLRA	KKVTFDRMQV	LDAHYSVLK	DIKLAASKVS	ARLLTLEEAC
NZLI	TSSRSASQORQ	KKVTFDRLQV	LDDHYKTALK	EVKERASRVK	ARMLTIEEAC

SA13	TSSRSAGQRQ	KKVTFDRLQV	LDDHYREVVD	EMKRLASKVK	ARLLPLEEAC
Th580	TSSRSAGLRQ	KKVTFDRLQV	VDQHYQDVLK	EIKLRASTVH	ARLLSTEEAC
Type_3a_CB	TSSRSASQRQ	RKVTFDRLQV	LDDHYKTVLK	EVKERASRVK	ARMLTIEEAC
TypeV_D	TSSRSASQRQ	KKVTFDRLQV	LDDHYKTALK	EVKERASRVK	ARMLTIEEAC
VN004	TSSRSAATRQ	KKVTFDRVQL	LDQHYYDTVK	EIKLRASHVK	AQLLSTEEAC
VN235	TSSRSASLRQ	KKVTFDRVQV	VDQHYYDVLK	EIKTKASGVS	AKLLSVEEAC
VN405	TTTRSAAMRQ	KKVTFDRLQI	LDQHYNVVK	EVKLASGVT	AKLLSVEEAC

	2551				2600
BEBE1	ALTPPHSARS	KYGFGAKEVR	SLSRRAVDHI	KSVWEDLLED	HCSPIDTTIM
D89815	KLTPPHSAKS	KFGYGAKDVR	SLSSRAVNHI	RSVWKDLLED	TDTPITTTIM
ED43type_4	DLTPPHSARS	KFGYGKQDVR	SHSRKAINHI	SSVWKDLLED	NNTPIPTTIM
HC_C2	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HC_G9	SLTPPHSARS	KFGYGAKDVR	SHSSKAIKHI	NSVWQDLLED	NTTPIDTTIM
HCU16326	KLTPPHSARS	KFGYGAKDVR	SLSSRAVTHI	RSVWKDLLED	TETPISTTIM
HCV_H_CMR	SLTPPHSARS	KFGYGAKDVR	CHARKAVAH1	NSVWKDLLED	SVTPIDTTIM
HCV_J1	SLTPPHSARS	KFGYGAKDVR	CHARKAVNHI	NSVWKDLLED	SVTPITTTIM
HCV_J483	KLTPPHSARS	KFGYGAKDVR	NLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HCV_J8	ALTPPHSARS	RYGFGAKEVR	SLSRRAVNHI	RSVWEDLLED	QHTPIDTTIM
HCV_JK1	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	HSVWKDLLED	TETPIDTTIM
HCV_JS	KLTPPHSARS	KYGFGAKEVR	NLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HCV_K1_R1	RLTPPHSARS	KFGYGAKDVR	NLSSGAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_R2	KLTPPHSARS	KFGYGAKDVR	NLSSRAINHI	RSVWKDLQED	TETPIDTTIM
HCV_K1_R3	KLTPPHSARS	KFGYGKQDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTVM
HCV_K1_S1	RLTPPHSARS	KFGYGAKDVR	NLSSGAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S2	KLTPPHSARS	KFGYGAKDVR	NLSSRAINHI	RSVWKDLLED	TETPIDTTIM
HCV_K1_S3	KLTPPHSARS	KFGYGKQDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTVM
HCV_L2	KLTPPHSARS	KFGYGAKDVR	NLSSRAVNHI	RSVWKDLLED	TETPIDTTIM
HCV_N	RLTPPHSARS	KFGYGAKDVR	NLSSRAINHI	RSVWEDLLED	TVTPIDTTVM
HCV12083	DLTPPHSARS	KYGFGAQDVR	SRASKAVDHI	PSVWEGLLED	SDTPITTTIM
HCV1480	GLTPPHSARS	KYGFGAKEVR	SLDKKALKHI	EGVWQDLLED	SDTPLPTTIM
HCVPOLYP	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HD_1	KLTPPLSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWEDLLED	NVTPIDTTIM
HPCCGAA	SLAPPHSARS	KFGYGAKDVR	CHARKAVAH1	NSVWKDLLED	SVTPIDTTIM
HPCFG	SLVPPHSGRS	KYGYSADVR	SLSSKAMNHI	RSVWEDLLED	NSTPIPTTIM
HPCGENANTI	KLTPPHSARS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCGENOM	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	RSVWKDLLED	NETPINTTIM
HPCHUMR	KLTPPHSARS	KFGYGAKDVR	NLSSKAVNHI	HSVWKDLLED	TVTPIDTTIM
HPCJ	KLTPPHSARS	KFGYGAKDVR	SLSSRAVNHI	TSVWKDLLED	TKTPIDTTIM
HPCJCG	KLTPPHSARS	KFGYGAKDVR	SLSSRAVNHI	RSVWEDLLED	TETPIDTTIM
HPCJK046	DLTPPHSARS	KFGYGAKDVR	GRTSKALNHI	NSVWEDLLED	NVTPITTTIM
HPCJK049	RLVPPHSARS	KFGYGAKDVR	SLSSKAINHI	NSVWEDLLED	NTTPITTTIM
HPCJTA	KLTPPHSARS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCJTB	KLTPPHSARS	KFGYGAKDVR	NLSSKAINHI	RSVWKDLLED	TETPIDTTIM
HPCK3A	ALVPPHSARS	KFGYSADVR	SLSSKAINHI	RSVWEDLLED	TTTPITTTIM
HPCPLYPRE	SLTPPHSARS	KFGYGAKDVR	CHARKAVTHI	NSVWKDLLED	NVTPIDTTIM
HPCPOLP	QLTPPHSARS	KYGFGAKEVR	SLSGRAVNHI	KSVWKDLLED	TQTPITTTIM
HPCPP	KLTPPHSARS	KFGYGAKDVR	SLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
HPCUNKCD	KLTPPHSARS	KFGYGAKDVR	SLSSRAVTHI	RSVWKDLLED	TETPISTTIM
MKC1A	KLTPPHSARS	KFGYGAKDVR	SLSSKAVNHI	RSVWKDLLED	TETPIDTTIM
NDM59	QLTPPHSARS	KYGFGAKEVR	SLSGRAVNHI	KSVWKDLLED	SQTPITTTIM
NZLI	ALVPPHSARS	KFGYSADVR	SLSSRAINHI	RSVWEDLLED	TTTPITTTIM
SA13	GLTPPHSARS	KYGFGAKEVR	SLDKKALNHI	KGVWQDLLED	SDTPLPTTIM
Th580	SLTPPHSARS	RYGYGARDVR	SHTSKAVKHI	DSVWEDLLED	NATPIPTTIM
Type_3a_CB	ALVPPHSARS	KFGYSADVR	SLSSRAINHI	RSVWEDLLED	TTTPITTTIM
TypeV_D	ALVPPHSARS	KFGYSADVR	SLSSRAIDHI	RSVWEDLLED	TTTPITTTIM
VN004	DLTPPHSARS	KFGYGAKDVR	SHASKAINHI	NSVWADLLED	TQTPITTTIM
VN235	ALTPPHSARS	KFGYGAKDVR	GLASKAVNHI	NSVWEDLLED	NSTPIPTTIM
VN405	SLTPPHSARS	KFGYGAKDVR	SHTSKAINHI	NSVWEDLLED	NQTPITTTIM

	2601				2650
BEBE1	AKNEVFCVDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIT	QKLPVAVMGQ
D89815	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
ED43type_4	AKNEVFAVNP	AKGGRKPARL	IVYPDLGSRV	CEKRALHDVI	KKTALAVMGA
HC_C2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HC_G9	AKNEVFCVKP	EKGGRKPARL	IVYPDLGVRV	CEKRALYDVV	KQLPIAVMGT
HCU16326	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_H_CMR	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPLAVMGS
HCV_J1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPPAVMGS
HCV_J483	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_J8	AKNEVFCIDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIA	QKLPKAIMGP
HCV_JK1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_JS	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_R1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_R2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGA
HCV_K1_R3	AKNEVFCVQP	EKGGRKAARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_S1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_K1_S2	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HCV_K1_S3	AKNEVFCVQP	EKGGRKAARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV_L2	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HCV_N	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HCV12083	AKNEVFCVDP	SKGGRKPARL	IVYPDLGVRV	CEKMALYDVT	QKLPQAVMGP
HCV1480	AKNEVFAVEP	SKGGKKPARL	IVYPDLGVRV	CEKRALYDVA	QKLPALMGP
HCVPOLYP	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HD_1	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPHTVMGS
HPCCGAA	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	SKLPLAVMGS
HPCFG	AKNEVFSVNP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLSIATMGP
HPCGENANTI	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCGENOM	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCHUMR	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCJ	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCJCG	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGP
HPCJK046	AKNEVFCVDP	SKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	RKLPAVAVMGA
HPCJK049	AKNEVFAVAP	HKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLPVAVMGA
HPCJTA	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCJTB	AKSEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCK3A	AKNEVFCVDP	AKGGRKAARL	IVYPDLGVRV	CEKRALYDVI	QKLSIETMGS
HPCPLYPRE	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	TKLPLAVMGS
HPCPOLP	AKNEVFCVDP	TKGGKKPARL	IVYPDLGVRV	CEKMALYDIT	QKLPQAVMGA
HPCPP	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
HPCUNKCD	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
MKC1A	AKNEVFCVQP	EKGGRKPARL	IVFPDLGVRV	CEKMALYDVV	STLPQAVMGS
NDM59	AKNEVFCVDP	AKGGRKAARL	IVYPDLGVRV	CEKMALYDVT	QKLPQAVMGA
NZLI	AKNEVFCVDP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLSIETMGP
SA13	AKNEVFAVEP	SKGGKKPARL	IVYPDLGVRV	CEKRALYDIA	QKLPALMGP
Th580	AKNEVFCVDP	SKGGRKPARL	IVYPDLGVRV	CEKMALYDVT	QKLPKTMGS
Type_3a_CB	AKNEVFCVDP	AKGGRKPARL	IVYPDLGVRV	CEKRALYDVI	QKLAETIGS
TypeV_D	AKNEVFCVDP	ARGGRKRRL	IVYPDLGVRV	CEKRVLVDVI	QKLSIETMGT
VN004	AKNEVFCVDA	SKGGRKSARL	IVYPDLGVRV	CEKRALFDVT	RKLPTAIMGD
VN235	AKNEVFCVDA	QKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	QKLPVAVMGA
VN405	AKNEVFCADV	SKGGRKPARL	IVYPDLGVRV	CEKRALYDVT	RKLPTAIMGD
	2651				2700
BEBE1	SYGFQYSPAQ	RVDFLLQAWK	EKKTPMGFSY	DTRCFDSTVT	ERDIRTEESI
D89815	SYGFQYSPKQ	RVEFLVNTWK	AKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
ED43type_4	AYGFQYSPAQ	RVEFLLTAWK	SKNDPMGFSY	DTRCFDSTVT	EKDIRVEEEV
HC_C2	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRIEESI
HC_G9	SYGFQYSPAQ	RVDFLLNAWK	SKKNPMGFSY	DTRCFDSTVT	EADIRTEEDL
HCU16326	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV_H_CMR	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFPY	DTRCFDSTVT	ESDIRTEEAI

HCV_J1	SYGFQYSPGQ	RVEFLVQAWK	SKRTPMGFSY	DTRCFDSTVT	ESDIRTEEAI
HCV_J483	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRVEESI
HCV_J8	SYGFQYSPAE	RVDFLKAWG	SKKDPMGFSY	DTRCFDSTVT	ERDIRTEESI
HCV_JK1	SYGFQYSPGQ	RVEFLVNAWK	SKKNPMGFAY	CTRCFDSTVT	ESDIRVEESI
HCV_JS	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
HCV_K1_R1	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_R2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV_K1_R3	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
HCV_K1_S1	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_S2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HCV_K1_S3	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV_L2	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRTEESI
HCV_N	SYGFQYSPGQ	RVEFLVNAWK	SKKNPMGFAY	DTRCFDSTVT	ENDIRVEESI
HCV12083	AYGFQYSPNQ	RVEYLLKMWR	SKKVPMGFSY	DTRCFDSTVT	ERDIRTENDI
HCV1480	SYGFQYSPAQ	RVDFLKAWG	SKKIPMAFSY	DTRCFDSTIT	EHDIMTEESI
HCVPOLYP	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFAY	DTRCFDSTVT	ESDIRVEESI
HD_1	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFAY	DTRCFDSTVT	ENDIRVEESI
HPCCGAA	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGLSY	DTRCFDSTVT	ESDIRTEEAI
HPCFG	AYGFQYSPKQ	RVEHLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EHDIRTEEGI
HPCGENANTI	SYGFQYSPGQ	RVEFLVNAWK	SKKCPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCGENOM	SYGFQYSPGQ	RVEFLVNAWK	SKENPMGFAY	DTRCFDSTVT	QNDIRVEESI
HPCHUMR	SYGFQYSPGQ	RVEFLVNTWK	SKKNPMGFAY	DTRCFDSTVT	ENDIRVEESI
HPCJ	SYGFQYSPGQ	RVEFLVKTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
HPCJCG	SYGFQYSPGQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRTEESI
HPCJK046	AYGFQYSPSQ	RVEYLLKIWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEESI
HPCJK049	AYGFQYSPKQ	RVEYLLKMWN	SKKTPLGFSY	DTRCFDSTVT	EQDIRVEESI
HPCJTA	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCJTB	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFSY	DTRCFDSTVT	ESDIRVEESI
HPCK3A	AYGFQYSPRQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	GQDIRVEEAV
HPCPLYPRE	SYGFQYSPGQ	RVEFLVQAWK	SKKTPMGFSY	DTRCFDSTVT	ESDIRTEEAI
HPCPOLP	SYGFQYSPAQ	RVEFLKAWA	EKKDPMGFAY	DTRCFDSTVT	ERDIRTEESI
HPCPP	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
HPCUNKCD	SYGFQYSPKQ	RVEFLVNTWK	SKKCPMGFSY	DTRCFDSTVT	ENDIRVEESI
MKC1A	SYGFQYSPGQ	RVEFLVNAWK	SKKSPMGFAY	DTRCFDSTVT	ENDIRTEESI
NDM59	SYGFQYSPAQ	RVEFLKAWA	EKKDPMGFAY	DTRCFDSTVT	ERDIRTEESI
NZLI	AYGFQYSPQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EQDIRVEEAI
SA13	SYGFQYSPAQ	RVEFLKAWA	SKKTPMAFSY	DTRCFDSTVT	EHDIMTEESI
Th580	AYGFQYSPSQ	RVEYLLKMWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEEDI
Type_3a_CB	AYGFQYSPQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EQDIRVEEAI
TypeV_D	AYGFQYSPQ	RVERLLKMWT	SKKTPLGFSY	DTRCFDSTVT	EQDFRVEEAI
VN004	AYGFQYSPQ	RVDRLKMWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEQDI
VN235	AYGFQYSPKQ	RVDYLLKMWR	SKKTPMGFSY	DTRCFDSTVT	ERDIRTEEDI
VN405	AYGFQYSPKQ	RVDQLKMWR	SKKTPMGFSY	DTRCFDSTVT	EHDIKTERDV

2701

2750

BEBE1	YLSCSLPEEA	RTAIHSLTER	LYVGGPMTNS	KGQSCGYRRC	RASGVLTTSM
D89815	YQCCDLAPEA	RQAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
ED43type_4	YQCCDLPEEA	RKVITALTDR	LYVGGPMHNS	KGDLGCGYRRC	RATGVYTTSF
HC_C2	YQCCDLAPEA	KQAIKSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HC_G9	YQSCDLVPEA	RAAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HCU16326	YQCCDLAPEA	KLAIKSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HCV_H_CMR	YQCCDLDPQA	RVAIKSLTER	LYVGGPMTNS	RGENCYRRC	RASGVLTTSC
HCV_J1	YQCCDLDPQA	RVAIRSLTER	LYVGGPMTNS	RGENCYRRC	RASGVLTTSC
HCV_J483	YQCCDLAPEA	RQAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HCV_J8	YQACSLPQEA	RTVIHSLTER	LYVGGPMTNS	KGQSCGYRRC	RASGVFTTSM
HCV_JK1	YQCCDLAPEA	RQVIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTNC
HCV_JS	YQCCDLAPEA	KLAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R1	YQCCDLAPEA	RQAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R2	YQCCDLAPEA	RQAIRSLTER	LYIGGPMTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_R3	YQCCDLAPEA	RQVIRSLTER	LYVGGPMTNS	KGQNCGYRRC	RASGVLTTSC

HCV_K1_S1	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S2	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_K1_S3	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HCV_L2	YQCCDLAPEA	KQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASVVLTTSC
HCV_N	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQSCGYRRC	RASGVLTTSC
HCV12083	YQSCQLDPVA	RRVSSSLTER	LYVGGPMANS	KGQSCGYRRC	RASGVLPTSM
HCV1480	YQSCDLQPEA	RVAIRSLTQR	LYCGGPMYNS	KGQQCGYRRC	RASGVFTTSM
HCVPOLYP	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HD_1	YQCCDLGPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCCGAA	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASRVLTTSF
HPCFG	YQCCDLPEA	RKAISALTER	LYIGGPMYNS	KGLQCGYRRC	RASGVLPTSF
HPCGENANTI	YQCCDLAPEA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCGENOM	YQCCDLAPEA	RRAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCHUMR	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJ	YQCCDLAPEA	RQVIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJCG	YQCCDLAPEA	RQAIRSLTER	LYVGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJK046	YQCCBLDPVA	RKAISSLTER	LYVGGPMYNS	KGQSCGYRRC	RASGVLPTSM
HPCJK049	YQACDLKDEA	RRVITSALTER	LYCGGPMFNS	KGQHCYRRC	RASGVLPTSF
HPCJTA	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCJTB	YQCCDLAPEA	RQAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
HPCK3A	YQCCNLEPEP	GQAISSLTER	LYCGGPMNNS	KGAQCGYLRC	RASGVLPTSF
HPCPLYPRE	YQCCDLDPQA	RVAIKSLTER	LYVGGPLTNS	RGENCYRRC	RASGVLTTSC
HPCPOLP	YRACSLPEEA	HTAIHSLTER	LYVGGPMFNS	KGQTCGYRRC	RASGVLTTSM
HPCPP	YQCCDLDPQA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RVSGVLTTSC
HPCUNKCD	YQCCDLAPEA	KLAIKSLTER	LYIGGPLTNS	KGQNCGYRRC	RASGVLTTSC
MKC1A	YQCCDLDPQA	RQAIRSLTER	LYIGGPLTNS	KGQNCGYRRC	RVSGVLTTSC
NDM59	YRACSLPEEA	HTAIHSLTER	LYVGGPMFNS	KGQTCGYRRC	RASGVLTTSM
NZLI	YQCCNLEPEA	RKVISSSLTER	LYCGGPMFNS	KGAQCGYRRC	RASGVLPTSF
SA13	YQSCDLQPEA	RAAIRSLTQR	LYCGGPMYNS	KGQQCGYRRC	RASGVFTTSM
Th580	YQSCQLDPTA	RKAISSLTER	LYCGGPMFNS	KGESCGYRRC	RASGVLTTSL
Type_3a_CB	YQCCNLEPEA	RKVISSSLTER	LYCGGPMFNS	KGAQCGDRRC	RASGVLPTSF
TypeV_D	YQCCNLEPEA	RKVISSSLTER	LYCGGPMFNS	KGAQCGYRRC	RASGVLPTSF
VN004	YLSCQLDPEA	RKVIESLTER	LYVGGPMYNS	KGQLCGQRRRC	RASGVLPTSM
VN235	YQCCQLDPVA	KKAITSLTER	LYCGGPMYNS	RGQSCGYRRC	RASGVLTTSL
VN405	YLSCQLDPVA	RKAIESLTER	LYIGGPMYNS	RGQLCGTRRC	RASGVLTTSL

2751

2800

BEBE1	GNTLTCTYVKA	KAACNAAGIV	APTMLVCGDD	LVVISESQGV	EEDERNLRVF
D89815	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
ED43type_4	GNTLTCTYLKA	TAAIRAAALR	DCTMLVCGDD	LVVIAESDGV	EEDNRALRAF
HC_C2	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HC_G9	GNTITCTYLKA	SAACRAAKLR	DCTMLVCGDD	LVVICESAGV	QEDAANLRAF
HCU16326	GNTLTCTYLKA	TAACRAAKLR	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HCV_H_CMJ	GNTLTCTYIKA	RAARRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRVF
HCV_J1	GNTLTCTYIKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRVF
HCV_J483	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAAALRVF
HCV_J8	GNTMTCTYIKA	LAACKAAGIV	DPVMLVCGDD	LVVISESQGN	EEDERNLRAF
HCV_JK1	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_JS	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R1	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R2	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_R3	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S1	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S2	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_K1_S3	GNTLTCTYLKA	AAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HCV_L2	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAANLRAF
HCV_N	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	RVVICESAGT	QEDAASLRVF
HCV12083	GNTLTCTYLKA	QAACRAANIK	DCDMLVCGDD	LVVICESAGV	QEDTASLRAF
HCV1480	GNTMTCTYIKA	LASCRAAKLR	DCTLLVCGDD	LVAICESQGT	HEDEASLRAF
HCVPOLYP	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF

HD_1	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAANLRVF
HPCCGAA	GNTLTCTYLKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HPCFG	GNTITCTYLKA	TAASRAAGLK	NPSFLVCGDD	LVVISESCGV	EEDRTALRAF
HPCGENANTI	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICESAGT	QEDAASLRVF
HPCGENOM	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCHUMR	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJ	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJCG	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAAALRAF
HPCJK046	GNTLTCTYLKA	MAACKAAGLK	NFDMLVCGDD	LVVISESLGV	SEDASALRAF
HPCJK049	GNTVTCYLKA	KAATKAAGIK	DPSFLVCGDD	LVVIAESAGI	DEKKSALRAF
HPCJTA	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCJTB	GNTLTCTYLKA	TAACRAAKLQ	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
HPCK3A	GNTITCTYLKA	TAAARAAGLR	NPDFLVCDD	LVVVAESDGV	DEDRATLRAF
HPCPLYPRE	GNTLTCTYLKA	RAACRAAGLQ	DCTMLVCGDD	LVVICESAGV	QEDAASLRAF
HPCPOLP	GNTITCTYLKA	LAACKAAGII	APTMLVCGDD	LVVISESQGT	EEDERNLRAF
HPCPP	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
HPCUNKCD	GNTLTCTYLKA	TAACRAAKLR	DCTMLVNGDD	LVVICESAGT	QEDAASLRVF
MKC1A	GNTLTCTYLKA	SAACRAAKLQ	DCTMLVCGDD	LVVICDSAGT	QEDAASLRVF
NDM59	GNTITCTYLKA	LAACKAAGIV	APTMLVCGDD	LVVISESQGT	EEDERNLRAF
NZLI	GNTITCTYLKA	TAAAKAANLR	NPDFLVCDD	LVVVAESDGV	DEDRALRAF
SA13	GNTMTCYLKA	LASCRAAKLR	DCTLLVCGDD	LVAICESQGT	HEDEASLRAF
Th580	GNTLTCTYLKA	QAACRAANIK	NFDMLVCGDD	LVVICESAGV	QEDVVALRAF
Type_3a_CB	GNTITCTYLKA	TAAANGAGLR	DPDFLVCDD	LVVVAESDGV	DEGGAALRAF
TypeV_D	GNTITCTYLKA	TAAAKAAGLR	NPDFLVCDD	LVVVAESDGV	DEDRATLRAF
VN004	GNTVTCFLKA	TAACRAAGFT	DYDMLVCGDD	LVVVITESAGV	NEDIANLRAF
VN235	GNTLTCTYLKA	QAACRAAKLK	DFDMLVCGDD	LVVISESMGV	AEDASALRAF
VN405	GNTMTCFIKA	EAACRAAGLT	NYDMLVCGDD	LVVIAESAGV	QEDASNLRAF

2801

2850

BEBE1	TEAMTRYSAP	PGDPPKAEYD	LELITSCSSN	VSVALDPRGR	RRYYLTRDPT
D89815	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
ED43type_4	TEAMTRYSAP	PGDAPQPAYD	LELITSCSSN	VSVAHVDGTGK	KVYYLTRDPE
HC_C2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HC_G9	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDGAGK	RVYYLTRDPE
HCU16326	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_H_CMR	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDGAGK	RVYYLTRDPT
HCV_J1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHDGAGK	RVYYLTRDPT
HCV_J483	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_J8	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_JK1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVALDSRGR	RRYFLTRDPT
HCV_JS	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_R1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_R2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_R3	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_S1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_S2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_K1_S3	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_L2	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV_N	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HCV12083	TDAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVAHAGNGK	KYYLTRDCT
HCV1480	TEAMTRYSAP	PGDPPVPAYD	LELITSCSSN	VSVARDASGN	RIYYLTRDPQ
HCVPOLYP	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HD_1	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HPCCGAA	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HPCFG	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVAHDGAGK	RVYYLTRDPT
HPCGENANTI	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVACDGAGK	RVYYLTRDPE
HPCGENOM	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HPCHUMR	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HPCJ	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT
HPCJCG	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSVAHASGK	RVYYLTRDPT

HPCJK046	TDAMTRYSAP	PGDEPHPEYD	LEHITSCSSN	VSAHDHTGQ	RYYYLTRDPT
HPCJK049	TEAMTRYSAP	PGDPPQPTYD	LELITSCSSN	VSAHDGAGK	RYYYLTRDPE
HPCJTA	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCJTB	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCK3A	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVARDDKGR	RYYYLTRDAT
HPCPLYPRE	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDGAGK	RVYYLTRDPT
HPCPOLP	TEAMTRYSAP	PGDPPRPEYD	LELITSCSSN	VSVLGPQGR	RRYYLTRDPT
HPCPP	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
HPCUNKCD	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
MKC1A	TEAMTRYSAP	PGDPPQPEYD	LELITSCSSN	VSAHDASGK	RVYYLTRDPT
NDM59	TEAMTRYSAP	PGDPPRPEYD	LELITSCSSN	VSVAXGPQGR	RRYYLTRDPT
NZLI	TEAMTRYSAP	PGDAPQATYD	LELITSCSSN	VSVARDDKGR	RYYYLTRDAT
SA13	TEAMTRYSAP	PGDPPVPAYD	LELITSCSSN	VSAHDASGN	RVYYLTRDPQ
Th580	TDAMIRYSAP	PGDAPQPTYD	LELITSCSSN	VSAHDGTGQ	RYYYLTRDCT
Type_3a_CB	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVARDDKGR	RYYYLTRDAT
TypeV_D	TEAMTRYSAP	PGDAPQPTYD	LELITSCSSN	VSVLGNKGR	RYYYLTRDAT
VN004	TEAMTRYSAT	PGDEPSPTYD	LELITSCSSN	VSAHDGDGR	RYYYLTRDPV
VN235	TEAMTRYSAP	PGDDPQPEYD	LELITSCSSN	VSAHDGAGQ	RYYYLTRDPL
VN405	TEAMTRYSAP	PGDEPHPAYD	LELITSCSSN	VSAHDHTGQ	RYYYLTRDPT

2851

2900

BEBE1	TPLARAAWET	ARHSPVNSWL	GNIQYAPT	VWRVLMTHF	FSVLMAQDTL
D89815	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
RD43type_4	TPLARAVWET	VRHTPVNSWL	GNIIVYAPTI	VWRMILMTHF	FSILQSQBAL
HC_C2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HC_G9	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	VWRVLMTHF	FSILLAEHL
HCU16326	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_H_CMR	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMTHF	FSVLIARDQL
HCV_J1	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMTHF	FSVLIARDQL
HCV_J483	IPLARAAWET	ARHTPVNSWL	GNIIMYAPAL	WARMILMTHF	FSILLAEQQL
HCV_J8	TPITRAAWET	VRHSPVNSWL	GNIQYAPTI	VWRMVIMTHF	FSILLAEQQL
HCV_JK1	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_JS	TPIARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_K1_R1	TPLARAAWET	AKSTPVNSWL	GNIIMFAPTL	VWRMILMTHF	FSILLAEQQL
HCV_K1_R2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_K1_R3	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_K1_S1	TPLARAAWET	ARSTPVNSWL	GNIIMFAPTL	VWRMILMTHF	FSILLAEQQL
HCV_K1_S2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_K1_S3	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_L2	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV_N	TPIARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HCV12083	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTI	VWRVLMNHF	FSILQSQBAL
HCV1480	VPLAKAAWET	AKHSPVNSWL	GNIIMYAPTL	WARIVLMTHF	FSVLQSQBAL
HCVPOLYP	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HD_1	TPLARAAWET	ARHTSVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCCGAA	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMTHF	FSVLIARDQL
HPCFG	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTI	VWRVLMTHF	FSILLAEQQL
HPCGENANTI	TPLARAAWAT	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCGENOM	IPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCHUMR	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCJ	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCJCG	TPLARAAWET	VRHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCJK046	NVLARAAWET	ARHTPVNSWL	GNIIMYAPTI	VWRVLMTHF	FGILQPQEQQL
HPCJK049	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	VWRMVIMTHF	FSILLAEQQL
HPCJTA	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCJTB	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL
HPCK3A	TPLARAAWET	ARHTPVNSWL	GSIIMYAPTI	VWRVMMTHF	FSILQSQEIL
HPCPLYPRE	TPLARAAWET	ARHTPVNSWL	GNIIMFAPTL	WARMILMTHF	FSVLIARDQL
HPCPOLP	TPIARAAWET	VRHSPVNSWL	GNIQYAPTI	WARMVLMTHF	FSILMAQDTL
HPCPP	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAEQQL

HPCUNKCD	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
MKC1A	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTL	WARMILMTHF	FSILLAQEQL
NDM59	TPLSRAAWET	VRHSPVNSWL	GNIIQYAPTI	WVRMVLMTTHF	FSILMAQDTL
NZLI	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMTHF	FSILQSQEIL
SA13	VPLARAAWET	AKHSPVNSWL	GNIIMYAPTL	WARIVLMTTHF	FSVLQSQEQL
Th580	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FSILQCQEQL
Type_3a_CB	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMTHF	FSILQSQEIL
TypeV_D	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVMTHF	FSILQSQEIL
VN004	TPLARAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FQILQAQETL
VN235	TPLSRAAWET	ARHTPVNSWL	GNIIMYAPTI	WVRMVLMTTHF	FAILQSQEIL
VN405	TPLSRAAWET	ARHTPVNSWL	GNIIMYAPAI	WVRMVLMTTHF	FQILQAQEQL

2901

2950

BEBE1	DQDLNFEMYG	AVYSVSPLDL	PAIIERLHGL	EAFLSHSYSP	HELTRVAAAL
D89815	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
ED43type_4	EKALDFDMYG	VTYSITPLDL	PAIIQRLHGL	SAFTLHGYS	HELN RVAGAL
HC_C2	EKALECQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HC_G9	EKALDCEIYG	AVHSVQPLDL	PEIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HCU16326	EKTLDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_H_CMR	EQALNCEIYA	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HCV_J1	EQALDCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HCV_J483	EQALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_J8	NQNLNFEMYG	AVYSVNPLDL	PAIIERLHGL	EAFLSHSYSP	HELTRVAAAL
HCV_JK1	EKALGDCQIYG	ATYFIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_JS	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_R1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_R2	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_R3	DKALDCQIYE	AIYSIGPLDL	PQVIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_S1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_S2	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_K1_S3	DKALDCQIYE	AIYSIGPLDL	PQVIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCV_L2	EKALECQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV_N	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HCV12083	EKALDFDIYG	VTYSVSPLDL	PAIIQRLHGM	AAFLSHGYSP	VELNRVAGAL
HCV1480	EKTLAFEMYG	SVYSVTPLDL	PAIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HCVPOLYP	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HD_1	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HPCCGAA	EQALNCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HPCFG	ERALDFEMYG	ATYSVTPLDL	PAIIERLHGL	SAFLSHGYSP	TELNRVAGAL
HPCGENANTI	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCGENOM	EKALDCQIYG	AYYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCHUMR	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCJ	GKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCJCG	EKALDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
HPCJK046	HKALDFDMYG	VTYNITPLDL	PQIIQRLHGM	AAFLSHGYSP	GELNRVAGAL
HPCJK049	EKALDFEMYG	AVYSVTPLDL	PAIIERLHGL	SAFLSHSYSP	VELNRVAGAL
HPCJTA	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HPCJTB	EKALDCQIYG	ACYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASSL
HPCK3A	DRPLDFEMYG	ATYSVTPLDL	PAIIERLHGL	SAFLSHSYSP	VELNRVAGTL
HPCPLYPRE	EQALDCEIYG	ACYSIEPLDL	PPIIQRLHGL	SAFLSHSYSP	GEINRVAACL
HPCPOLP	DQNLNFEMYG	AVYSVSPLDL	PAIIERLHGL	DAFLSHYTP	HELTRVASAL
HPCPP	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
HPCUNKCD	EKTLDCQIYG	ACYSIEPLDL	PQIIERLHGL	SAFLSHSYSP	GEINRVASCL
MKC1A	EKALDCQIYG	ATYSIEPLDL	PQIIQRLHGL	SAFLSHSYSP	GEINRVASCL
NDM59	DQNLNFEMYG	XVYSVSPLDL	PAIIERLHGL	DAFLSHYTP	HELTRVASAL
NZLI	DRPLDFEMYG	ATYSVTPLDL	PAIIERLHGL	SAFTLHSYSP	VELNRVAGTL
SA13	EKALAFEMYG	SVYSVTPLDL	PAIIQRLHGL	SAFTLHSYSP	SEINRVSSCL
Th580	EKALNDFMYG	VTYSVTPLDL	PAIIQRLHGM	AAFLSHGYSP	TELNRVAGSL
Type_3a_CB	DRPLDFEMYG	ATYSVTPLDL	PAIIERLHGL	SAFTLHSYSP	VELNRVAGTL
TypeV_D	DRPLDFEMYG	ATYSVTPLDL	PAIIERLHGL	SAFTLHSYSP	VELNRVAGTL

VN004	DRALDFDIYG	VTYSITPLDL	PVIIQRLHGM	AAFSLHGYSP	DELNRVASCL
VN235	HKALDFDMYG	VTYSVTPLDL	PYIIQRLHGM	AAFSLHGYSP	GELNRVASCL
VN405	DKVLDFDMYG	VTYSVSPLQL	PAIIQRLHGM	AAFSLHGYSP	TELNRVGACL

	2951		3000
BEBE1	RKLGAPPLRA	WKSARAVRA	SLISRGGSAA
D89815	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
ED43type_4	RKLGVPPLRA	WRHRARAVRA	KLIAQGGRAK
HC_C2	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HC_G9	RKLGVPPLRA	WRHRARAVRA	TLLSQGGRAA
HCU16326	RKLGVPPLRA	WRHRARAVRA	KLLSQGGRAA
HCV_H_CMR	RKLGVPPLRA	WRHRARAVRA	RLLSRGGRAA
HCV_J1	RKLGVPPLRA	WRHRARAVRA	RLLSRGGRAA
HCV_J483	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_J8	RKLGAPPLRA	WKSARAVRA	SLIAQGARA
HCV_JK1	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_JS	RKLGVPPLRV	WRHRARGVRA	KLLSQGGRAA
HCV_K1_R1	RKLGVPPLRT	WRHRARAVRA	KLLSQGGRAA
HCV_K1_R2	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_K1_R3	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_K1_S1	RKLGVPPLRT	WRHRARAVRA	KLLSQGGRAA
HCV_K1_S2	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_K1_S3	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_L2	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HCV_N	RKLGVPPLRV	WRHRARNVRA	KLLSQGGRAA
HCV12083	RKLGVLPSRA	WRHRARAVRA	KLIAQGGKAA
HCV1480	RKLGVPPLRA	WRHRARAVRA	KLIAQGGRAA
HCVPOLYP	RKLGVPPLRA	WRHRARAVRA	KLLSQGGRAA
HD_1	RKLGVPPLRV	WRHRARAVRA	KLLSPGGEGS
HPCCGAA	RKLGVPPLRA	WRHRAWVRA	RLLARGGKAA
HPCFG	RKLGIPPLRA	WRHRARAVRA	KLIAQGGKAR
HPCGENANTI	RKLGVPPLRA	WRHRARAVRA	KLLSQGGRAA
HPCGENOM	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HPCHUMR	RKLGVPPLRV	WRHRARAVRA	RLLSQGGRAA
HPCJ	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HPCJCG	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HPCJK046	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA
HPCJK049	RKLGIPPLRA	WRHRARAVRA	KLISQGGKAK
HPCJTA	RKLGVPPLRV	WRHRARAVRA	RLLSQGGRAA
HPCJTB	RKLGVPPLRV	WRHRARAVRA	RLLSQGGRAA
HPCK3A	RKLGCPPLRA	WRHRARAVRA	KLIAQGGRAK
HPCPLYPRE	RKLGVPPLRA	WRHRARAVRA	RLLARGGRAA
HPCPOLP	RKLGAPPLRA	WKSARAVRA	SLISRGGSAA
HPCPP	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
HPCUNKCD	RKLGVPPLRA	WRHRARAVRA	KLLSQGGRAA
MKC1A	RKLGVPPLRV	WRHRARAVRA	KLLSQGGRAA
NDM59	RKLGAPPLRA	WKSARAVRA	SLISRGGSAA
NZLI	RKLGCPPLRA	WRHRARAVRA	KLIAQGGKAK
SA13	RKLGVPPLRA	WRHRARAVRA	KLIAQGGKAA
Th580	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA
Type_3a_CB	RKLGCPPLRA	WRHRARAGRA	KLIAQGGKAK
TypeV_D	RKLGCPPLRA	WRHRARAVRA	KLIAQGGKAK
VN004	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKAA
VN235	RKLGAPPLRA	WRHRARAVRA	KLIAQGGKHA
VN405	RKLGAPPLRA	WRHRARAVRA	KLIAQGGGAA

	3001		3050
BEBE1	PAARLLDLSS	WFTVSAGGGD	IYHSVSRARP
D89815	PEASQLDLSS	WFWAGYSGGD	IYHSLSRARP
ED43type_4	PAAAKLDLSS	WFTVGAGGGD	IYHSMHARP

HC_C2	PAASRLDLSG	WVAGYGGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HC_G9	PSASQLDLSN	WFTGGYSGGD	IYHSVSHVRP	RWFFWCLLLL	SVGVGIYLLP
HCU16326	PAASRLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV_H_CMR	AAAGRLDLSG	WFTAGYSGGD	IYHSVSHARP	RWFWFCLLLL	AAGVGIYLLP
HCV_J1	AAAGRLDLSG	WFTAGYSGGD	IYHSVSHARP	RWFWFCLLLL	AAGVGIYLLP
HCV_J483	PAASQLDLSG	WVAGYSGGD	IYHSLSRARP	RWFLLCLLLL	SVGVGIYLLP
HCV_J8	PEASRLDLSG	WFTVGAGGGD	IYHSVSHARP	RLLLLCLLLL	SVGVGIFLLP
HCV_JK1	PAASQLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_JS	PAASRLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_K1_R1	PAASQLDLSN	WVAGYSGGD	VYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_K1_R2	PAASQLDLSG	WVAGYSGGD	IYHSVSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_K1_R3	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_K1_S1	PAASQLDLSN	WVAGYSGGD	VYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV_K1_S2	PAASQLDLSG	WVAGYSGGD	IYHSVSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_K1_S3	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HCV_L2	PAASRLDLSS	WVAGYSGGD	IYHSVSHARP	RWFMLCLLLL	SVGVGIYLLP
HCV_N	PAASQLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HCV12083	VSASKLDLSG	WVAGYDGGD	IYHSVSQARP	RFLLLGLLLL	TVGVGIFLLP
HCV1480	ADADRLDLSS	WFTVGAGGGD	IYHSMRARP	RNLLLCLLLL	SVGVGIFLLP
HCVPOLYP	PAASQLDLSN	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HD_1	PAAFQLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HPCCGAA	TAAGRLDLSG	WFTAGYSGGD	IYHSVSHARP	RWFWFCLLLL	AAGVGIYLLP
HPCFG	PTAGQLDLSS	WFTVGVGND	IYHSVSRART	RHLLLCLLLL	TVGVGIFLLP
HPCGENANTI	PAASQLDLSS	WVAGYGGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCGENOM	PAASRLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCHUMR	PAASRLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCJ	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCJCG	PAASQLDLSG	WVAGYNGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
HPCJK046	RDADRLDLSG	WVAGYSGGD	IFHSVSHARP	RVLLLCLLLL	TVGVGIFLLP
HPCJK049	PQAGLLDLSS	WFTVGAGGND	IYHSVSRARS	RHLLLGLLLL	TVGVGIFLLP
HPCJTA	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HPCJTB	PAASQLDLSS	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HPCK3A	PAAGQLDLSS	WFTVGVGND	IYHSVSRART	RYLLLCLLLL	TVGVGIFLLP
HPCPLYPRE	AAAGQLDLSG	WFTAGYSGGD	IYHSVSHARP	RWIWFCLLLL	AAGVGIYLLP
HPCPOLP	PEARLLDLSS	WFTVGAGGGD	IYHSVSRARP	RLLLLGLLLL	TVGVGIFLLP
HPCPP	PEASQLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
HPCUNKCD	PAASRLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMLCLLLL	SVGVGIYLLP
MKC1A	PEASQLDLSG	WVAGYSGGD	IYHSLSRARP	RWFMCLLLL	SVGVGIYLLP
NDM59	PEARLLDLSS	WFTVGAGGGD	IYHSVSRARP	RLLLLSLLLL	LVGVGLFLLP
NZLI	PAAGQLDLSS	WFTVGVGND	IYHSVSRART	RHLLLCLLLL	TVGVGIFLLP
SA13	ADADRLDLSS	WFTVGAGGGD	IYHSMRARP	RCILLCLLLL	TVGVGIFLLP
Th580	AAASQLDLSG	WVAGYDGGD	IYHSVSRARP	RLLLLGLLLL	TVGVGIFLLP
Type_3a_CB	PRAGQLDLSS	WFTVGVGND	IYHSVSRART	RYLLLCLLLL	TVGVGIFLLP
TypeV_D	PATGQLDLSS	WFTVGVGND	IYHSVSRART	RYLLLCLLLL	TVGVGIFLLP
VN004	RGASALDLSG	WFTSGYGGGD	VYHSASRARP	RFLLLCLLLL	SVGVGIFLLP
VN235	RGAANLDLSG	WVSGGSGGD	IFHSVSRARP	RNLLLCLLLL	TVGVGIFLLP
VN405	PDAARLDLSG	WFISGFSGGD	IYHSVSRARP	RIFLLCLLLL	SVGVGIFLLP

3051

BEBE1	AR
D89815	NR
ED43type_4	AR
HC_C2	NR
HC_G9	NR
HCU16326	NR
HCV_H_CMR	NR
HCV_J1	NR
HCV_J483	NR
HCV_J8	AR
HCV_JK1	NR

HCV_JS	NR
HCV_K1_R1	NR
HCV_K1_R2	NR
HCV_K1_R3	NR
HCV_K1_S1	NR
HCV_K1_S2	NR
HCV_K1_S3	NR
HCV_L2	NR
HCV_N	N.
HCV12083	AR
HCV1480	AR
HCVPOLYP	NR
HD_1	NR
HPCCGAA	NR
HPCFG	AR
HPCGENANTI	NR
HPCGENOM	NR
HPCHUMR	NR
HPCJ	NR
HPCJCG	NR
HPCJK046	PR
HPCJK049	AR
HPCJTA	NR
HPCJTB	NR
HPCK3A	AR
HPCPLYPRE	NR
HPCPOLP	AR
HPCPP	NR
HPCUNKCD	NR
MKC1A	NR
NDM59	AR
NZLI	AR
SA13	AR
Th580	AR
Type_3a_CB	AR
TypeV_D	AR
VN004	AR
VN235	AR
VN405	AR

60458026 . 032903

Table 23. HIV Fusion Construct

EP-HIV-1020

MGMQVQIQSLFLLLLWVFGSRGKLVOKLNWAGAILKEPVHGVNAACPKVSFEPIKIPHYCAPA
KAKFVAAWTLKAAAKAFVVRPQVPLGAAKLTPLCVTLGAAAVLAHAMSQVKVYLAWVPAHKG
AAAAIFQSSMTKKTTLFCABDAKNIPYNFQSQGVVHKPVHAGPIANVTVYYGVVWKKAAAQMA
VFIHNFKNAAAYPLASLRSLFNLTFGWCFKLNRLQQLLFNAKIQNFRVYYRKAADVTKIGGQLKK
VPLQLPFLKAMTNPPPV

ATGGGAATGCAGGTGCAOATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAAGCTGGTGGGCAAACCTCAACTGGGCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
GOTGAATGCCGCTTGCCCTAAAGTCAAGCTTCGAACCAATTAAGATCCCCATTCACTACTGTGC
AOC TGCCAAAGCTAAGTTTGTGGCCGCTTGGACCTCAAGGCCGCTGCAAAAGCCTTCCAGT
GAGGCCCCAGGTGGCTCTGGGCGCGCTAAACTCACACCACTGTGGCTCACTCTGGGAGCCGC
TGCAGTGTCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCACAA
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAAACAACCTCTGTCTGTGCCTC
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC
CGAOCCTATTGCTAACGTGAACGTGTACTATGGGTGCCAGTGTGGGAAGAAAGCCGCTGCACA
GATGGCCGTGTTTATTACAAATTTCAAAAACGCGCTGCATACCCCTCGCCAGCCTGAGATC
CCTCTTCAACCTGACATTGGGCTGGTGTCTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTT
ATCAATGCTAAATCCAGAACTTCCGCTCTACTATAGGAAGGCTGCAGTGAATATCAAAATT
GGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC
CCCTATCCAGTCTGA

Table 24. HBV GCR-3697 Fusion Construct

<p>GCR-3697</p> <p>SEQ ID NO: _</p>	<p><i>Polynucleotide</i></p> <p>1 Start ↑***</p> <p>ATGGGCATGCAGGTGCAGATCCAGAGCCTGTTCTGCTCCTGCTGTGGGTGCCAGGAAGCAGAGGCTTTCTC CTGTCCCTGGGCATCCACCTGAACGCCGCTGCAAAGTACACCAGCTTCCCCTGGCTGCTCAACGCCGCTGCC CGTTTCAGCTGGCTGTCCCTGCTCGTGCCCTTCAACGCAGCCTTCCCCACTGCCTGGCCTTACGTACATGA AAGCAGCCCTGGTGGTGCAGTTCTCCAGTTACGCCGGGAGCCATCCTGCTCCTGTGCCTGATCTTCTGCT CAACGCCGCTGCCACACCCCTGTGGAAGGCTGGCATCCTGTACAAGAAAGCCTGGATGATGTGGTACTGGG GACCCAGCCTGTACAAGGCATATCCAGCCCTGATGCCCTGTACGCCCTGCATCGGAGCTGCCGCATGGCTGA GCCTCCTGGTGCCCTTCGTGAACGCCGCTGCCGGTTCTGCTGACAAGAATCCTGACCATCAACGCCGAG CCATTCTATCCCTCCAGCTGGGCCTTCAAGGCAGCCGCCGAGTACCTGGTGAAGCTTCGGAGTCTGGAACC TGCCAGCGACTTCTTTCCAGCGTGAAAGCCGCGAGCCTTCTGCTCCGACTTCTTTCCAGCGTGAAGGC CGACGCCGATCTCCTGGACACCGCTAGCGCCTGTACAACAGCTGGCCCAAGTTCCGCCGTGCCCAACCTGAA GGCCGACGCCAGGCCATCTGCAGCGTGGTCAGACCGGAAGCTGTCCCTCGATGTGAGCCGCGCTTCTACAA CGCCGCCGAAAGTTCTGTGGCCGCTGGACCTGAAAGCCGCTTCCCAAGGCAGCAACCTGAGCATCCCCCT GGACCCACAAAGGAGCCGAGGACTGAGCCGCTATGTGGCCAGACTGAACGCCGCTGCCAGCACCCCTGCC GAGACCAGAGTGGTCAGACGGAAGCACCCCGCCGATGCCCAACCTGCTGAAGGCCGAGCCCGTGGAT GTGCTCAGACGGTTTCATCAACGCTTCTTCTGTGGCAGCCCTACAAGGCCGCTACATGGATGACGT GGTCTGGGAGTGAACGCCCTCTGGTTCCATCAGCTGCTGACCTTCAAAGCCGCTGCCACACCCGCAAG AGTGACCGGAGGCGTGTCAAGGCTGCAGCCCTGACCTTCGCCUGGAGACCGTGTGGAGTACAAGCAGG CCTTACCTTCAGCCCCACCTACAAGAAGCCGCGCACCAGCTTTGTGTACGTCCCAAGGCCCTGAATCCCG CAGACGCCGCCCGGCCGACTGTGCCAGGTGTGCCGATGCCACACCAACCGGATGGGGCCTGGGCCCT GGACCCGGCAGACACTACCTGCATACCTGTGGAAGGCAAGGAATCCTGTACAAGGCCGCCGCTGGACC CCATCACACCGCTCTGCCGAGGCCATCCTGTGCTGGGGCGAGTCTATGACTCTGGCAGGACCCGCCCGG CGAATCCAGGCTGGTGGTGGACTTTAGCCAGTTCTCCAGAGGCAACGGACCCGCCAGGACCCCTTCTGCT CGCCAGTTACACAGCGCCATCTGCAGCGTGGTGGACCTGGCCAGGACTGGTGCCTTCGTGCACTGGTT CGTCCGCCCTCAGCCACCGCTCGGACCTGGCCCGGCTGCACCTCTACAGCCACCTATCATTTCTGGGCTT CAGAAAGATCGGACCGCCCGGCTCCAGCAACCTGTCTGCTGACCTGAGCCTGAGCGCAGCCTTCG GACCCGCCCTGGCCTGCAGAGCCTGACCAACCTGCTCAGCAGCAACCTCAGCTGGTGGGCCAGGACCC GGCGCAGGCTTCTTTCTGCTCACAGAACTCTGACCATCCCCTCAGAGCGGCCCGGACCCAGGCTTC GGCGTGTGGATTCGGACTCTCCCGCTCAGACCCCAATGCCCCATCGGCCAGGACCCGGCGTGGGA CCTCTGACTGTGAACGAGAAGCGGAGACTGAAGCTGATCGGCCCGGACCCAGGCAACAGTGTTCAGGAA GCTCCCTGTGAACAGACCTATCGACTGGGGCCCGGACCCGCCGAGCAACTGGATTCTGAGAGGCCACA GCTTCTGTACGTCCTGGACCCGCCCTGGCAAGCAAGCCTTACCTTCAGCCCACTACAAGGCATTCC TGTGCGGAATAC</p> <p>↓ Stop 2232</p>
<p>GCR-3697</p> <p>SEQ ID NO: _</p>	<p><i>Polypeptide</i></p> <p>1 ↑</p> <p>MGMQVQIQSLFLLLLWVPGSRGFLSLGIHLNAAKYTSFPWLLNAAARFSWLSLLVPFNAAPHCLAFSYMKA ALVVDIFSQFSRGAILLLCLIFLLNAAHTLWKAGILYKKAWMMWYWGPSLYKAYPALMPLYACIGAAAWSLL VPFVNAAGFLLTRILTINAAAIPISSWAFKAAAEYLVSFGVWNLPSDFFPSVKAAAFPSDFFPSVKAAADLLD TASALYNSWPKFAVPNLKAAASAICSVVRRKLSLDVSAAFYNAAAFVAAWTLKAAAKAANVSIPWTHKGAA GLSRVYARLNAAASTLPETTIVRRKJIPAAAPHLLKAAARWMCLRRFIINASFCSPIKAAAYMDDVVLGVNAL WFHISCLTFKAAATPARVTGGVFKAAALTFGRETVLEYKQAFSTPYKNAGTSFVYVPSALNPADGPGPGLCQ VFADATPTGWGLGPGPRHYLHLWKAGIIYKPGPGPHHTALRQAILCWGELMTLAGPGPGESRLVVDIFSQFS RNGNPGPGPFLLAQFTSAICSVVGPGLVPFVQWFGVLSPTVGPGLHLHYSHPIILGFRKIGPGPGSSNLSWLSL DVSAAFGPGPGLQSLTNLSSNLWLGPAGFFLLTRILTIPQSGPGPGVSFGVWIRTPPAYRPPNAPIGPGPV OPLTVNEKRRLLKIGPGPKQCFRKLFPVNRIDWGPFGAANWILRGTSFVYVGPGPGLKQAFSTPYKALFCG</p> <p>↓ 744</p>

Table 25. HBV AOSIb2 Fusion Construct

HBV AOSIb2	<i>Polynucleotide</i>
SEQ ID NO: __	<p>1 Start ↑ ATG GGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCTGTGGGTGCCCGGGTCCAGAGGACACAC CCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCT GCCTAGCGATTCTTTCCTAGCGTGAACCTTCCTGCTGCTGACCAGAATCCTGACCATCTCCACCCTG CTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCTGCTGACCAGAATCCTGACCATCTCCACCCTG CCAGAGACCACCGTGGTGAGGAGGCAGGCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCTGGCT GAGCCTGCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTCAAGACCCAGCCAGGGTGAC CGGAGGAGTGTTTAAGGTGGGAAACTTCACCGGCTGTATAACCTGCCAGCGATTCTTTCCTAGCGTGAA GACCTGTGGAAGGCCGGAATCCCTGTAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGG TGGTGGACTTTTCCAGTTCAGCAGAAATTCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGT ATGCCTGTATCTGA ↓ Stop 657</p>
HBV AOSIb2	<i>Polypeptide</i>
SEQ ID NO: __	<p>1 ↑ MGMQVQIQSLFLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAFLPSDFFPSVNFLSLGIHLYMDDVVL GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPYKGAAA WLSLLVPFVNIPSSWAFKTPARVTGGVFKV GNFTGLYNLPDFFPSVKTLWKAGILYKNVSIPTWTHKGAALVVDFSQFSRNSAICSVVRRALMPYACI ↓ 219</p>

Table 26. HCV Fusion Construct

HCV4312(1P)

MGMQVQIQSLFLLLWVPGSRORLOVRATRKKAAAKTSRRSQPRNLPOCSFSTFNDLMQVIPLVK
 YLLPRRGPRINTLCGFADLMOYRMYVGGVEHRKLLFNILGGWYKAAALADGGCSOGAYRLIVFP
 DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSRRNGYLVAIQATVAAALLFLLLADALIFCHS
 KKKYLVRHADVLGFQAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLA
 AFLLLADARVLSAFSLHSYILAQYGAGVWMNRLLAFANAAAFVAAWTLKAAA*

GAATTGGGCGCAACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCTGTGG
 GTGCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAAGCTGCCGCTAAAAAC
 AAGGAGCGCTCCAGGCCAGGAACCTGCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT
 GGGGTACATTCCACTGGTGAAGTATCTGCTCCCAQACGGGGCCCTCGCTGAACACTCTCTG
 TGGATTGCTGATCTGATGGGGTACAGGATGTATGTGGGGGAGTGGAAACACAGAAAACCTGCT
 CTTCACATCTCGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGGG
 GAGCTTACAGGCTCATTGTCTTCCCGATCTGGAGTCAAATTTTGGGCAAAGCACATGTGGA
 ATTTTCATCGGGGTGGCCGAGCCCTGGTGGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCAA
 GACGGAAACGGATACCTCGTGGCTAACAGGCCACTGTGGCTGCAGCTCTGCTCTTCTGCTCC
 TGGCCGATGCACCTCATCTTCTGOCATTCCAAGAAAAAGTATCTGGTCAACAGACATGCTGACG
 TGCTGGGGTTTGGGGCTACATGAGCAAGTGACCTGTGGCAGCTCCGACCTGTATCACATGT
 GGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAAGAAAGCGGCTGCAG
 TCCTGGTGGGCGGCTCTGTCAGCGCTTTCTCTCTCTGGCAGACGCCAGGGTGCTGTCTG
 CCTCAGGCTCCACTCTACATCTCTCGAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA
 TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG
 GATCC

Table 27. *Plasmodium falciparum* Fusion Construct

PE3
 MOMQVQIQSLFLLLWVFGSRGFMKAVCVBNVTCONGIQVRKGLIMVLSFLNAAALFHIFDGDN
 EIKAAALLACAGLAYKKSFLFVBALFNAAPSDOKNLKAAQTNFKSLRLNLPSENERGYKAAQVS
 ENIFLKNAAYFILVNLLKAAAILSVSSFLFVNTPYAGEFAPFKAAAKYKLATSVLKAAVFLIFFDL
 FLNYYIPHQSSLKAAAGLLGNVSTVGAVLLGGVGLVNLACAGLAYKKAKFKSLFHIFKAAFYFIL
 VNLLKAFILIFFDLFLVKALFFHFNKNFYGKQENWYSLKFVEALFQBYNAAAKFVAAWTLKAAAK
 ILSVFFLANAVLAGLLGNVNFQDRENIGIYKAAALYISFYTIKAFILVNLLIFHNAALPYGRNLKAA
 HVLSHNSYEKNAAAKYLVVFLI

GGCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCC
 GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCCGTAAACGGAAT
 TCAGGTGAGAAAAGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT
 TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCGGACTAGCCTATAAAAAGA
 GTTTCCTTTTGGTTGAAGCACTATTTAAGGCAGCACCCAGTGACCGTAAATGCAACCTATATA
 AAGCAGCTCAGACTAATTTCAAAGCCTGTAAAGAAATCTGCCCTCAGAGAATGAAAGGGGT
 TACAAAGCCGCGGGGTGTCCGAGAATATTTTCTGAAGAAAGCCGCTGCTTATTTTATACTC
 GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTTCAGTGTCCAGCTTTCTGTTTGTAAACACAC
 CATATGCCGGGAGCGGGCTCCTTTCAAGGCTGCAGCAAAATACAAAGCTTGCCACATCAGTAT
 TGAAAGCAGCTGTGTTTTGATATTCCTTTGATCTTTTTTAACTACTACATACTCATCAGTCT
 AGTCTTAAAGCAGCCGGGCTACTGGGGAACCTCTCTACTGTGGGGGGCGTCTTACTTGGAGGA
 GTTGGCCTCGTGTGAAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAGCGAAATTCATCAAG
 TCTCTGTTCCACATTTTAAAGCCGCATTCTATTTTCATACTAGTGAAACCTTCTCAAAGCTTTCT
 GATCTTCTCGATCTATTCTCGTAAAGCCGCTATTCTTCATTATCTTTAAACAAAAATTATTAC
 GGCAAGCAAGAAAATTGGTACTCACTCAAGTTGTAGAAAGCTCTGTTCCAGGAATACAACGCC
 GCTGCTAAATTCGTTGCAGCTTGGACCCGTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTC
 TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACCTTTCAAGACGAAGAGAATATAG
 GCATCTACAAAGCCGCAGCACTGTACATTTTATTCTACTTCATCAAGGCCCTTCATACTGGTCAA
 CCTTCTGATATTTTATAATGCAGCACTGCCATATGGGAGAACCACTTGAAAGCGGCCACGT
 GTTGAGCCACAACCTCTACGAGAAGAACCCGCGGAAATATCTGTCATTGTCTTCTCGAT
 TTGA

Table 28. *Mycobacterium tuberculosis* Fusion Construct**TE1**

MQVQIQSLFLLLWVFGSRGRMSRVTTFTVKALVLLMLPVVNLMTAAAVVKALVLLMLFVGA
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRPLVLPVNAATAAKFVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLVNMITYAAPLFVGAATAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCTCTGTGGGTGCCCGGATCCAGAGGAAGG
ATGAGCAGAGTGACACATTCATGTCAGGCCCTGGTGCTCTGATGCTCCCGTCTGTGAAC
CTGATGATCGGCACCGCTGCAGCCGTCTGTAAGCTCTGCTCTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCCGTGTACCTGGTCCGGCTGCAGOCATGGCCCTCTGCGGCTGCCA
GTGAAGCGCATGTTTGTGCAATCTGGGAGTCAACTCCCTCTATTTGGGGGCATTTCGCTG
GGAAGGCTGCCCTCTGTGCTGCTGTGAAATGCAGCCCTGCCAAATTTGTGCGCGCTTGG
ACTCTGAAGGCAGCCGCTAAGGCCCTGCAAGACTGATGATCGGGACCGCGCTGCCGGCTT
CGTGGTCCCGCTGATCCCTGGTGAACGCCATGACATAAGCAGCTCTCTGTTTGTGGGAGC
CGCTGCAGCCATGGCTCTCTGCGGCTGCCACTGGTGTGA

Table 29. Hepatitis B Virus Core Protein (SEQ ID NO:)

MQLFHLCLIISCSCPTVQASKLCLGWLWGMDIDPYKEFGATVELLSFLPSDFFPSVRD
 LLDTASALYREALSPEHCSPHHTALRQAILCWGELMTLATWVGVNLEDPASRDLVV
 SYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLVSFSGWIRTPPAYRPPNAPILSTLPE
 TTVVRRRGRSPRRRTSPRRRRSQSPRRRRSQSRESQC

WHAT IS CLAIMED IS:

1. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and
 - b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.
2. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;
 - b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
 - c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.
3. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
 - b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and
 - ii) a variant which occurs with high frequency within the population of variants; and

- c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.
- 4. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
 - b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and
 - ii) a variant which occurs with high frequency within the population of variants; and
 - c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
 - d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.
- 5. The method of claim 1, wherein (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.
- 6. The method of claim 2 or 3, wherein (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.
- 7. The method of claim 4, wherein (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

8. The method of any of claims 1-4, wherein (a) comprises aligning the sequences of said antigens.
9. The method of claim 3 or 4, wherein (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif.
10. The method of claim 3 or 4, wherein (b) comprises choosing a variant which occurs with high frequency within said population.
11. The method of claim 10, wherein (b) comprises ranking said variants by frequency of occurrence within said population.
12. The method of claim 3 or 4 wherein (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif and which occurs with high frequency within said population.
13. The method of claim 12, wherein (b) comprises ranking said variants by frequency of occurrence within said population.
14. The method of any of claims 1-13, wherein the identified variant comprises the fewest conserved anchor residues in comparison to each of the remaining variants.
15. The method of any of claims 1-4, wherein the remaining variants comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, or 300 variants.
16. The method of any of claims 1-15, wherein the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis*, *Chlamydia*, *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, *Aspergillus fumigatus*, *Plasmodium spp.*, *Trypanosoma spp.*, *Schistosoma spp.*, and *Leishmania spp.*
17. The method of claim 16, wherein the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus.
18. The method of claim 16, wherein the infectious agent is HIV and the antigen is selected from the group consisting of: Gag, Env, Pol, Nef, Rev, Tat, Vif, Vpr, and Vpu.

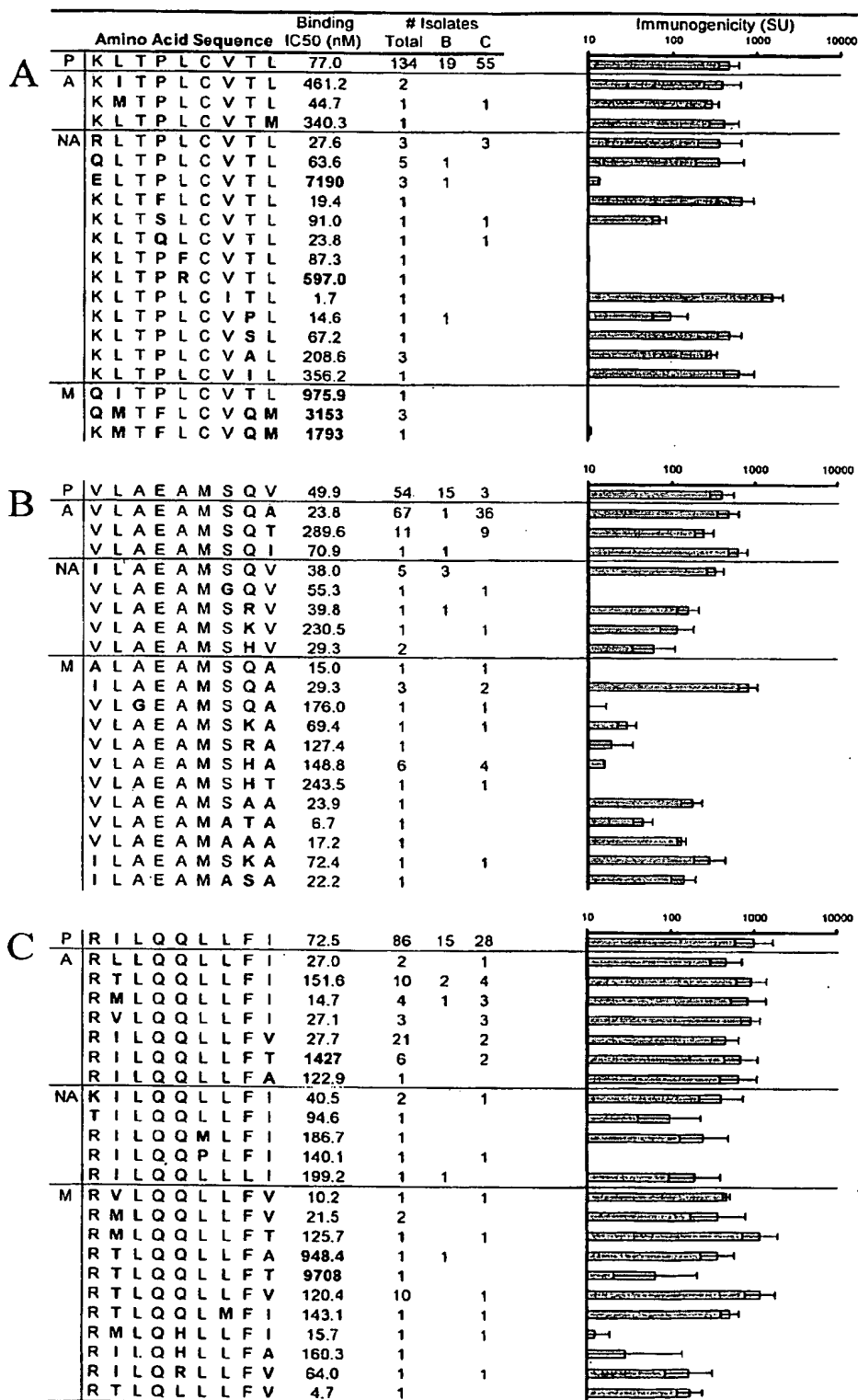
19. The method of claim 16, wherein the infectious agent is HBV and the antigen is selected from the group consisting of: Pol, Env, Core, and NS1/Env2.
20. The method of claim 16, wherein the infectious agent is HCV and the antigen is selected from the group consisting of: Core, E1, E2, NS1, NS2, NS3, NS4, and NS5.
21. The method of claim 16, wherein the infectious agent is HPV and the antigen is selected from the group consisting of: E1, E2, E3, E4, E5, E6, E7, L1, and L2.
22. The method of claim 16, wherein the infectious agent is *Plasmodium falciparum* and the antigen is selected from the group consisting of: CSP, SSP2, EXP1, LSA1.
23. The method of any claims 1-4, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.
24. The method of any of claims 1-4, wherein the motif or supermotif is selected from the group consisting of those in Tables 1-2.
25. The method of any of claims 1-4, wherein the conserved non-anchor residues are at any of positions 3-7 of said variant.
26. The method of any of claims 1-4, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.
27. The method of any of claims 26, wherein the variant comprises only 1-2 conserved non-anchor residues compared to at least one remaining variant.
28. The method of any of claims 27, wherein the variant comprises only 1 conserved non-anchor residue compared to at least one remaining variant.
29. The method of claim 16, wherein the infectious agent is HPV, and further wherein, the HPV infectious agent is selected from the group consisting of HPV strains 16, 18, 31, 33, 45, 52, 56, and 58.
30. The method of any of claims 1-29, wherein the variants are a population of naturally occurring variants.

METHODS OF IDENTIFYING OPTIMAL VARIANTS OF PEPTIDE EPITOPES

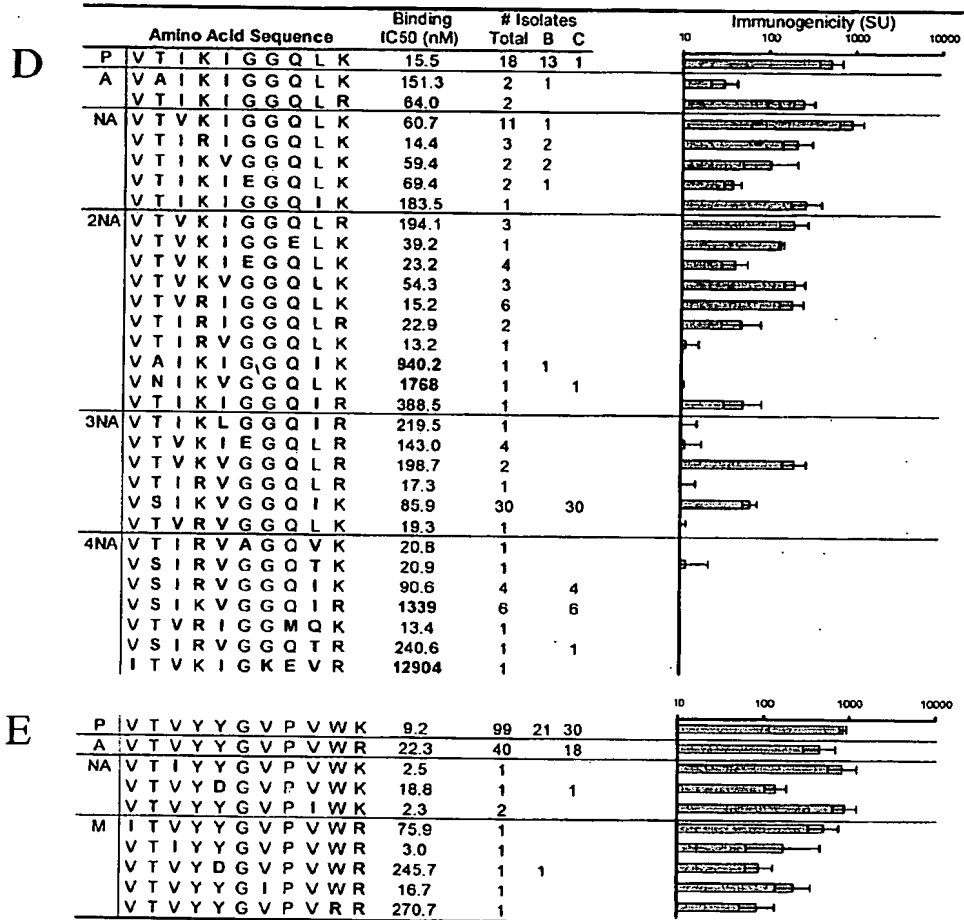
ABSTRACT OF THE DISCLOSURE

The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s). The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

FIGS. 1A-1C

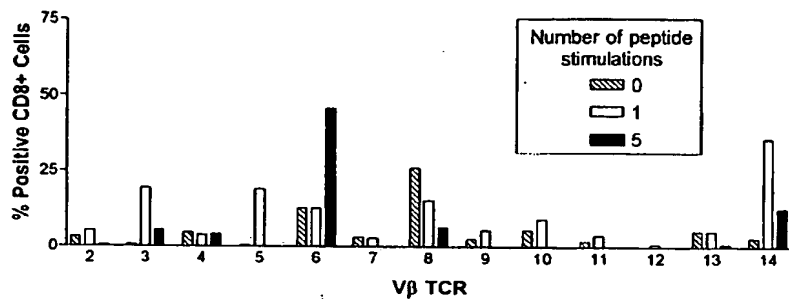


FIGS. 1D-1E

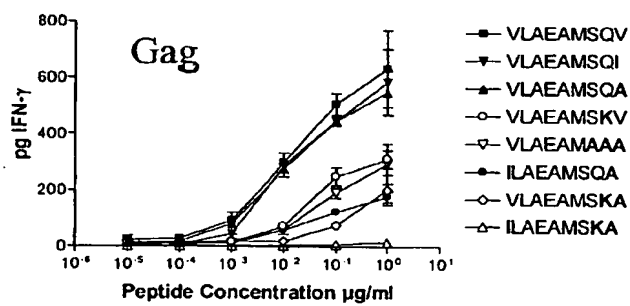


FIGS. 2A-2C

A



B



C

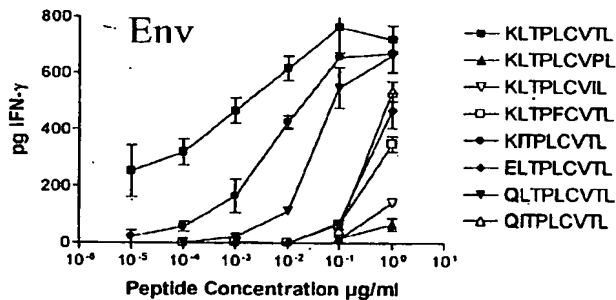
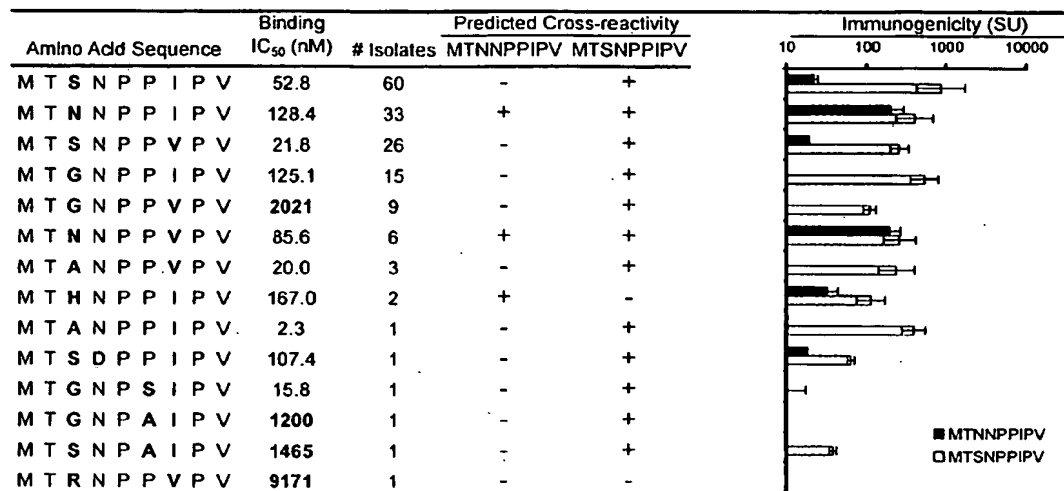


FIG. 4



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